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                                                                                                                          June 13, 2005, 13:22:36 ; Search time 118 Seconds (without alignments) 22.943 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzhaimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's diseaserike plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzhaimer's disease. represents an inhibitor of beta-secretase enzyme.
                                                                                                                                                                                 Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease; inhibitor.
                                                                                                                                                                                                                                                                                                                              93.1%; Score 27; DB 3; Length 7; 100.0%; Pred. No. 1.8e+06;
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ng S, Mcconlogue
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                                             /note= "hydroxyethylene"
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Tung J, Wang S,
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                              Location/Qualifiers
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                                                                                         10-FEB-2000; 2000WO-US003819
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Sinha S, Tatsuno G,
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Adr51049
Adh63159
Adh63159
                                                                                                                                             Aar47233
Aaw63844
Aaw63844
Aab84489
Aab84489
Adc49087
Adc18125
Adc18125
Adc18125
Adc5182
Adc51135
Adc65155
Adc61155
Adc61155
Adc61155
Adc61155
Adc61155
                                                                                                                                                                                                                                                                          Aar26337
Aau04699
Abr56164
Abr56166
Ade51698
Ade51709
Ade51709
Adf41057
Adp65260
Adp65260
Adp65260
Adp65260
Adp65260
                                                                                                                                                                                                                                                                                                                                                                                                                      Abm83107
                                                                                                                                             AAR47233
AAW63844
AAY06458
                                                                                                                                                                   AAB84383
ADO49087
ADS18125
ADS18122
ADS18132
AAR21080
ADE57113
ADD45446
                                                                                                                                                                                                                                                           AAR13549
AAR20750
AAR26337
                                                                                                                                                                                                                                                                                 AAU04694
AAE34488
ABR56164
                                                                                                                                                                                                                                                                                                              ADE55803
ADE61700
ADF45057
                                                                                                                                                                                                                                                                                                                                                           ADL61330
ADN03976
ADO42159
                                                                                                                      ADH63159
AAR10648
                                                                                                                                                                                                                                             ADH63156
ADO49089
                                                                                                                                                                                                                              ADF45058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB07871 standard; peptide; 7 AA
14-NOV-2000
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John V, nlogue L;

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Gaps

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/note= "hydroxyethylene"

WO200047618-A2

Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide; amyloid plaque component; Alzheimer's disease; amyloidogenic disease;

A beta-secretase inhibitor peptide.

AAB07871;

AAB07871
ID AAB
XX
XX
XX
DT 14:
XX
XX
DE A BEL
KW BEL
KW AMY

RESULT 1

Modified-site

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The invention describes an isolated taste transduction G-protein coupled receptor (I) e.g., T2R which is expressed in a taste cell, comprises or seceptor (I) e.g., T2R which is expressed in a taste cell, comprises or greater than 60% sequence identity to a fully defined sequence of 335 (S1), 333 (S2), 299 (S3), 310 (S4), 224 (S5), 77 (S6), 209 (S7), 266 (S16), 300 (S10), 155 (S11), 173 (S12), 94 (S13), 115 (S14), 68 (S15), 300 (S10), 186 (S16) amino acids as given in the specification. (S1) is useful for identifying a compound that modulates taste signaling in taste cells which involves contacting the compound with (I) and effect is determined by measuring che compound (I). The functional effect of the compound (I). The functional effect is determined by measuring binding of the compound to a call membrane. (The functional effect is determined by determined compound (I). (I) is sexpressed in the compound activity of calls (e.g., eukaryotic cell) expressing (I). (I) is captesing (I). (I) caste cells which involves contacting a compound with (I). The compound with the polynucleotide encoding (I) and determining the functional effect of the compound with the polynucleotide encoding (I) and determining the functional effect of the compound with the polynucleotide encoding (I) and determining the functional effect of the compound with the polynucleotide encoding (I) and determining the contacting the compound with the polynucleotide encoding receptor.
                                                                                                           Novel isolated taste transduction G-protein coupled receptor e.g., T2R useful for identifying compound that modulates taste signaling in taste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteus mirabilis infection; bacterial infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.1%; Score 27; DB 8; Length 68; 71.4%; Pred. No. 23; 1; Indels ive 1; Mismatches 1; Indels
Mueller K;
  Ryba N,
                                                                                                                                                                                                        Claim 22; SEQ ID NO 80; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF06975 standard; protein; 450 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENO-) GENOME THERAPEUTICS CORP.
  Hoon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-2000; 2000US-00543681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacterial polypeptide #3088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 71.4
Matches 5; Conservative
Zuker CS, Adler JE,
                                          WPI; 2004-203221/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 IMAVAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteus mirabilis.
                                                                  N-PSDB; ADJ84528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 68 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6605709-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF06975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. Is they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The present sequence represents an inhibitor of beta-secretase enzyme
                                                                                                                                                                                                                                                                                                                                         Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     taste transduction; G-protein coupled receptor; T2R; taste signaling; cAMP level; cGMP level; IP3 level; Ca(2+) level; electrical activity; human; G-protein coupled receptor; receptor.
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                                                                                                                                                                                                                                Power M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.1%; Score 27; DB 3; Length 8; 100.0%; Pred. No. 1.8e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                             F, Frigon N, John V, Wang S, Mcconlogue L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human T2R G-protein coupled receptor seq id 80
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 12; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ84527 standard; protein; 68 AA.
                                                                                                                                                                                                                             Doane MT,
                                                                                                                                                                                                                                                   Tung J,
                                                                                                           99US-0119571P.
99US-0139172P.
                                                              10-FEB-2000; 2000WO-US003819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-FEB-2003; 2003US-00364861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00393634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                                                                                                                                                                (ELAN-) ELAN PHARM INC
                                                                                                                                                                                                                             Basi G,
                                                                                                                                                                                                                           Anderson JP, Basi G,
Sinha S, Tatsuno G,
                                                                                                                                                                                                                                                                                                WPI; 2000-533011/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZUKE/) ZUKER C S.
(ADLE/) ADLER J E.
(HOON/) HOON M.
(RYBA/) RYBA N.
(MUEL/) MUELLER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-1999;
                                                                                                           10-FEB-1999;
15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2004.
                   17-AUG-2000
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The invention relates to new Proteus mirabilis polypeptides and polymucleotides. The invention also relates to antibodies against the polypeptides, amethod of generating vaccines for producing the polypeptides, amethod of polypeptides and method of polypeptides and amethod for screening test compounds for mirabilis, and polymeptide and a method for screening test compounds for antibation activity. The polypeptides and polymucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial days or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                        New Proteus mirabilis polypeptides and polynucleotides, useful reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or biocontrol agents for plants.
                                                                                                                                                                                                             Disclosure; SEQ ID NO 7260; 870pp; English.
                         2003-895291/82
                      WPI; 2003-895291
N-PSDB; ADF02803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 450 AA;
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Gaps ö Score 27; DB 7; Length 450; Pred. No. 1.8e+02; 0; Mismatches 1; Indels 93.1**%**; 85.7**%**; Query Match Best Local Similarity 85., Pest Local 6; Conservative VMXVAEF 7

VMVVAEF 292 286 н ઠે 셤

ADN46338 standard; protein; 457 AA. ADN46338; RESULT 5 ADN46338

(first entry) 01-JUL-2004

gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.

Thermococcus kodakaraensis KOD1 protein sequence SeqID216.

Thermococcus kodakaraensis

WO2004022736-A1.

18-MAR-2004.

29-AUG-2003; 2003WO-IB003597

30-AUG-2002; 2002JP-00319011.

(NISC-) JAPAN SCI & TECHNOLOGY

CORP.

Imanaka T, Atomi H;

WPI; 2004-257583/24.

organism particularly analysis, applicable in genome of c Method for disrupting targeted gene in thermostable bacterium and with genome studying gene structure and functions.

Claim 9; SEQ ID NO 216; 598pp; Japanese.

This invention relates to a novel method for targeting disruption of an

whole sequential data of the genome of such organism, selecting at least I arbitrary region in the sequence, providing a vector that contains a sequence homologous with the selected region and a marker gene, transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly thermococcus kodakaraensis KODI. The method is for targeting the disruption of a gene in the genome of an organism, which is applicable in studying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology, with this method, the disruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein concoded by the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at arbitrary gene in a genome of an organism which comprises providing the ftp.wipo.int/pub/published_pct_sequences

0X00000000000000000X0

aB aB Sequence 457 AA;

ö Score 27; DB 8; Length 457; Pred. No. 1.8e+02; 0; Mismatches 1; Indels n Similarity 85.7%; 6; Conservative (Best Local Similarity Matches 6; Conser Query Match

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Gaps

1 VMXVAEF 7 VMEVAEF

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RESULT 6 ABB93074

ABB93074 standard; protein; 802 AA.

ABB93074;

(first entry) 31-MAY-2002

SEQ ID NO 2285. Herbicidally active polypeptide

Herbicidal; plant; agriculture; herbicide.

Arabidopsis thaliana

WO200210210-A2.

07-FEB-2002

28-AUG-2001; 2001WO-EP009892

28-AUG-2001; 2001WO-EP009892

(FARB) BAYER AG.

Weidler M; Tietjen K,

WPI; 2002-269010/31.

Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms

Claim 5; SEQ ID NO 2285; 261pp + Sequence Listing; English

The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as

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ABU36167;
                                                                                                                                                                     Query Match
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Wall D,
                                                                                                                                                                                                                                                                           ABU36167
ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a activity of a gene in an operon required for proliferation or the activity of against a biological pathway required for that has an activity against a biological pathway; che gene product or that has an activity against a biological pathway; che gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound; activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                            Antisense, prokaryotic essential gene, cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind JW;
Xu HH;
                                                                      Gaps
                                                                       ö
                                               Length 802;
                                                                    1; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #21019.
                                              Score 27; DB 5; I
Pred. No. 3.4e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID NO 63416; 1766pp; English
                                                                                                                                                                              ABU35492 standard; protein; 223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                              93.1%;
llarity 71.4%;
Conservative 1
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                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                    Mycoplasma genitalium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zamudio C,
Trawick JD,
                                                                                                                    629 VMSIAEF 635
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                                                         Local Similarity
Les 5, Conserv
                                                                                            1 VMXVAEF
                       Sequence 802 AA;
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                                                                                                                                                                                                                                                                                                                            WO200277183-A2
                                                                                                                                                                                                                              19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                   03-OCT-2002.
 herbicides
                                                                                                                                                                                                      ABU35492
                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                    Matches
                                                                                                                                                      RESULT 7
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strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at five published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening
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(1) a vector comprising a promoter operably linked to the nucleic acid; a vector comprising a promoter operably linked to the nucleic acid nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DB 6; Length 223;
Pred. No. 1.5e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #21694.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 64091; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU36167 standard; protein; 224 AA.
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-0362699P.
06-MAR-2002; 2002US-0362699P.
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71.4%;
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Trawick JD,
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93 VMNIAEF
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 223 AA;
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required for proliferation, or that inhibits a biological pathway required for proliferation, or that inhibits callular proliferation; (8) required for proliferation, or that inhibits callular proliferation; (8) identifying a gene required for callular proliferation or the biological pathway in which a proliferation required for callular proliferation of the pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or compound's activity; (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense mucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for callular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids capter in the proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained for the printed specification.
proliferation; (7) identifying a compound that influences the activity of
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Gaps ö 89.7%; Score 26; DB 6; Length 224; 71.4%; Pred. No. 1.5e+02; ive 1; Mismatches 1; Indels Local Similarity 71.4 nes 5; Conservative Query Match Matches

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ADN47550 standard; protein; 304 AA ADN47550

ADN47550;

01-JUL-2004 . (first entry)

Thermococcus kodakaraensis KOD1 protein sequence SeqID1428

gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.

Thermococcus kodakaraensis.

MO2004022736-A1

29-AUG-2003; 2003WO-IB003597

30-AUG-2002; 2002JP-00319011.

(NISC-) JAPAN SCI & TECHNOLOGY CORP.

Imanaka T, Atomi H;

WPI; 2004-257583/24

Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in studying gene structure and functions.

Claim 9; SEQ ID NO 1428; 598pp; Japanese.

This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least

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ransformation, which the selected region and a marker gene, transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly Thermococcus kodakaraensis KODI. The method is for targeting the disruption of a gene in the genome of an organism, which is applicable in studying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology. With this method, the disruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein encoded by the genome of Thermococcus kodakaraensis which was derived to sing the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
a vector that contains a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Margetts MB;
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Pred. No. 2.1e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              AAY34479 standard; protein; 821 AA.
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98AU-00001546
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98AU-00002911
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98AU-00003654
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Hocking DM, Webb EA;
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20-MAR-2003
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09-APR-1998
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RESULT 12
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             AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAX94583. AAX91802 to AAX91899 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used to detect Porphorymonas gingivalis. Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34318 to
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                                                                                                                                  Length 821;
                                                                                                                                Score 26; DB 2; Length 821
Pred. No. 6.3e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                        gingivalis protein PG21.
Page 460-461; 588pp; English.
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                                                                                                                                                                                                                                  AAY34354 standard; protein; 869 AA.
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                                                                                                                                89.7%;
85.7%;
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97AU-00001182
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98AU-00005028
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(revised)
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                                                                                                                                          Local Similarity 85.7
                                                                                                                                                                                                                                                                                                                                                   Porphyromonas gingivalis
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                                                                                                                Sequence 821 AA;
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                                                                                                                                                                                                                                                                                                        Porphorymonas
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20-MAR-2003
25-AUG-1999
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Hocking DM,
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AAY34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation be used to prophorymonas gingivalis is involved in periodontal disease especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid comprising a sequence encoding an Enterococcus fecalis polypeptide, useful for preparing a composition for diagnosing or treating E. fecalis infection.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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85.7%; Pred. No. 6.7e+02;
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Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
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Matches 6; Conserv
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Best Local Similarity
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the inventor fracter to an inclear acts compitating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid conditions are inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or list fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway confideration; (7) identifying a compound that inhibits proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling the extent or agene on which the test compound that inhibits proliferation of the strains in spresent in a culture or collection of the craning the trains in spresent in a culture or collection of the strains in spresent in a culture or collection of the strains in present in a culture or collection of the strains in present in a culture or collection of the strains in present in a culture or collection of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational cauged are useful or required for proliferation in cells other than S. aureus, S. typhimurium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to an isolated nucleic acid comprising any one of
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Xu HH;
     Gaps
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Forsyth RA,
       1; Indels
                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #14856.
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Yamamoto R,
     1; Mismatches
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                                                                                                                                                                                                                       ABU29329 standard; protein; 406 AA.
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Carr GJ,
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2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                      (first entry)
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis
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Trawick JD,
                                                                                                VLSVAEF 118
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                                                  1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200277183-A2
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Wall D,
     Matches
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                             the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forestores forensic science; Good; drug inspection; molecular biology; immunology.
K. pneumoniae or P. aeruginosa. The present sequence is encoded by one
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                                                                                                                                                                                                                                                                                                                             Length 406;
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                                                                                                                                                                                                                                             Sequence 406
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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperporliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
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                                                                                                                                                                                    Human ORFX protein sequence SEQ ID NO:6058
                                           ABP03038 standard; protein; 64 AA.
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29-AUG-2000; 2000US-0228716P.
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                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                 myasthenia gravis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                        24-JUN-2002
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                     ABP03038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises beta-secretase inhibitory peptides. The beta-secretase inhibitory peptides of the invention are useful for the prevention or treatment of neurodegenerative diseases, such as:
Alzheimer's disease, Parkinson's disease, neuropathy, postencephalitis, cerebral palsy, and memory loss. The beta-secretase inhibitory peptides of the invention are also useful in the manufacture of an sAPPR secretion promoter or neurotropic factor-like agent. The present amino acid sequence represents a beta-secretase inhibitory peptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel compound such as beta-secretase inhibitor, useful as preventive or therapeutic agent for treating neurodegenerative disease such as Alzheimer's disease, Parkinson's disease and neuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-secretase inhibitory peptide; neurodegenerative disease;
Alzheimer's disease; Parkinson's disease; neuropathy; postencephalitis;
cerebral palsy; memory loss; AAPPA secretion promoter;
neurotropic factor-like agent.
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                                                                 86.2%; Score 25; DB 8; Length 583; 71.4%; Pred. No. 7.9e+02;
                                                                                                                1; Indels
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Pred. No. 1.8e+06;
1; Mismatches 0; Indels
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                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                               ADS09499 standard; peptide; 8 AA.
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6; Conservative
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439 VMAVAEY 445
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                                                                                                                                                              1 VMXVAEF 7
                                                                                     Local Similarity
                     Sequence 583 AA;
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Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                                                    Query Match
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Best Local 8
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleoride sequences can be used in gene therapy. ORFX sequences can be used in the transplantation, reloid, degenerative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, disorders related to organ storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for treating burns, inclisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from restemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 82.8%;
Similarity 71.4%;
5; Conservative
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Best Local Similarity
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P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of p. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and activity of P. acnes polypeptides and activity of P. acnes polypeptides and activity of P. acnes proteins. The antibodies and also be used as the activity of P. acnes proteins of the analyses of the activity of P. acnes proteins of the analyses of the activity of P. acnes proteins activity of P. acnes proteins activities and the activity of P. acnes proteins activity of P. acnes proteins activities and the activities activities and the activities activities activities and the activities activities activities activit
                                                                                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uvaitis; endopthalnitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; engryme linked immunosorbent assay; dermatological; osteopathic; neuroprotectent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides and nucleic acids useful for diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bhatia A;
                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes immunogenic protein #17674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitcham JL, Wang SS, , Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 17973; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky YAW, Persing DH, Mitcham J
L'maisonneuve J, Zhang Y, Jen S,
                                                                                                                                                                                    AAU56778 standard; protein; 75 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-2000; 2000US-0199047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2001; 2001WO-US012865
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes vaccinating against and treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                VMDVAEY 59
7
VMXVAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200181581-A2
                                                                                                                                                                                                                                                                                                27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-2001.
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                                                                                                                                                                                                                                          AAU56778;
                                                                                                                                  RESULT 17
                                                                                                                                                           AAU56778
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Gaps

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Score 24; DB 4; Length 75; Pred. No. 1.6e+02; 0; Mismatches 2; Indels

82.8%; 71.4%;

Query Match
Best Local Similarity 71.4
Matches 5; Conservative

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The invention relates to an isolated polymucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM643536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a comprising a polypeptide of the invention; a polymucleotide of the invention; antibodies against polypeptides of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared to polymucleotides, autibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit of detecting or determining the presence or absence of P. acnes in a patient; The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polympeptides are useful for diagnosing, preventing or treating acne proteins, T cell populations or antigen-presenting cells that express the polympeptides are useful for diagnosing, preventing or treating acne protein. The polymucleotides can also be used as probes or primers for uncleic acid hybridisation; an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form tart of the printed specification, but an electronic form the directly and the polymention and the polymention and the polymention and patent did not form part of the printed specification, but an electronic form the polyment of the printed specification, but an electronic form the polyment of the printed specification, but an electronic form the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                Propionibacterium acnes predicted ORF-encoded polypeptide #17973.
                                                                                                                                                                                                                                                                                                                                                                 Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
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Lodes MJ, Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 17973; 1481pp; English
                                                                                                                                                                  ABM53297 standard; protein; 75 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitcham JL, Skeiky YAW, Persi
Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-2001; 2001US-00978825.
                                                                                                                                                                                                                                                                20-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes.
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1 VMXVAEF 7
                                           VMAVCEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003033515-A1
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                                                                                                                  RESULT 18
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Homo sapiens.
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25-APR-2000;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang J,
Zhou P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia; asthma; Crohn's disease; neurological disorder; epilepsy; cancer; Huntington's disease; Alzheimers disease; Creutzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; cell proliferative disorder; anti-inflammatory; immunosuppressive; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic; antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus; secretory polynucleotide; secretory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an AB, Dahl CR, Gietzen D, Chinn J;
Yu JY, Tuason O, Yap PE, Amshey SR;
Liu TF, Nguyen DA, Kleefeld Y, Gerstin BH;
Lewis SA, Chen AJ, Panzer SR, Harris B;
Lo A, Lan RY, Urashka ME;
                                                                          Gaps
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                      Length 75;
                   Score 24; DB 6;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                               Human secretory polypeptide SPTM SEQ ID NO 770.
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                    ABP75586 standard; protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-2001, 2001US-0280067P.
29-WAR-2001; 2001US-0280068P.
16-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291839P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-029448P.
20-JUN-2001; 2001US-029476P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lo A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2002; 2002WO-US009921
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                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                  5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dufour GE, Hiliman
Daughtery SC, Dam TC,
David MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peralta CH, David MH
Flores V, Marwaha R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-075543/07.
                      Query Match
Best Local Similarity
                                                                                                                    VMXVAEF
                                                                                                                                                                   VMAVCEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  10-FEB-2003
                                                                                                                                                                                                                                                                                                                                   ABP75586;
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                                                                     Matches
                                                                                                                                                                                                                                          RESULT 19
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ID ABP
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Zhao QA;
disease), neurological disorders (e.g. epilepsy, Huntington's disease, dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease, multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety, schizophrenia or amnesia), or cell proliferative disorders (e.g. psoriasis, polycythemia vera, or cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain, breast, cervix or prostate). The present sequence is one of the SpTM proteins of the invention (ABP75384-ABP75962). Note: The sequence data for this patent did not form part of the printed specfication, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                       Gaps
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Zhang J,
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                                                                                                                                                                                                                                               Score 24; DB 6; Length 97;
Pred. No. 2.1e+02;
0; Mismatches 1; Indels
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Yang Y,
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Xue AJ,
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                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM41985 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 6916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00471275.
2000US-0048B725.
2000US-00552317.
2000US-00598042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-00620312.
2000US-00653450.
2000US-00662191.
2000US-00693036.
                                                                                                                                                                                                                                                     82.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                       5; Conservative
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N-PSDB; AAI61141.
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                  Sequence 97 AA;
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Example 2; SEQ ID NO 6917; 10078pp; English.
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          immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                              system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzeimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic as the activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang D;
, Zhao Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J,
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                                                                                                                                                                                                                   82.8%; Score 24; DB 4; Length 132; 71.4%; Pred. No. 2.9e+02; ive 1; Mismatches 1; Indels
encoded polypeptides (AAM38642-AAM42213) with nootropic,
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Yang Y,
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Xue AJ,
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rman T, Xu C,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                              AAM41986 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO 6917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 2000US-00488725.
; 2000US-0055317.
; 2000US-00598042.
; 2000US-00620312.
; 2000US-00653450.
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Wang Z, Wehrman T
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                 Query Match 82.8
Best Local Similarity 71.4
Matches 5; Conservative
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Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-442253/47.
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                                                                                                                                                                                                                                                                                     Sequence 132 AA;
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia.
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Wang J,
                                                                                                                                                                                                                                                                                                                                                                                       AAM41986;
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Zhou P;
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ID AAM4
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

N-PSDB; AAI61142

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic.

Immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, ancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and State and Alzeimer and the sequence data for this patent did not form
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Zhang J, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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peripheral nervous system, neuropathy, central nervous system, CNS;
Alzheimer's, Parkinson's disease; Huntington's disease, haemostatic,
amyotrophic lateral sclerosis, Shy-Drager Syndrome, chemotactic,
chemokinetic, thrombolytic, drug screening; arthritis, inflammation,
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                                                                                                                                                                                                                                                                                                                                                                 Length 132;
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Pred. No. 2.9e+02;
1; Mismatches 1; Indels
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Yang Y,
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Xue AJ,
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irman T, Xu C, X
Drmanac RT;
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                                                                                                                                                                                                                                                                                  part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 6915.
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25-APR-2000; 2000US-00552317.
20-UIN-2000; 2000US-0059042.
19-UIL-2000; 2000US-005312.
03-AUG-2000; 2000US-0065450.
14-SEP-2000; 2000US-0065191.
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71.4%;
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Wang Z, Wehrman T,
Goodrich R, Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 LMVVAEF 70
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                         Sequence 132 AA;
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Zhou P,
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encoded polypeptides (AAM36642-AAM42213) with nootropic.

immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous foralised neuropathies and central nervous system diseases, and as Alzheimer's, parkinson's disease, system disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activity, inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel three dimensional structure of Thermus thermophilus 70S ribosome resolved using x-ray crystallography upto 5.5 Angstroms resolution, useful for screening and designing compounds that alter ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.8%; Score 24; DB 4; Length 132; 71.4%; Pred. No. 2.9e+02; ive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        x-ray crystallography; protein coordinate data.
                                                                                                   Example 2; SEQ ID NO 6915; 10078pp; English.
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                                       as central nervous system injuries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   part of the printed specification
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22-MAR-2001; 2001US-0278013P.
30-MAY-2001; 2001US-0294394P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 132 AA;
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ID ABG6

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XX XX ABG9

XX XX ABG9

YX ABG9

YX XX ABG9

YX YX YX ABG9

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YX YX YX YX ABG9

YX YX YX ABG9

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This invention relates to a three dimensional structure of Thermus thermophilus 70S ribosome resolved using x-ray crystallography up to 5.5

Disclosure; Page 502; 525pp; English.

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Angstrom resolution. The invention also discloses a method for identifying a compound that binds to a bacterial 70S ribosome or its portion. The method comparises designing a compound based upon a three-dimensional structure of the bacterial 70S ribosome, where the structure co-ordinates are given in the specification, contacting the compound with the bacterial 70S ribosome or its portion and determining whether the compound binds to the bacterial 70S ribosome or its portion. The 70S ribosome of the invention can be used to screen and design ribosome 3D structure of the invention can be used to screen and design compounds that bind to sites on the 70S ribosome and that alter the ribosome function. The present sequence represents a ribosomal protein sequence used in the method of the invention
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated applypeptide or its fragment whose expression is inhibited by the antisense aucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                              Score 24; DB 5; Length 145; Pred. No. 3.2e+02; 0; Mismatches 1; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #10141.
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Yamamoto R,
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362699P.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Trawick JD,
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                                                                                                                                                                                                                                           Sequence 145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      1 MSVAEF
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 24
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drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                       the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for callular proliferation to isolate candidate molecules for rational
proliferation; (7) identifying a compound that influences the activity of
$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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Sequence 191 AA;

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82.8%; Score 24; DB 6; Length 191; 57.1%; Pred. No. 4.3e+02; ive 2; Mismatches 1; Indels
Query Match 82.6
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                          131 LMAIAEF 137
                                                                      1 UMXVAEF 7
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Gaps ; 0

> ABU23979 standard; protein; 195 AA. RESULT 25 ABU23979

ABU23979;

Protein encoded by Prokaryotic essential gene #9506.

(first entry)

19-JUN-2003

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Clostridium acetobutylicum.

WO200277183-A2

03-OCT-2002,

21-MAR-2002; 2002WO-US009107

06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0326599P. 21-MAR-2001; 2001US-00815242

(ELIT-) ELITRA PHARM INC.

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, Wang L, Wall D,

WPI; 2003-029926/02. N-PSDB; ACA27849 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 51903; 1766pp; English.

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the inversion relaters to an isolated muchalc acts comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated continued in a polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway or that has an activity against a biological pathway or the proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture computing strains in which the each of the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of proliferation of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids are pational for dentifying proteins or screening for homologous nucleic acids are pational for dentifying proteins or screening for homologous nucleic acids are pational for dentifying proteins or screening for homologous nucleic acids are pational for dentifying the description of the description of the strains is solutions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent din not form part of the printed specification, but was obtained in electronic format directly from NIPO at from the properties of the printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences
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57.1%;
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Score 24; DB 6; Length 195; Pred. No. 4.4e+02; 2; Mismatches 1; Indels Query Match Best Local Similarity 57.1%, Best Local Similarity 4; Conservative 1 VMXVAEF ò

131 LMAIAEF 137 g

ADJ48536 standard; protein; 195 AA. ADJ48536; ADJ48536

RESULT 26

Oil-associated gene related protein #36.

06-MAY-2004 (first entry)

oil-associated gene; transgenic; enhanced seed oil; vegetable oil. Unidentified.

JS2004025202-A1.

05-FEB-2004.

15-MAR-2002; 2002US-0365301P. 26-JUN-2002; 2002US-0391786P. 26-JUN-2002; 2002US-0392018P. 14-MAR-2003; 2003US-00389566. LAUR/)

LAURIE C C. RAVANELLO M. SAVAGE T. LEDEAUX J R. ROGERS J A. (SAVA/) (LEDE/) (ROGE/) RAVA/)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see AAZ96173-Z96494) and their encoded proteins (see AAX961792.Y86182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of
                                                           Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic
                                                                                                                                                                                         genome
                                                                                                                                                                    promoter functional in plants operably linked to an oil-associated gene. The construct is useful for transgenic plant seed which has in its genome the construct, that is functional in the plant to transcribe the oil-associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents the amino acid sequence of an oil-associated gene related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae proteins and related DNA - useful for screening
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment; prevention; disease; diagnosis; gene therapy; screening; bacterial; antimicrobial; antibiotic; pathogenesis; infection.
                                                                                                                                                         The invention relates to a recombinant DNA construct comprising a
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   Rogers JA;
                                                                                                                                                                                                                                                                                                                                            Length 195;
                                                                                                                                                                                                                                                                                                                            Score 24; DB 8; Length 15., Pred. No. 4.4e+02;
   Ledeaux JR,
                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                          Example 3; SEQ ID NO 540; 22pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae proteins and compounds for antibacterial activity.
Savage T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY85820 standard; protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S. pneumoniae derived protein #29.
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                                                                                                                                                                                                                                                                                                                                             82.8%;
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Best Local Similarity 71.*v.,
Best Local Si Conservative
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 Ravanello M,
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                             WPI; 2004-142683/14
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                                                                                                                                                                                                                                                                                                               Sequence 195 AA;
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Laurie CC,
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such a polypeptide. They can also be used to screen for compounds which interact with and inhibit or activate such a polypeptide. The polypeptides (or DNA encoding them, via gene therapy) are also useful for inducing an immunological response in a mammal. The antagonists are useful to inhibit such bacterial polypeptides. The polypeptides are particularly useful to identify antimicrobial compounds and antibiotics. They are also useful to determine their role in pathogenesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris.
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                                                                                                                                                                                                          Length 225;
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                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes immunogenic protein #11698.
                                                                                                                                                                                                          1 82.8%; Score 24; DB 2; Le:
Similarity 71.4%; Pred. No. 5.1e+02;
5; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitcham JL, Wang S;
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 11997; 1069pp; English
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                                                                                                                                  infection, dysfunction and disease
                                                                                                                                                                                                                                                                                                                                                                                                                  AAU50802 standard; protein; 236
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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e J, Zhang 1
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                                                                                                                                                                                                                                                                                                                      115 VMSAAEF 121
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Matches 5; Conserv
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                                                                                                                                                                        Sequence 225 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to an isolated polynucleotide (ACF64435-ACF64733)
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Jones R, Carter D;
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                     Length 236;
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Benson DR,
                                                                                                                                                                                                                   Score 24; DB 4; 1
Pred. No. 5.4e+02;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunostimulant; immune response; vaccine
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Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM47321 standard; protein; 236 AA
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Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-OCT-2002; 2002WO-US032727.
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                                                                                                                                                                                                                                         71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                               Query Match
Best Local Similarity '1...
Best Local Similarity '1...
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VMELAEF 175
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N-PSDB; ACF64478.
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                                                                                                                                                                                Sequence 236 AA;
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proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present and the kit is useful for performing a diagnostic assay. The present reading frame) contained within the P. acnes polymucleotides of the invention. Note: The sequence data for this patent did not form part of from WIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the 6113 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated antisense appression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to an isolated nucleic acid comprising any
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Forsyth RA,
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                                                                                                                                                                                                                                                                                82.8%; Score 24; DB 6; I
71.4%; Pred. No. 5.4e+02;
iive 1; Mismatches 1;
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 54190; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU26266 standard; protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362859P.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                              169 VMELAEF 175
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                                                                                                                                                                                                                                                                                                                                                            1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                             Sequence 236 AA;
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Wall D,
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                        Matches
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proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the strains; or (13) identifying the target of a compound that inhibits for identifying proteins or screening for homologous nucleic acids required for callular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                              drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine, eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 238;
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Pred. No. 5.4e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a Chlamydia trachomatis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 786; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY36930 standard; protein; 254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.8%;
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98US-0107077P.
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VLSIAEF 78
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 238 AA;
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04-NOV-1998;
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AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
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vaccines against Chlamydia trachomatis. Antisense and ribozyme sequent can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perity perihepatitis, bartholinitis; pneumopathy in breast feeding infants; wenereal lymphogranulomatosis. The polypeptides of the invention may of use in treating these diseases
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                            82.8%; Score 24; DB 2; Length 254; 71.4%; Pred. No. 5.8e+02; ive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #18325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG18334 standard; protein; 286 AA.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                     5; Conservative
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                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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VMIVADE
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N-PSDB; AAS82521.
                                                                                                                                                                                                                                                                                                                          1 VMXVAEF
                                                                                                                                                                                                         Sequence 254 AA;
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responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the vipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated binding pocket of receptor tyrosine kinase that regulates the kinase domain of the receptor, useful for identifying modulator of the receptor for treating lymphoproliferative conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor tyrosine kinase; RTK; kinase domain; cytostatic; antiarthritic; antiinflammatory; immunosuppressive; antirheumatic; virucide; noctropic; neuroprotective; cerebroprotective; antiparkinsonian; dermatological; nephrotropic; tranquilizer; vulnerary; anticonvulsant; VAB-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "residues Xaa are not clearly indicated in the specification"
                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                       Score 24; DB 4; Length 286;
Pred. No. 6.6e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .332
                                                                                                                                                                                                                                                                                                                                                                                                ABB81185 standard; protein; 332 AA
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                                                                                                                                                                                       y Match 82.8%;
Local Similarity 71.4%;
hes 5; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAB-1 protein sequence.
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                                                                                                                                                                                                                                                                                                      29
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                                                                                                                                                      Sequence 286 AA;
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          make a model for (1) or its complexes or parts, in X-ray crystallography techniques, or for determining three-dimensional structures of polypeptides with unknown structures. Pharmaceutical compositions comprising the ligand or modulator is useful for treating lymphoproliferative conditions, malignant and pre-malignant conditions lymphoproliferative conditions, malignant and pre-malignant conditions lupus erythematosus, immune-related glomerulonephritis, rheumatoid arthritis), viral infection, inflammation, gaft versus host disease, neurodegenerative diseases and conditions involving trauma and injury to the nervous system (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease and multiple sclerosis). The present sequence represents a VAB-1 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carr GJ;
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
or ligands that associate with the binding pocket,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae cellular proliferation protein #182.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                           Length 332;
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Pred. No. 7.8e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
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                                                                                                                                                                                                                                                                       Similarity 71.4%; 5; Conservative
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Xu HH;
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                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                          Sequence 332 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000; 23-MAY-2000; 26-MAY-2000; 2
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-FEB-2002
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 34
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sequence not defined in the specification, for amplifying a target

cequence contained within a Streptococcus nucleic acid sequence, where

the first primer is substantially complementary to the target sequence

and the second primer is substantially complementary to the complement

the target sequence, and where the parts of the primers having

the target sequence and where the parts of the primers having

considerably assay comprising contacting a test compound with the

protein, and determining whether the test compound binds to the protein

and a Streptococcus pneumoniae bacterium, where one or more genes

concoding the proteins has been renderive. The proteins, nucleic

acid molecules, antibody and compositions are useful as medicaments for

treating or preventing a disease or infection due to streptococcus

bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis

media or ear infection. They are also useful in developing vaccines,

diagnostics and antibiotics. The methods are useful for identifying

immunodominant proteins. The present sequence is one of the 2469 proteins

expressed by the identified coding regions from the genomic sequence.

Note: The sequence data for this patent did not form part of the printed

specification, but was obtained in electronic format directly from WIPO

at ftp.wipo.int/pub/published_pot_sequences. (Updated on 23-OCT-2003 to

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        development. The antisense muckels adids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antinflammatory; antibacterial; immunostimulant; auditory; respiratory;
for the identification of potential new targets for antibiotic
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                    S. pneumoniae type 4 strain protein from coding region #869.
                                                                                                                                                                                             Length 335;
                                                                                                                                                                                 Score 24; DB 4; Lengua compress. Pred. No. 7.9e+02;
                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae; type 4 strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Masignani V, Tettelin H, Fraser C;
                                                                                                                                                                                                                                                                                                                                          ABU01294 standard; protein; 335 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-MAR-2001; 2001GB-00007658.
                                                                                                                                                                                             82.8%;
                                                                                                                                                                              Query Match
Best Local Similarity 71.**,
S; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
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(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; vaccine.
                                                                                                                                                                                                                                                                           224 VMSAAEF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-040579/03.
                                                                                                                                                                                                                                                 1 VMXVAEF 7
                                                                                                                                                                     Sequence 335 AA;
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11-FEB-2003
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Sequence 335 AA;

Query Match

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                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preventing S. pneumoniae infections, or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Streptococcus pneumoniae polynucleotides, useful for treating
                                                                                                                                                                                                                                                        Streptococcus pneumoniae; infection; otitis media; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Russell DP;
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Score 24; DB 6; Length 335;
Pred. No. 7.9e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chakravarti DN,
                                                                                                                                                                                                                              Streptococcus pneumoniae polypeptide SEQ ID NO 654.
                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 42; Page 921-923; 1091pp; English
                                                                                                                                                  ABP81576 standard; protein; 335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zagursky RJ, Masi AW, Green BA,
 82.8%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                               L2-APR-2002; 2002WO-US011524.
                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-2001; 2001US-0283948P.
18-APR-2001; 2001US-028443P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMCY ) AMERICAN CYANAMID CO
                                                                                                                                                                                                      (first entry)
             Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                        diagnosis; gene therapy.
                                                                              224 VMSAAEF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-093010/08.
                                                     1 VMXVAEF 7
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                                                                                                                                                                                                      04-MAR-2003
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                                                                                                                      RESULT 36
ABP81576
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New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or

N-PSDB; ABX06581

Claim 1; SEQ ID NO 1738; 56pp; English.

infection

The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the 6113 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8)
               one of the polymucleotides. The S. pneumoniae polymucleotides and encoded bolymeptides (ABPR1299-ABPR1674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for detecting S. pneumoniae in a biological sample or disgnosing S. pneumoniae in a biological sample or disgnosing S. pneumoniae infection in a subject. The polymucleotides have antibacterial activity and are useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an isolated nucleic acid comprising any one of
 of the polynucleotide or a nucleic acid sequence 95% identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                     Score 24; DB 6; Length 335;
Pred. No. 7.9e+02;
0; Mismatches 2; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #31517.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID NO 73914; 1766pp; English.
                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           ABU45990 standard; protein; 335 AA.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00572851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                       82.8%;
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Best Local Similarity 71.**,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae
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Trawick JD,
                                                                                                                                                                                                                                                                                                                 224 VMSAAEF 230
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                                                                                                                                                                   Sequence 335 AA;
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Wall D,
 variant
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pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which he gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. T. promumoniae or P. aaruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Mote: The sequence data for this present did not form part of the printed specification, but was obtained the control of the printed specification, but was obtained the control of the printed specification, and the control of the printed specification, but was obtained the control of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated Streptococcus pneumoniae nucleic acids and polypeptides. The nucleic acids and proteins are useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, such as S. pneumoniae infection. These may also be used for drug screening procedures. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecules and polypeptides useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, e.g. Streptococcus pneumoniae infection, and in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae protein, Seq ID No 5099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 5099; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zeng O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK48584 standard; protein; 335 AA.
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98US-0085131P.
98US-00107433.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        82.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 71.4%;
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Matches 5, Conser
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 335 AA;
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99US-0137222P

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99US-0138044P

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15-JUL-1999;
16-JUL-1999;
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21-JUL-1999;
21-JUL-1999;
22-JUL-1999;
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04-AUG-1999;
04-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-1999;
13-JUL-1999;
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Streptococcus pneumoniae polypeptide of the invention. Note: The sequence data for this parent did not appear in the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                               Gaps
                                                                                               ;
0
                                                                         Score 24; DB 8; Length 335;
Pred. No. 7.9e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 23321
                                                                                                                                                                                            AAG20945 standard; protein; 361 AA
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99US-0123548P

99US-0126264P

99US-0126768P

99US-01267462P

99US-0128234P

99US-0128734P

99US-013843P

99US-0130077P

99US-0130443P

99US-01314449P

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99US-0132464P

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99US-013248P

99US-013248P
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99US-0136392P.
99US-0136782P.
                                                                        Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative 0
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                                                                                                                                                                                                                                    17-OCT-2000 (first entry)
                                                                                                                                      224 VMSAAEF 230
                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                  1 VMXVAEF 7
                                                     Sequence 335 AA;
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
26-APR-1999;
06-APR-1999;
19-APR-1999;
21-APR-1999;
21-APR-1999;
21-APR-1999;
21-APR-1999;
30-APR-1999;
30-APR-1999;
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44-MAY-1999;
45-MAY-1999;
45-MAY-1999;
45-MAY-1999;
45-MAY-1999;
46-MAY-1999;
46-MAY-1999;
46-MAY-1999;
46-MAY-1999;
46-MAY-1999;
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        PR
        05-AUG-1999 j.
        94US-0147192P.

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        06-AUG-1999 j.
        94US-0147146P.

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        06-AUG-1999 j.
        94US-0147146P.

        PR
        06-AUG-1999 j.
        94US-0147446P.

        PR
        09-AUG-1999 j.
        94US-0147416P.

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        10-AUG-1999 j.
        94US-0147135P.

        PR
        11-AUG-1999 j.
        94US-0148111P.

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        11-AUG-1999 j.
        94US-014811P.

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        11-AUG-1999 j.
        94US-0149172P.

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        12-AUG-1999 j.
        94US-0149172P.

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        20-AUG-1999 j.
        94US-0149172P.

        PR
        21-AUG-1999 j.
        94US-0149172P.

        PR
        21-AUG-1999 j.
        94US-0149173P.</
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Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter, termination sequence.
                     Gaps
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0
Score 24; DB 3; Length 361;
Pred. No. 8.5e+02;
1; Mismatches 1; Indels
                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 57658.
                                                                                                AAG45883 standard; protein; 361 AA
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9905-0123180P

9905-0123180P

9905-0125788P

9905-012664P

9905-0126281P

9905-0120714P

9905-0130044P

9905-013044P

9905-013044P

9905-013044P

9905-0131448P

9905-013248P

9905-0134218P

9905-0134218P

9905-013422P

9905-013422P

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9905-013422P
  82.8%;
ilarity 71.4%;
Conservative
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                                                                                                                                    (first entry)
                                                                                                                                                                                                          Arabidopsis thaliana
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VMNMAEF 37
           Best Local Similarity
Matches 5; Conserv
                                    1 VMXVAEF 7
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   Query Match
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990S-0148319P.
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990S-016135P.
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Best Local Similarity
Matches 5; Conserv
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VMNMAEF
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 11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
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16-AUG-1999;
18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
23-AUG-1999;
23-AUG-1999;
27-AUG-1999;
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Gaps

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02 - AUG - 1999

02 - AUG - 1999

03 - AUG - 1999

04 - AUG - 1999

05 - AUG - 1999

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06 - AUG - 1999

06 - AUG - 1999

11 - AUG - 1999
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18-AUG-1999;
                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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99US-0131449P.
99US-0132048P.
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99US-0136782P.
99US-0137222P.
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                                                                                                     (first entry)
                                                                                                                                                                                                             Arabidopsis thaliana
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05 - MAR - 1999

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24 - MAR - 1999

10 - APR - 1999

11 - MAY - 1999

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                                                                                                     17-OCT-2000
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                                                                           AAG24458;
                       RESULT 41
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
                      Protein encoded by Prokaryotic essential gene #9133
                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 51530; 1766pp; English.
                                                                                                                             06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                    21-MAR-2001; 2001US-00815242.
                                                                                                    21-MAR-2002; 2002WO-US009107
                                                                                                                                                     06-MAR-2002; 2002US-0362699P
                                                      Clostridium acetobutylicum
        19-JUN-2003 (first entry)
                                                                                                                                                                    ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                   Wang L, Zamudio C,
Wall D, Trawick JD,
                                                                                                                                                                                                            WPI; 2003-029926/02
                                                                                                                                                                                                                     N-PSDB; ACA27476.
                                                                      WO200277183-A2
                                                                                     03-OCT-2002
 82.8%; Score 24; DB 3; Length 361; 71.4%; Pred. No. 8.5e+02;
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99US-016076P.
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99US-0159293P.
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30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
10-SEP-1999;
13-SEP-1999;
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22-OCT-1999;
25-OCT-1999;
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13-OCT-1999;
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13-OCT-1999;
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14-0CT-1999;
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21-OCT-1999
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Zyskind JW; Xu HH;

Haselbeck R, Ohlsen KL, Yamamoto R, Forsyth RA,

Malone C, Carr GJ,

the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense contisense mucleic acid; (2) a host cell containing the vector; (3) an isolated of polypeptide or its fragment whose expression is inhibited by the antisense contisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular or the activity of the gene product or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) required for cellular proliferation or the biological contained for cellular proliferation or the biological contained for cellular proliferation or the biological contained agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling the extent or organism or the strains is present in a culture or collection of contains; or (13) identifying the target of a compound that inhibits the contained contains; or (13) identifying the target of a compound collection of an organism. The antisense nucleic acids are useful for cellular proliferation or product antidetes molecules for rational contains or for extension or antidetense nucleic acids are useful for cellular proliferation or sorganism or prover andideted molecules for rational ö drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences The invention relates to an isolated nucleic acid comprising any one of Gaps ; 0 DB 6; Length 367; 82.8%; Score 24; DB 6; Length 367 ilarity 71.4%; Pred. No. 8.7e+02; Conservative 1; Mismatches 1; Indels Local Similarity Sequence 367 AA; . د Query Match Best Loc Matches

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Gaps

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1; Indels

1; Mismatches

5; Conservative

Matches

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ABU23606 standard; protein; 367 AA.

RESULT 42
ABU23606
ID ABU236
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AC ABU236

ABU23606;

Gaps

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Indels

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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Pred. No. 8.8e+02;
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                 5; Conservative
                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                 termination sequence
 Best Local Similarity
Matches 5; Conserv
                                              1 VMXVAEF 7
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10-JUN-1999;
14-JUN-1999;
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07-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoded polypeptides (AAM38642-AAM42213) with nootropic, immonsuppressant and cytostatic activity. The polymorleotides are useful in gene therapy. A composition containing a polymorleotide are useful of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic utilisation of the activities such as: Immune system suppression, and thrombolytic activity, cancer disagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAIS7798-AAI61369) and the
                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren F, Wang D;
Zhang J, Zhao
                                                                                                                                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's Parkinson's disease; hamenstatic; amyotrophic lateral sclerosis; Shy-Brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.8%; Score 24; DB 4; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ma Y, (
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; SEQ ID NO 3345; 10078pp; English.
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Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen R,
                                                                                                         AAM40200 standard; protein; 373 AA
                                                                                                                                                                                                 Human polypeptide SEQ ID NO 3345
                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1999; 99US-00471275.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00552317.
20-JUN-2000; 2000US-0059042.
19-JUL-2000; 2000US-0059042.
19-APR-2000; 2000US-0065312.
14-SEP-2000; 2000US-0065319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Asundi V,
Wang Z, Wehrman T,
Goodrich R, Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2000; 2000WO-US034263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-00727344
                                                                                                                                                                      (first entry)
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VMEVAEY 35
VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                         WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                      22-OCT-2001
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                                                                                                                                                                                                                                                                                                             leukaemia.
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Wang J, 1
Zhou P, 0
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12 - AUG - 1999; 13 - AUG - 1999; 13 - AUG - 1999; 14 - AUG - 1999; 15 - AUG - 1999; 16 - AUG - 1999; 17 - AUG - 1999; 18 - AUG - 1999; 18 - AUG - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - AUG - 1999; 20 - AUG - 1999; 20 - AUG - 1999; 21 - AUG - 1999; 22 - AUG - 1999; 23 - AUG - 1999; 24 - AUG - 1999; 25 - AUG - 1999; 26 - AUG - 1999; 27 - AUG - 1999; 28 - AUG - 1999; 29 - A	Query Match Best Local Simil Matches 5; C	1 VMXVAEF : 48 VMMAEF
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Gaps

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9905-014031P

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04-AUG-1999;
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18-AUG-1999;
20-AUG-1999;
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06-JUL-19
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14-JUL-19
15-JUL-19
16-JUL-19
    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 28135.
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9905-012548P

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25-MAR-1999;

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23-APR-1999;

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07-MAY-1999;
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04 JUN-1999;
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16 JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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-JUN-1999;
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                                                                AAG24457;
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Page 30

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Gaps
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Pred. No. 9e+02;
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99US-0161359P.
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ilarity 71.4%;
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28-EP-1
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Matches
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AAG45882 standard; protein; 378 AA.

AAG45882,

RESULT 46 AAG45882 ID AAG451 XX AC AAG451

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|| :||| VMNMAEF

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VMXVAEF 7

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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27-ANG-1999; 99US-0151066 P. 27-ANG-1999; 99US-0151060 P. 31-ANG-1999; 99US-0151000 P. 31-ANG-1999; 99US-0151000 P. 31-ANG-1999; 99US-0151301 P. 31-SEP-1999; 99US-0151301 P. 32-SEP-1999; 99US-015302 P. 32-SEP-1999; 99US-015307 P. 32-SEP-1999; 99US-015401 P. 32-SEP-1999; 99US-015540 P. 34-SEP-1999; 99US-015591 P. 35-SEP-1999; 99US-015691 P. 35-SEP-1999; 99US-01601 P. 35-SEP-1999; 99US-01601 P. 35-SEP-1999; 99US-01610 P. 35-SEP-199	Query Match 82.8%; Score 24; DB 3; Length 378; Best Local Similarity 71.4%; Pred. No. 9e+02; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0; (1 VMXVAEF 7	LT 47 1056 AAY71056 standard; protein; 384 AA. AAY71056; 29-AUG-2000 (first entry) Human membrane transport protein, MTRP-1. Human; membrane transport protein, MTRP-1; antiinflammatory; cytostatic; antithyroid; immunosuppressive; thyromimetic; antidiabetic; nootropic; antidiabraric; neuroprotective; antidiapressant; nephrotropic; virucide;
***************************************	Que Bes Mat Qy Db	RESULT AAY7100 ID AAY7100 XX AX AX XX

09730329-60ed.rag

bacterial, fungal, parasitic, protozoal or helminthic infections and cell proliferative disorders such as cancer. Fragments of MTRP polymucleotides are useful as targets in microarrays. WTRP DNA is useful for generating hybridisation probes useful in mapping genomic sequences and detecting differences in sequences among normal, carrier and affected individuals.

is also used for screening libraries of compounds in drug screening

Page 32

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Gaps

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Score 24; DB 3; Length 384; Pred. No. 9.1e+02;

82.8%; 71.4%;

1; Mismatches

5; Conservative

Local Similarity

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Query Match

Sequence 384 AA;

techniques

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diagnosis; prevention; treatment; membrane transport disorder; epilepsy; Menkes disease; diabetes; Parkinson's disease; neurological disorder; Alzheimer's disease; depression; schizophrenia; immune disorder; allergy; inflammatory disorder; ADDS, Addison's disease; atherosclerosis; gout; Graves disease; Hashinoto's thyroiditis; microbial infection; cancer; cell proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human membrane transport proteins useful for diagnosis, prevention and treatment of membrane transport disorders, immune/inflammatory disorders and cell proliferative disorders including cancer.
                                                                                                                                                                                                                                                                             /note= "P-type cation transporter signature sequence"
antihelminthic; protozoacide; antibacterial; neuroleptic; antigout;
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                                                                                                                                                                       35. 115
/note= "El-E2 ATPase signature sequence"
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/note= "E1-E2 ATPase signature sequence"
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                                                                                                                                      'note= "Phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                               130. .351
|label= Transmembrane_domain
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/label= Transmembrane_domain
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                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, L
Y, Lu DAM;
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98US-0172214P.
99US-0121896P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-365576/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AADOO600
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22-DEC-1998;
26-FEB-1999;
                                                                                          Homo sapiens
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM3213) with nootropic, fimunosuppressant and cyrostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
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, Zhao Q
                                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
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Zhang J,
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Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                       AAM40198 standard; protein; 384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as central nervous system injuries.
                                                                                                                                                                Human polypeptide SEQ ID NO 3343.
                                                                                                                                                                                                                                                                                                                                                                                  99US-00471275.
2000US-00582317.
2000US-00552317.
2000US-0058042.
2000US-00620312.
2000US-0063450.
2000US-0063450.
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Vang Z, Wehrman T,
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                                                                                                                                        (first entry)
                         305 LMVVAEF 311
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1 VMXVAEF 7
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29-NOV-2000;
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25-APR-2000;
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Wang J,
                                                                                                                AAM40198;
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Zhou P,
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AAM40198
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The present sequence is a membrane transport protein, WTRP-1 from Incyte clone 961344 isolated from human BRSTYTUTO3 CDNA library. WTRP-1 shows homology to the mouse E1-E2 ATPase and is expressed in reproductive, nervous and haematopoietic/immune tissues. The present sequence is useful in diagnosis, prevention and treatment of disorders related with increased or decreased expression of WTRP such as familial goitre, Menkes disease, diabetes, Parkinson's disease, neurological disorders such as ALDS. ALAbimer's disease, depression, epilepsy, schizophrenia, immune/inflammatory disorders such as ALDS, Addison's disease, allergies, atherosclerosis, Graves disease, gout, Hashimoto's thyroiditis, viral,

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          localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic as the transport of the activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang D;
Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rel nucleic acids and polypeptides, useful for treating disorders such central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Humenostatic; amyotrophic lateral sclerosis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 such as peripheral nervous injuries, peripheral neuropathy and
                                                                                                                                                                                                Gaps
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Zhang J,
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Yang Y,
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Xu C,
                                                                                                                                                                                                                                                                                                                   AAM40199 standard, protein, 384 AA
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Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                              Human polypeptide SEQ ID NO 3344.
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19-JUL-2000; 2000US-00620312
03-AUG-2000; 2000US-00623450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
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Wehrman T,
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Wang Z,
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                                                                                                                                            Sequence 384 AA;
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Zhou P,
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              in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous totalised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Auntington's disease, amyotrophic lateral seclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, ancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid encoding an insect gustatory receptor (Gr) or odorant receptor (Or) protein which comprises seven transmembrane domains and a C-terminal domain comprising consecutive amino acids. The invention is useful for identifying a compound which activates the insect receptor or inhibits the activity of a lipid bilayer. The purified insect receptor protein is embedded in a lipid bilayer. The invention is sprayed for combating ingestion of crops by pest insects, combating disease-carrying insects in an area and controlling a pest population in an area. The invention is useful for detecting the presence of insect gustatory or odorant receptor and for inhibiting the function of the receptor in humans or animals or in biological fluids isolated from them. The invention is also useful for identifying or isolating other insect receptors and for combating pest
immunosuppressant and cytostatic activity. The polynucleotides are useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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ilarity 71.4%;
Conservative
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Best Local Similarity
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Matches
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                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                        Gaps
nuisances. The present sequence is fruit fly gustatory receptor (Gr)
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                                        Length 409;
                                                      1; Indels
                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 57656.
                                       Score 24; DB 5; I
Pred. No. 9.8e+02;
1; Mismatches 1;
                                                                                                                             AAG45881 standard; protein; 414 AA
                                                                                                                                                                                                                                                                                                                                                              990S-0139845P
990S-0130077P
990S-0130649P
990S-0131449P
990S-0131449P
990S-0132484P
990S-0132484P
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990S-0132487P
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990S-0134218P
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990S-0134318P
990S-0134318P
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990S-0134318P
990S-0135124P
990S-0135124P
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99US-0123548P.
99US-0125548P.
99US-0126264P.
99US-0126785P.
99US-0126785P.
99US-0126785P.
                                      Query Match 82.8%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                         25-FEB-2000; 2000EP-00301439
                                                                                                                                                             18-OCT-2000 (first entry)
                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                |: ||||
24 VLLVAEF 30
                                                                       VMXVAEF 7
                        Sequence 409 AA
                                                                                                                                                                                                                                                                                        25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
19-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
06-MAY-1999;
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         protein
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5; Conservative
                                                                                    84 VMNMAEF
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16-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
10-APR-1999;
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09-MAR-1999;
23-MAR-1999;
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29-MAR-1999;
01-APR-1999;
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06-MAY-1999;
06-MAY-1999;
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03-JUN-1999;
04-JUN-1999;
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27-MAY-1999;
28-MAY-1999;
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14-MAY-1999
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24-MAY-1999
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                                                                                                                                                                                                                            AAG24456;
      Matches
                                                                                                                                               RESULT 52
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990S-0147303P-990S-0147416P-990S-0147411P-990S-0147411P-990S-014791P-990S-014791P-990S-014811P-990S-0148131P-990S-0148131P-990S-0148131P-990S-0148131P-990S-0149328P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0151303P-990S-0159233P-990S-0159233P-990S-0159233P-990S-0159233P-990S-0159233P-990S-0159233P-990S-0159233P-990S-0159233P-990S-0159233P-990S-0160980P-990S-0160980P-990S-0160989P-990S-016135P-990S-016135P-990S-016135P-990S-016135P-990S-016135P-990S-016135P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-0161932P-990S-016193
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Best Local Similarity
  06-AUG-1999

06-AUG-1999

10-AUG-1999

110-AUG-1999

113-AUG-1999

113-AUG-1999

113-AUG-1999

113-AUG-1999

113-AUG-1999

113-AUG-1999

120-AUG-1999

120-AUG-1999

120-AUG-1999

120-AUG-1999

121-AUG-1999

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08-071-1999

13-071-1999

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18-071-1999

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21-071-1999
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22-0CT-1999;
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25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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                                                                                                                   Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter,
Gaps
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Indels
                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 28134.
1;
Mismatches
                                                              AAG24456 standard; protein; 414 AA.
1,
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99US-0123180P.
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99US-0132481P.
99US-013423P.
99US-0136782P.
99US-0136782P.
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                                                                                         17-OCT-2000 (first entry)
                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                    termination sequence
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14-JUN-1999;
16-JUN-1999;
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Length 414;
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Pred. No. 9.9e+02;
1; Mismatches 1;
9905-0148655P.
9905-0148684P.
9905-0149175P.
9905-0149175P.
9905-0149172P.
9905-014929P.
9905-0149929P.
9905-0149929P.
9905-0150884P.
9905-0151080P.
9905-015923P.
9905-015923P.
9905-015923P.
9905-015923P.
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9905-015923P.
9905-015923P.
9905-015923P.
9905-0160981P.
9905-0160980P.
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Similarity 71.4%;
5; Conservative
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VMNMAEF
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 13-AUG-1999

13-AUG-1999

118-AUG-1999

108-AUG-1999

20-AUG-1999

20-AUG-1999

20-AUG-1999

21-AUG-1999

22-AUG-1999

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25-AUG-1999

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27-AUG-1999

28-SEP-1999

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Best Local S:
Matches 5
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9900S-0139453P

9900S-0139452P

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9900S-0139452P

9900S-0139462P

9900S-0140334P

9900S-0142842P

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9900S-0144334P

9900S-0144632P

9900S-0144632P

9900S-0144632P

9900S-014518P

9900S-0147302P

9900S-0147332P
16 - 70N - 1999 | 18 - 70N - 1
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Gaps

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990S-0139461P
990S-0139461P
990S-0139461P
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990S-0139750P
990S-0139753P
990S-01405354P
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18 - JUN - 1999;
21 - JUN - 1999;
23 - JUN - 1999;
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24 - JUN - 1999;
25 - JUN - 1999;
26 - JUN - 1999;
27 - JUN - 1999;
27 - JUN - 1999;
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04-AUG-1999
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09-AUG-1999
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112-AUG-1999
113-AUG-1999
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02-AUG-1999;
02-AUG-1999;
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12-JUL-1999
   signal transduction pathway; metabolic pathway; netic mapping; gene expression control; promoter;
                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 23319.
                                  AAG20943 standard; protein; 414 AA
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9905-012548P-
9905-012548P-
9905-0126785P-
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9905-0128744P-
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9905-013421P-
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99US-0139457P.
99US-0139458P.
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99US-0139492P
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                                                                                                  (first entry)
                                                                                                                                                                     Protein identification;
hybridisation assay; gen
termination sequence.
                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                              25 - FEB - 1999; 05 - MAR - 1999; 25 - MAR - 1999; 25 - MAR - 1999; 26 - MAR - 1999; 26 - MAR - 1999; 26 - MAR - 1999; 27 - MAR - 1999; 27 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 29 - MAR - 1999; 20 - MAR - 1999; 20 - MAR - 1999; 20 - MAR - 1999; 21 - MAR - 1999; 22 - MAR - 1999; 23 - MAR - 1999; 24 - MAR - 1999; 25 - MAR - 1999; 26 - MAR - 1999; 27 - M
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10 - JUN - 1999)
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18-JUN-1999;
18-JUN-1999;
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                                                                    AAG20943;
RESULT 53
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New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                 osteoporosis; neurological disease; Alzheimer's disease;
Parkhison's disease; dementia; short memory; cancer;
sense or motor function; emoctional reaction; fear response; panic;
osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
        Human protein useful for treating neurological disease Seq 2913.
                        human; oligo-capping method; diagnostic marker; gene therapy;
                                                                                                                                                                                                     Nishikawa T, Iso
Nagai K, Irie R;
                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2913; 2686pp; English.
                                                                                                                                                                                    (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                          14-FEB-2003; 2003JP-00102207. 09-MAY-2003; 2003JP-00131452.
                                                                                                                                         12-FEB-2004; 2004EP-00003145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 71.4
Matches 5, Conservative
                                                                                                                                                                                                     Isogai T, Yamamoto J,
Wakamatsu A, Ishii S,
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389 LMVVAEF 395
                                                                                                                                                                                                                               WPI; 2004-583265/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 457 AA;
                                                                                                                                                                                                                                         N-PSDB; ADR07451
                                                                                                       EP1447413-A2.
                                                                      tranquiliser.
                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.8%; Score 24; DB 3; 71.4%; Pred. No. 9.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                        99US-0158369P.
99US-0159293P.
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                                                                   99US-0151303P.
99US-0151438P.
99US-0151930P.
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99US-0161405P.
                                 99US-0150884P
                                                                                              99US-0152363P.
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                                                                                                                                                                                                                                                                                                                                                                  99US-0160814P.
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                                                                                                                                 99US-0154039P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 71.4%;
5; Conservative
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VMNMAEF 90
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Best Local Similarity
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                                                                                                                                                                                           04-0CT-1999
05-0CT-1999
06-0CT-1999
12-0CT-1999
13-0CT-1999
13-0CT-1999
14-0CT-1999
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14-0CT-1999
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14-0CT-1999
18-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
                        25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
                                                                           31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
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24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
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25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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15-SEP-1999;
16-SEP-1999;
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22-OCT-1999;
22-OCT-1999;
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22-SEP-1999
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28-OCT-1999
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Isono Y, Sugiyama T, Otsuki T;

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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to convacious and the encoded proteins thereof. Specifically, it refers to convacious describes an immunoassay to identify agonists and antagonists, as well as attibodies, antisense molecules and siRNAs that can all be used to bind to antibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these concludes are useful for diagnostic markers or therapeutic targets for the various diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, noctropic, antiparkinsonian, encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.8%; Score 24; DB 8; Length 457; 71.4%; Pred. No. 1.1e+03; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB96296 standard; protein; 584 AA.
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ADR09407 standard; protein; 457 AA.

RESULT 54 ADR09407 04-NOV-2004 (first entry)

ADR09407;

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the 6113 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid;

(2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or gene on which the test compound that inhibits spilling a companial acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or compound, and the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for
                                                                                                                                                                                                               screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. arreus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at
                                                                                                                                                                                                                                                                                                                                                  invention relates to an isolated nucleic acid comprising any one of
                                                                   Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
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0
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Pred. No. 2e+03;
0; Mismatches 1; Indels
                                                                   ¥,ĕ
                                                                   Ohlsen |
Forsyth |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 36873.
                                                                   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 46060; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB70027 standard; protein; 817 AA.
                                                                   Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 82.8%;
Similarity 83.3%;
5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                          (ELIT-) ELITRA PHARM INC.
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                                                                   Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5, Conserv
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                                                                                                                                                             N-PSDB; ACA22006
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                                                                   Wang L,
Wall D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is a hyperthermophilit archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade. Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Weissenbach J, Saurin W, Heilig R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.8%; Score 24; DB 4; Length 584; 57.1%; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                             Hyperthermophilic archaeon; hyperthermophilic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #3663.
Putative P. abyssi queuine tRNA-ribosyltransferase.
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                                                                                                                                                                                                                                                                                                                          (CNRS ) CNRS CENT NAT RECH SCI.
(IFRE-) IFREMER INST FR RECH EXPL MER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 957-959; 1657pp; French.
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2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
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nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Thierry JC,
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440 VMAIAEY 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-126236/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus anthracis.
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                                                                                         Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 584 AA;
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                                                                                                                                                                                                                                                                                                                                                                                              Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2001;
25-OCT-2001;
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06-MAR-2002;
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                                                                                                                                                                                                                                21-APR-1999;
                                                                                                                                    FR2792651-A1
                                                                                                                                                                                                                                                                              21-APR-1999;
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Matches

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or screening

Xu HH;

Forsyth RA,

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The invention fracters to an interior action where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operor required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation of an identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profifing a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed, (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for contilieration of an organism. The antisense nucleic acids are useful for an inhibits and acids required for cellular proliferational according an encoding and according an encoding and according an encoding and according an encoding according according according according a collection of an organism. The antisense nucleic acids are useful for cellular proliferation of sections or screening for homologous nucleic acids are useful for according accordin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid comprising any
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #28340.
Carr GJ, Yamamoto R,
                                                                                                                                                                                                                    Claim 25; SEQ ID NO 46068; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU42813 standard; protein; 919 AA.
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Trawick JD,
                                                2003-029926/02
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                                                                          N-PSDB; ACA22014
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Wall D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA aequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zyskind JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 36873; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; DB 4; Length 817;
Pred. No. 2.1e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haselbeck R, Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #3671.
                                                                                                                                                                                                                                                                          Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU18144 standard; protein; 902 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malone C,
                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.8%;
71.4%;
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06-SEP-2001, 2001US-0094893.
25-OCT-2001, 2001US-0192923P.
08-FEB-2002, 2002US-00072851.
06-MAR-2002, 2002US-0362699P.
                                                                                                                                               23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                 23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.8
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432 VLLVAEF 438
                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zamudio C,
                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VMXVAEF 7
                                                                                                                                                                                                                    (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABL14130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 817 AA;
WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   interactions
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                                                27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 58
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ð 셤 ö

Gaps

cold tolerance, heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

Recombinant DNA construct, transformed plant; improved plant property,

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the 613 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell contening the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for cellular proliferation of an organism cellular proliferation of an organism of the candidate molecules for rational additional acciding the description of an organism of the activity of a compound that inhibits the proliferation of an organism of the candidate molecules for rational additional acciding the capage of a compound.
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                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                           Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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83.3%; Pred. No. 2.3e+03;
iive 0; Mismatches 1; Indels
                                                                                                                                           Ohlsen KL,
Forsyth RA,
                                                                                                                                        Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 70737; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                          Carr GJ,
                                                                                                                                           Malone C,
         21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Query Match
Best Local Similarity 83.33,
Bernative
5; Conservative
                                                                                                            (ELIT-) ELITRA PHARM INC.
                                                                                                                                          Zamudio C,
Trawick JD,
                                                                                                                                                                                        WPI; 2003-029926/02.
N-PSDB; ACA46683.
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                                                                                                                                          Wang
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promoter positioned to provide

Goldman BS;

Chen X,

Slater SC,

WPI; 2004-061375/06.

20-FEB-2003; 2003US-00369493 21-FEB-2002; 2002US-0360039P

JS2003233675-A1.

Bacteria.

18-DEC-2003

CAO Y. HINKLE G J. SLATER S C.

CAOY/)

HINK/ CHEN/

GOLDMAN B S. Hinkle GJ,

(GOLD/) SLAT/)

Cao Y,

CHEN X

New recombinant DNA construct comprising a promoter positioned to provious expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Claim 1, SEQ ID NO 5367; 122pp; English.

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of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant thaving an improved property. The plant is a crop plant such as malze or soybean. The method of producing a transformed plant ecombinant DNA construct and stransforming a plant with the recombinant DNA construct and growing the transformed plant polynucleotide or polypeptide is useful for improving plants with the polynucleotide or polypeptide is useful for producing plants with improved plant properties. Figure osen cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VMXVAEF 7
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RESULT 61 ADB11880

ADN22714 standard; protein; 919 AA.

RESULT 60

Bacterial polypeptide #5367

(first entry)

02-DEC-2004

ADN22714;

BXXXXXX

Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.

Staphylococcus epidermidis.

JS6380370-B1

30-APR-2002

Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4831

(first entry)

24-JUL-2002

ABP39986;

ABP39986 standard; protein; 927 AA.

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The present invention describes an isolated polymucleotide (I) of Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. Alloiococcus otitidis is a Gram-positive bacterium. Also described: (I) an isolated polypeptide that is encoded by the polymucleotide (I), its complement, despendente variant or fragment; (3) a genetically engineered comparison vector comprising the polypeptide of (I); (5) an immunogenic composition comprising the polypeptide, its complement, biological composition comprising the polypeptide, its composition comprising the polypeptide, its composition comprising the polypeptide of (I); (8) an immunogenic composition for the polypeptide (II) a protein chip comprising in the expression vector; (6) a pharmaceutical composition comprising an array of the polypeptides of (I), their biological equivalent or fragment; (8) immunogenic composition; (9) detecting and/or identifying Alloiococcus otitidis by administering to a host the contraining the novel polymucleotide, its degenerate variant or fragment; or the antibody of (4); and (11) producing a polypeptide by culturing the genetically engineered host cell under conditions suitable to produce the polypeptide from the culture. (I) can be used in gene therapy. The polypeptide from the culture. (I) can be used in gene therapy. The polymucleotides prosent and and angening and detecting Alloiococcus oritidis. The present sequence represents an Alloiococcus otitidis. The present sequence represents an Alloiococcus otitidis. The present from the navelent for expressing and detecting Alloiococcus otitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                  Alloiococcus otitidis; antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zagursky RJ;
                                                                                                                             Alloiococcus otitis antigenic protein SEQ ID NO:5180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigen protein from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 33; SEQ ID NO 5180; 1019pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mcmichael JC, Russell DP,
ADB11880 standard; protein; 926 AA
                                                                                                                                                                                                                                                                                                                                                                25-NOV-2002; 2002WO-US036123.
                                                                                                                                                                                                                                                                                                                                                                                                     29-NOV-2001; 2001US-0333777P.
18-NOV-2002; 2002US-0426742P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMHP ) WYETH HOLDINGS CORP.
                                                                                   (first entry)
                                                                                                                                                                                                                                  Alloiococcus otitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-505284/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADB11883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 926 AA;
                                                                                                                                                                                                                                                                              WO2003048304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fletcher LD,
                                                                                   20-NOV-2003
                                                                                                                                                                                                                                                                                                                      12-JUN-2003
                                            ADB11880,
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(GENO-) GENOME THERAPEUTICS CORP.

'n

Bush

Doucette-Stamm LA,

2002-381255/41.

N-PSDB; ABN92531

97US-0055779P 97US-0064964P

13-AUG-1998;

14-AUG-1997; 08-NOV-1997;

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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis; recombinant expression vector; infection; computer readable medium; computer based system.
                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 5; Length 927;
Pred. No. 2.4e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermis polypeptide segid 5691.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4831; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADS06396 standard; protein; 927 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus epidermidis.
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Best Local Similarity 83.3
Matches 5; Conservative
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115 MSVAEF 120 MXVAEF 7

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Alloiococcus otitidis, antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
                                                                                                                         25-NOV-2002; 2002WO-US036123
                                                                                                                                                    29-NOV-2001; 2001US-033377P
18-NOV-2002; 2002US-0426742P
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                                                                                                                                                                                             AMHP ) WYETH HOLDINGS CORP
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                                                                                                                                                                                                                                                   WPI; 2003-505284/47.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 MXVAEF 7
                                                                                                                                                                                                                                                                N-PSDB; ADB11881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 938 AA;
                                                                     WO2003048304-A2.
                                                                                               12-JUN-2003
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TD ADB1
XX
AC ADB1
XX
DT 20-N
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                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and enrociding an Staphylococcus epidermidis polypeptide with any of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as given in the specification. Also described are: a recombinant expression vector; a cell comprising a recombinant expression vector of (1); producing an S. epidermidis polypeptide; an isolated nucleocide signature of a least 8 nucleocides in length; a vaccine composition for prevention or treatment of an S. epidermidis infection, comprising a nucleocide acid cited above and a carrier; treating a subject for S. epidermidis infection; a recombinant or substantially cure preparation of an S. epidermidis polypeptide or its fragment; a vaccine composition for prevention or treatment of an S. epidermidis infection; detecting the presence of a Staphylococcus mucleic acid in a sample; a computer readable medium having recorded in it the nucleotide sample; a computer readable medium having recorded in it the nucleotide system for identifying fragments of the Staphylococcus genome of commercial importance; a computer based system for identifying fragments of the Staphylococcus genome and/or plasmids of commercial important nucleic acid fragments of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment commercially important in the present invention are useful for the diagnosis, prevention and/or treatment of an Staphylococcus poidermidis bacterial infection. This is the amino acid sequence of a S. epidermidis bacterial of the antico.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                            New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB 8; Length 927;
Pred. No. 2.4e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alloiococcus otitis antigenic protein SEQ ID NO:5182.
                                                                                                                                                                                                                                                                                                                      Claim 17; SEQ ID NO 5691; 741pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB11878 standard; protein; 938 AA.
                                                                                          97US-0064964P.
98US-00134001.
99US-00450969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.8%;
                                                                  01-DEC-2003; 2003US-00724972.
                                                                                                                                                                                             Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                 DOUCETTE-STAMM L.
BUSH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 83.3
Matches 5, Conservative
                                                                                                                                                                                                                     WPI; 2004-580138/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 MSVAEF 131
                                                                                                                                                                                             Doucette-Stamm L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 MXVAEF 7
                                                                                                                                                                                                                                    N-PSDB; ADS02624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 927 AA;
            US2004147734-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention.
                                                                                            08-NOV-1997;
                                                                                                         13-AUG-1998;
29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-2003
                                      29-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB11878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                 (DOUC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 64
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2622252
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The present invention describes an isolated polymucleotide (I) of Alloiococcus otitidis genomic DNA, which encodes an antigenic protein. Alloiococcus otitidis ganomic DNA, which encodes an antigenic protein. Alloiococcus otitidis is a Gram-positive bacterium. Also described: (I) an isolated polypeptide that is encoded by the polymucleotide (I); (2) an isolated polypeptide that is encoded by the polymucleotide (I); (2) an expression vector comprising the novel isolated polymucleotide (I); (2) an expression vector fragment or fragment; (3) a genetically engineered host cell, transfected, transformed or infected with the vector of (2); (4) an antibody specific for the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide of (1); (6) a pharmaceutical composition comprising the expression vector; (6) a pharmaceutical composition comprising an array of the polypeptide of (1) and a carrier; (7) a protein chip comprising the expression vector; (6) a pharmaceutical composition composition; (9) detecting and/or identifying Alloiococcus of the polypeptides of (1), their biological equivalent or fragment, (8) immunogenic composition; (9) detecting and/or identifying Alloiococcus otitidis in the biological sample; (10) a kit comprising a container containing the movel polymucleotides, polymeptide from the culture. (I) can be used in gene therapy. The colypeptide from the culture. (I) can be used in gene therapy. The polymucleotides, and onlicoting and diagnosing diseases, drug invention can be used for treating and diagnosing diseases, drug creening assays and monitoring of effects during drug clinical trials. The polymucleotides are useful for expressing and detecting officials antigen protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                             New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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Pred. No. 2.4e+03;
0; Mismatches 1; Indels
Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 33; SEQ ID NO 5182; 1019pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB11876 standard; protein; 940 AA.
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is expressed in COSI or CHO cells. The recombinant antigen is used in a vaccine for the protection of mammals and animals against the parasite H. contortus. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Haemonchus contortus enzyme antigen H110D is an aminopeptidase, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expression of parasite gut membrane bound antigen - for protective immunity against parasites \ensuremath{\mathsf{esp}} . Haemonchus contortus.
                                                                    Aminopeptidase H110D helminthic antigen.
                                                                                                                     Aminopeptidase; H110D; antigen; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 23-27; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 (MLCW ) MALLINCKRODT VETERINARY INC. (AGRI-) AGRIC & FOOD RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith TS,
                                                                                                                                                                                                                                                                                                            94WO-GB000204
                                                                                                                                                                                                                                                                                                                                                        93GB-00002302
  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                   Haemonchus contortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemonchus contortus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1994-279741/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Munn E, Graham M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 5: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VMXVAEF 7
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532 VISVAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB, AAQ71611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 962 AA;
                                                                                                                                                                                                                                                                                                       04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                        05-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9323542-A1.
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                                                                                                                                                                                                               WO9418320-A1
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  25-MAR-2003
25-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR51280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an isolated polymucleotide (I) of
Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.
Alloiococcus otitidis ganomic DNA, which encodes an antigenic protein.
Alloiococcus otitidis is a Gram-positive bacterium. Also described: (I)
an isolated polypeptide that is encoded by the polymucleotide (I); (2) an expression vector comprising the novel isolated polymucleotide (I); (2) an expression vector of (2);
(4) an antibody specific for the polypeptide of (I); (5) an immunogenic composition comprising the polypeptide of (I); (5) an immunogenic composition comprising the polypeptide of (I); (5) an immunogenic composition comprising the polypeptide of (I) and a carrier; (7) a protein chip comprising the expression vector; (6) a pharmaceutical composition comprising an array of the polypeptide of (I) and a carrier; (7) a protein chip comprising the expression vector; (6) a detecting and/or identifying an array of the polypeptide of (I) and a carrier; (7) a protein chip comprising an array of the polypeptide of (I) and a carrier; (7) a protein chip comprising the composition; (8) detecting and/or identifying Alloiococcus of the polypeptide from the culture. (I) a kit comprising a container composition; (9) detecting and/or identifying Alloiococcus of the present invention can be used for treating and diagnosing diseases, drug creaming assays and monitoring of effects during drug clinical trials.

The polyputleotides, polypeptides, antibodies and compositions of the present invention culture. (I) can be used distorbed by culturing Alloiococcus officials. The present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                           Alloiococcus otitidis; antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.8%; Score 24; DB 6; Length 940;
83.3%; Pred. No. 2.4e+03;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Zagursky RJ;
Alloiococcus otitis antigenic protein SEQ ID NO:5184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 33; SEQ ID NO 5184; 1019pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Russell DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR58701 standard; protein; 962 AA.
                                                                                                                                                                                                                                                           25-NOV-2002; 2002WO-US036123.
                                                                                                                                                                                                                                                                                                       2001US-0333777P.
                                                                                                                                                                                                                                                                                                                                                                           (AMHP ) WYETH HOLDINGS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                            Mcmichael JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                  Alloiococcus otitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-505284/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 MXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADB11879.
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                                                                                                                                                              WO2003048304-A2
                                                                                                                                                                                                                                                                                                       29-NOV-2001;
18-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                            Fletcher LD,
                                                                                                                                                                                                             12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5,
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Newton SE;

Rolph TP,

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Gaps
                                                                                                                                                                                                                             Helminth; aminopeptidase; H11-3; H11-2; H11-1; integral membrane; alpha-amino acyl peptide hydrolase (microsomal); multigene family; antigen; vaccine; parasite; human; virus; microbe.
                                                                                                                                                                                                        Helminth aminopeptidase H110D varient encoded by the H11-3 gene.
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Similarity 71.4%; Pred. No. 2.5e+03; 5; Conservative 1; Mismatches 1; Indels
                                                                                                                            AAR51280 standard; protein; 972 AA.
                                                                                                                                                                                                                                                                                                                                                                                           (AGRI-) AGRIC & FOOD RES COUNCIL.
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Matches

RESULT 66

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AARS8701 ID AAR: XX AC AAR: XX

N-PSDB; ABQ74274, ABQ74275

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                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAR51280-82 represent varients of the helminth aminopoptidase H110D encoed by the genes H11-3, -2 and -1 respectively. H110D is a protein doublet which shows homolay to a family of integral membrane aminopoptidases. The differences between the coding sequences and the translated products, can be attributed to different mRNAs of the willigene family, and also to different variants of the H110D-encoding sequence being present at different stages of the life cycle, or in strains differing in geographical origin. Antigenic fragments of these aminopoptidases may be used in vaccines to stimulate immune response against helminth parasites in humans or other animals. The DNA sequences encoding these proteins may be incorporated into a virus or microbe and used in a similar manner. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                    New DNA encoding amino-peptidase from Haemonchus contortus and derived peptide(s) - useful in protective vaccines, for new vectors, transformed cells and oligosaccharide, for incorporation in virus or microbe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
   Oliver JJ, Newton SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.8%; Score 24; DB 2; Length 972; 71.4%; Pred. No. 2.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 67084FL transporter protein SEQ ID NO:23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
   Knox DP,
                                                                                                                                                                                                                                                                                                         Claim 6; Page 82-84; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP52161 standard; protein; 1084 AA.
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Smith TS, - Munn EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2000; 2000US-0256588P. 21-DEC-2000; 2000US-0258028P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Query Match
Beet Local Similarity 71.4°,
Beet Local Similarity
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                WPI; 1993-386574/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VMXVAEF 7
                                                                                                N-PSDB; AAQ52489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 972 AA;
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Graham M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP52161;
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14 X B B X B A X B
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The present sequence represents the human 67084FL protein, which is a member of the transporter family. The transporter family proteins (1) of the present invention have anorectic, antidabetic, anti-Parkinsonian, nootropic, neuroprotective, hypotensive, antidaperseant, neuroleptic, cardiovascular and immunosuppressive activities, and can be used in gene therapy. The human transporter proteins from the present invention are cadiovascular and immunosuppressive activities, and can be used in gene therapy. The human transporter proteins from the present invention are casing assignated 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL and sasays (e.g. chromosome mapping, tissue typing, or in forensic biology), credictive medicine (e.g. diagnostic assays, prognostic assays, prognostic assays, controling clinical trials, or pharmacogenetics), as surrogate markers, and in methods of treatment (e.g. therapeutic or prophylactic). (1) are useful for treatment (e.g. therapeutic or prophylactic). (1) are useful for treatment (e.g. therapeutic or prophylactic). (1) are useful for treatment of 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084alt substrates or production of transport 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084alt inhibitors. Disorders associated with 8099 and 46455 include disorders associated with sugar homeostasis cuch as obesity, diabetes or anorexia. Disorders associated with Sugar homeostasis. Cc 53763, 67076, 67102, 44181, 67084FL or 67084alt are e.g. CNS disorders (e.g. Parkinson's disease or Alzheimer's disease), autonomic function disorders (e.g. ammesia or age-related disorders), cradiovascular disorders (e.g. hypothyroidism or hyporthyroidism), crestenosis), hormonal disorders (e.g. hypothyroidism or hyporthyroidism), cc restenosis), hormonal disorders (e.g. hypothyroidism or hypothyroidism), cc restenosis), hormonal disorders (e.g. hypothyroidism or hypothyroidism), cc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; transporter protein, anorectic, antidiabetic; anti-Parkinsonian, nootropic; neuroprotective; hypotensive; antidepressant; neuroleptic; cardiovascular; immunosuppressive; gene therapy; sugar homeostasis; obesity; diabetes; anorexia; central nervous system disorder; depression; CNS disorder; Parkinson's disease; Alzheimer's disease; hypetrension; autonomic function disorder; schizophrenia; learning disorder; amnesia; memory disorder; age-related disorder; cardiovascular disorder; ischemia reperfusion injury; restenosis; hypothyroidism; hypothyroidism; immune disorder; chronic mucocutaneous candidiasis.
                                            New 67076, 67102, 44181, 67084FL and 67084alt nucleic acids and proteins, useful in e.g. treating disorders characterized by insufficient or excessive production of the polypeptides, e.g. cardiovascular or immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.8%; Score 24; DB 5; Length 1084; 71.4%; Pred. No. 2.8e+03; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 67084alt related transporter protein SEQ ID NO:27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP52175 standard; protein; 1084 AA.
                                                                                                                                                                           Claim 13; Fig 32; 364pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 71.4%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Matches
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18-JUL-2002

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New isolated nucleic acid, useful for preparing a composition for treating PGC-1 associated disorders e.g. liver tumors, obesity, epilepsy or diabetes.
                                                                        22-MAY-2002; 2002US-00154419
                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-851783/79.
N-PSDB; ADD37495, ADD37497.
                US2003143675-A1.
                                                                                                                                                             25-SEP-2000;
05-OCT-2000;
                                                                                                                                                                                       14-NOV-2000;
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                                                                                                                                                                                                                                                                 22-JAN-2001;
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                                                                                                                                                                                                                                                                                                          31-JUL-2001;
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                                                                                                                                               19-SEP-2000;
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                                                                                                      12-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Curtie RAJ,
                                             31-JUL-2003
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Matches
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                                                                                                                                                                                                                                                                                                  transporter family. The transporter family proteins (1) of the present invention have anorectic, antidiabetic, anti-Parkinsonian, nootropic, neuroprotectitive, hypotensive, antidepressant, neuroleptic, cardiovascular neuroleptic, cardiovascular and immunosuppressive activities, and can be used in gene therapy. The human transporter proteins from the present invention are designated solys, 46455, 54444, 53763, 67076, 67102, 44181, 67084FL and 67084alt. The polynucleotides encoding (1) can be used in screening assays (e.g. chromosome mapping, tissue typing, or in forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical transment (e.g. therapeutic or prognesics), as surrogate markers, and in methods of treatment (e.g. therapeutic or prophylactic). (1) are useful for treating disorders characterised by insufficient or excessive production of 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084alt inhibitors Disorders associated with 8099 and 44181, 67084FL or 67084alt inhibitors Disorders associated with sugar homestals such as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obesity, diabetes or anorexia. Disorders associated with 54414, 53763, 67102, 44181, 67084FL or 67084alt are e.g. CNS disorders (e.g. Parkinson's disease or Alzheimer's disease), automaic function disorders (e.g. hypertension, depression or schizophrenia), or learning or memory disorders (e.g. amnesia or age-related disorders), cardiovascular disorders (e.g. ischaemia reperfusion injury or restenosis), hormonal disorders (e.g. hypothyroidism or hyperthyroidism), or immune disorders (e.g. chronic mucocutaneous candidiaeis). The present sequence represents a human transporter protein related protein from the present invention
                                                                                                                                                                                       New 67076, 67102, 44181, 67084FL and 67084alt nucleic acids and proteins, useful in e.g. treating disorders characterized by insufficient or excessive production of the polypeptides, e.g. cardiovascular or immune
                                                                                                                                                                                                                                                                                           present invention describes human proteins which are members of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.8%; Score 24; DB 5; Length 1084; 71.4%; Pred No. 2.8e+03;
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                                                                                                                                                                                                                                                              Disclosure; Page 334-339; 364pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD37496 standard; protein; 1084 AA.
17-DEC-2001; 2001WO-US049060
                           2000US-0256240P.
                                          2000US-0256588P
2000US-0258028P
                                                                                    (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 71.4
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                                                                                                                                            WPI; 2002-590672/63.
N-PSDB; ABQ74277.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1084 AA;
                                          18-DEC-2000;
21-DEC-2000;
                            15-DEC-2000;
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                                                                                                                   Curtis RAJ;
                                                                                                                                                                                                                                    disorders
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Glucksmann MA, Meyers RE;

2000US-0233790P. 2000US-0235107P. 2000US-0238336P. 2000US-0248364P. 2000US-0256240P. 2000US-0256240P.

2000US-0258028P. 2001US-0263169P. 2001US-00858194. 2001US-00957811. 2001US-00957664. 2001US-00964295.

2001US-00972724. 2001US-00002769. 2001US-00024623.

2002US-00055025

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encoding a human transporter protein, or its complement, a sequence that is 60 % identical to the CDNA, a fragment comprising at least 30 nucleotides of the CDNA, or a sequence encoding a fragment of the polypeptide comprising at least 10 contiguous amino acid residues of the CDNA. Also included are a vector comprising the novel nucleic acid molecule, producing the polypeptide, the isolated transporter polypeptide, an isolated antibody that specifically binds to the polypeptide, detecting the presence of the polypeptide or nucleic acid in a sample, a kit, identifying a compound that binds to, or that modulates the activity of, the polypeptide, and modulating the activity of the polypeptide. The nucleic acid is useful for preparing a composition for treating PGC-1 (not defined) associated disorders e.g. liver tumours, obesity, epilepsy or diabetes. The present sequence represents a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                             The invention relates to an isolated nucleic acid comprising a cDNA
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Claim 11; SEQ ID NO 73; 663pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI27975 standard; protein; 1084 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human transporter protein.
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1016 LMVVAEF 1022
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Human; transporter; cytostatic; anorectic; antidiabetic; anticonvulsant; gene therapy; PGC-1 associated disorder; liver tumour; obesity; epilepsy; diabetes.

Homo sapiens

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Claim 1; SEQ ID NO 19; 285pp; English
                                                                                   Sequence 1084 AA;
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25-OCT-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                 ADN33134;
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Ring HZ,
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Matches
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IC47615, HNWDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel

Emily (ICF) nucleic acids and proteins. The TWIK-7, IC23927,

TWIK-8, IC47611, IC47615, HNWDA-1, TWIK-9, alpha-2delta-4, 54414 and

Emily (ICF) nucleic acids and proteins may be used for preventing,

TWIK-8, IC47611, IC47615, HNWDA-1, TWIK-9, alpha-2delta-4, 54414 and

CHARLES ICF nucleic acids and proteins may be used for preventing,

CHARLES ICF nucleic acids and proteins may be used to treat disorders associated with decreased expression by rectifying

TRIP creat disorders associated with decreased expression by rectifying

TRIP creat disorders in a patient's genome that affect the activity of

CH proteins by expressing inactive proteins or to supplement the

patients own production of ICF proteins. The proteins may also be used as antigens in the production of antibodies against ICF proteins and in

assays to identify modulators of ICF protein expression and activity. The

anti-ICF protein expression and activity. The antibodies may also be

cregulate ICF protein expression and activity. The antibodies may also be

cred as diagnostic agents for detecting the presence of ICF proteins in

samples (e.g. by immunoassay). The nucleic acids and proteins may be used

to prevent, diagnose and treat a wide variety of disorders, e.g. cancers

and leukaemia, Alzheimer's disease, Parkinson's disoraes, multiple

sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disorders.
                                                                                                                  Human; 67084FL; ion channel family; ICF; cancer; leukaemia;
Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy;
hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective;
nootropic; antiparkinsonlan; hepatotropic; cardiovascular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Curtis RAJ, Glucksmann MA, Silos-Santiago I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 68; 638pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-SEP-2000; 2000US-0233537P.
25-SEP-2000; 2000US-0235018P.
25-SEP-2000; 2000US-0235018P.
15-DEC-2000; 2000US-025658P.
11-DEC-2000; 2000US-025658P.
28-PEB-2001; 2000US-025802BP.
28-PEB-2001; 2001US-00796720.
11-APR-2001; 2001US-00833081.
25-APR-2001; 2001US-00833081.
                                                                                                                                                                                                                                                                                                                                                                                           2000US-00515520.
2000US-0185938P.
2000US-0195934P.
2000US-0195993P.
2000US-0199799P.
2000US-0233537P.
2000US-0235018P.
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25-SEP-2001; 2001US-00964256
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                                                                                                                                                                                                                                                                                                                                                      15-MAY-2002; 2002US-00146733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADI27974, ADI27976.
                                      (first entry)
                                                                             Human 67084FL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2004-069000/07
                                                                                                                                                                                                                                                                    JS2003165891-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAR-2000;
07-APR-2000;
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                                                                                                                                                                                                                               Homo sapiens
                                        06-MAY-2004
                                                                                                                                                                                                                                                                                                           04-SEP-2003.
AD127975;
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sequence represents the human 67084FL protein of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at segdata.uspto.gov/sequence.html.
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Ison CH, Becha SD, Ding L, Warren BA, Lee SY, Swarnakar A;
VS, Richardson TW, Marquis JP, Ramkumar J, Murage J;
BE, Yao MG, Lu Y, Gietzen KJ, Yang YG, Chang H, Chaula NK;
Lee S, Yang J, Gandhi AR, Tribouley CM, Policky JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crohn's disease; renal disorder; Goodpasture's syndrome; infection; viral; bacterial; fungal; parasitic; protozoal; helminthic; cardiovascular disorder; atherosclerosis; hepatic disease; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                              Score 24; DB 8; I
Pred. No. 2.8e+03;
1; Mismatches 1;
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2002US-0421033P.
2002US-0421349P.
2002US-0423516P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
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Best Local Similarity
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Lee EA;
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Times liventon relates to novel numan transporters and ion channel convention may be useful for the production of compounds with a convention may be useful for the production of compounds with a convention may be useful for the production of compounds with a convention may be useful for the production of compounds with a convention of dermatological, immunosuppressive, antiinflammatory, thyromimetic, dermatological, immunosuppressive, antiinflammatory, thyromimetic, antiinflammatory, thyromimetic, antiparasitic, anticonvulsant, antiparkinsonian, antibacterial, antiparasitic, fungicide, protozoacide, virucide, uropathic, antirheumatic, cardiant, cardiavascular, anti-HIV or nootropic activity acting as TRICH agonists or antagonists. In addition the disclosed acting as TRICH agonists or antagonists. In addition the disclosed adiagnosing, preventing, and treating disorders associated with an abnormal expression or activity of TRICH, such as neurodegenerative disorders (for example Parkinson's disease, Alzheimer's disease), muscular disorders (for example myotonic dystrophy, catatonia), endocrine disorders (for example dabetes, Grave's disease), cancers (for example colopasture's syndrome), infections (for example viral, targies) assertial, fungal, parasitic, protozoal, helminthely, cardiavascular disorders (for example Goodpasture's syndrome), infections (for example viral, bacterial, fungal, parasitic, protozoal, helminthely, cardiavascular disorders (for example atherosclerosis), or hepatic diseases (for example compounds that specifically bind to and modulate the activity of TRICH. The nucleotides can be used to create humanised animals to model human disease. The present sequence is that of a human converse animals to model human disease. The present sequence is that of a human converse animals to model human disease. The present sequence is that of a human converse animals to model human despective or create human sequence is that of a human converse in the present sequence is that of a human converse in the p
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                    This invention relates to novel human transporters and ion channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.8%; Score 24; DB 8; Length 1084; 71.4%; Pred. No. 2.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human 67084alt transporter protein SEQ ID NO:26.
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18-DEC-2000; 2000US-0256588P.
21-DEC-2000; 2000US-0258028P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 71.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1016 LMVVAEF 1022
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The present sequence represents the fundamental process.

C member of the transporter family. The transporter family proteins (1) of the present invention have anorectic, antidiabetic, anti-Parkinsonian, cootropic, neuroprotective, well-depressant, neuroleptic, cardiovascular and immunosuppressive, activities, and can be used in gene therapy. The human transporter proteins from the present invention are designated 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL and 67084alt. The polynucleotides encoding (1) can be used in screening assays (e.g. chromosome mapping, tissue typing, or in forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, compitoring clinical trials, or pharmacogenetics), as surrogate markers, and in methods of treatment (e.g. pherapeutic or prophylactic). (I) are useful for treating disorders characterised by insufficient or excessive production of 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084alt substrates or production of transport 8099, 46455, 54414, 53763, 67076, 67102, 44181, 67084FL or 67084alt inhibitors. Disorders associated with sugar homeostasis cuch as obesity, diabetes or anorexia, Disorders associated with 54414, 53763, 67076, 67102, 44181, 67084FL or 67084alt are e.g. CNS disorders (e.g. parkinson's disease or Alzheimer's disease), autonomic function of disorders (e.g. hypertension, depression or schizophrenia), or learning or memory disorders (e.g. hypertension, depression or schizophrenia), or learning or cardiovascular disorders (e.g. hypertension, the hypertension of the hypertension of the hypertension of the hypertension of the hypertension, the hypertension of the hypertension of the hypertension of the hypertension of the hypertension, the hypertension of the hypertension of the hypertension of the hyperte
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                                                                                                                                                                                      New 67076, 67102, 44181, 67084FL and 67084alt nucleic acids and proteins, useful in e.g. treating disorders characterized by insufficient or excessive production of the polypeptides, e.g. cardiovascular or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restenosis), hormonal disorders (e.g. hypothyroidism or hyperthyroidism), or immune disorders (e.g. chronic mucocutaneous candidiasis)
                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the human 67084alt protein, which is a
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Pred. No. 2.8e+03;
1; Mismatches 1; Indels
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71.4%;
(MILL-) MILLENNIUM PHARM INC
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Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                           WPI; 2002-590672/63.
N-PSDB; ABQ74276.
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                                                       Curtis RAJ;
                                                                                                                                                                                                                                                                                   disorders.
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Human; transporter and ion channel; TRICH; atherosclerosis; cancer;

Human TRICH-16 protein.

24-MAR-2003

AAE32082;

'note= "Transmembrane domain"

.153

cocation/Qualifiers

Homo sapiens

Key Domain Domain Domain Domain

gene therapy

"Transmembrane

note= /note= 'note= /note=

"E1-E2 ATPase

.199 305 "Transmembrane domain"

"Transmembrane "Transmembrane "Transmembrane "Transmembrane "Transmembrane

326. .346

Domain Domain Domain Domain Domain

.371

'note=

900

/note= /note= 'note=

"El-E2 ATPase domain"

domain"

.978

Domain

Domain Domain

'note= /note=

.927

/note= "Transmembrane domain"

WO200283712-A2

Domain

24-OCT-2002

20-APR-2001; 2001US-0285592P. 27-APR-2001; 2001US-0287263P. 04-MAY-2001; 2001US-028666E. 18-MAY-2001; 2001US-0292042P. 25-MAY-2001; 2001US-0293724P.

12-APR-2002; 2002WO-US011760

12-APR-2001;

/note= "Transmembrane "Transmembrane

.1035 1006

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transporter family. The transporter family proteins (I) of the present invention have anorectic, antidiabetic, anti-Parkinsonian, nootropic, invention have anorectic, antidiabetic, anti-Parkinsonian, nootropic, and immunosuppressive activities, and can be used in gene therapy. The human transporter proteins from the present invention are designated (1) 2019, 44611, 67084F. and 67084att. The polynucleotides encoding (I) can be used in screening assays (e.g. chromosome mapping, tissue typing, or in forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trails, or pharmacogenetics), as surrogate markers, and in methods of transpentic or prophylactic). (I) are useful for treating disorders characterised by insufficient or excessive production of 8099, a 46455, 54414, 53763, 67076, 67102, 444181, 67084FL or 67084alt inhibitors. Disorders associated with 8099 and 44181, 67084FL or 67084alt inhibitors. Disorders associated with 8099 and 44181, 67084FL or 67084alt inhibitors. Disorders associated with 8099 and 44181, 67084FL or 67084alt inhibitors. Disorders associated with 8099 and 44181, 67084FL or 67084alt inhibitors. Disorders associated with 8040 and 67084alt inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                obesity, diabetes or anorexia. Disorders associated with 54414, 53763, 67102, 44181, 67084FL or 67084alt are e.g. CNS disorders (e.g. Parkinson's disease or Alzheimer's disease), autonomic function disorders (e.g. hypertension, depression or schizophrenia), or learning or memory disorders (e.g. amnesia or age-related disorders), cardiovascular disorders (e.g. ischaemia reperfusion injury or restenosis), hormonal disorders (e.g. hypothyroidism or hyperthyroidism), or immune disorders (e.g. chronic mucocutaneous candidiashs). The present sequence represents a protein given in comparison with a human transporter protein from the
                                                                                                                                                                                                                                                                                                                         New 67076, 67102, 44181, 67084FL and 67084alt nucleic acids and proteins, useful in e.g. treating disorders characterized by insufficient or excessive production of the polypeptides, e.g. cardiovascular or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.8%; Score 24; DB 5; Length 1095; 71.4%; Pred. No. 2.8e+03; ive 1; Mismatches 1; Indels
                                                                 /note= "unspecified"
                                       note= "unspecified"
           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 35; 364pp; English.
                                                                                                                                                                              15-DEC-2000; 2000US-0256240P.
18-DEC-2000; 2000US-0256588P.
21-DEC-2000; 2000US-0258028P.
                                                                                                                                                   17-DEC-2001; 2001WO-US049060
                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.**,
Best Local Similarity 71.**,
                                                      Misc-difference 1005
                                                                                                                                                                                                                                                                                               WPI; 2002-590672/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1095 AA;
                          Misc-difference
                                                                                               WO200255701-A2
                                                                                                                         18-JUL-2002
                                                                                                                                                                                                                                                                   Curtis RAJ;
                                                                                                                                                                                                                                                                                                                                                                     disorders
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The invention relates to human transporters and ion channels (TRICH) polypeptides and nucleic acid molecules encoding such polypeptides. TRICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human functional transporters and ion channels (TRICH) polypeptides, useful for preparing a composition for diagnosing or treating a disease associated with decreased expression or overexpression of TRICH e.g.
                                                                                                                                                                             Baughn MR, Elliott VS, Hafalia AJA, Yang J, Walia NK, Ramkumar J; Forseythe IJ, Lu Y, Tang YT, Yue H, Raumann BE, Lal PG, Azimzai Y Lu DAM, Gandhi AR, Thornton M, Nguyen DB, Arvizu CS, Emerling BM; Swarnakar A, Yao MG, Ding L, He A, Griffin JA, Sanjanwala MM; Gietzen KJ, Lee EA, Xu Y, Au-Young JK, Das D, Lee SY, Chang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 178-181; 204pp; English.
2002US-0351107P
                                                                                             (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-092996/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAD49514.
    22-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer
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Gaps

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AAE32082 standard; protein; 1095 AA.

RESULT 75
AAE32082
ID AAE320

1016 LMVVAÈF 1022

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1 VMXVAEF 7

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The invention relates to an isolated nucleic acid comprising a cDNA encoding a human transporter protein, or its complement, a sequence that is 60 % identical to the cDNA, or a sequence encoding at least 30 nucleotides of the cDNA, or a sequence encoding a fragment of the polypeptide comprising at least 10 contiguous amino acid residues of the cDNA. Also included are a vector comprising the novel nucleic acid molecule, producing the polypeptide, the isolated transporter polypeptide, an isolated antibody that specifically binds to the polypeptide, an isolated antibody that specifically binds to the polypeptide, a kit, identifying a compound that binds to, or that modulates the activity of, the polypeptide, and modulating the activity of the polypeptide. The nucleic acid is useful for preparing a composition for treating pGC-1 (not defined) associated disorders e.g. liver tumours, obesity, epilepsy or diabetes. The present sequence represents a species homologue of a novel human transporter protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, transporter; cytostatic; anorectic; antidiabetic; anticonvulsant;
gene therapy; PGC-1 associated disorder; liver tumour; obesity; epilepsy;
                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                                                        Score 24; DB 7; Length 1095;
Pred. No. 2.8e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  ADD37499 standard; protein; 1095 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0248364P.
2000US-0248878P.
2000US-0256240P.
2000US-0256888
2000US-0258028P.
2001US-0263169P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0221769P.
2000US-0233790P.
2000US-0235107P.
2000US-0238336P.
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2001US-00919781.
2001US-00957664.
2001US-00964295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-00972724.
2001US-00002769.
2001US-00024623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-2002; 2002US-00154419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-00055025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                         Query Match 82.8%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human transporter 67084alt
                                                                                                                                                                                                                                                                                                                                    :| ||||
1016 LMVVAEF 1022
                                                                                                                                                                                                                                Sequence 1095 AA;
                                                                                                                                                                                                                                                                                                                  1 VMXVAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003143675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2000;
05-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-NOV-2000;
15-NOV-2000;
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18-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD37499;
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 77
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  proteins are useful for preparing compositions for diagnosing or treating diseases or conditions associated with decreased expression or overexpression of functional TRICH e.g. atherosclerosis or cancer. The invention is useful in gene therapy. The present sequence is human TRICH
                                                                                                                                                                                                                                                                                                                                                                                    Transporter; cytostatic; anorectic; antidiabetic; anticonvulsant; gene therapy; PGC-1 associated disorder; liver tumour; obesity; epilepsy; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid, useful for preparing a composition for treating PGC-1 associated disorders e.g. liver tumors, obesity, epilepsy or diabetes.
                                                                                                                                               Gaps
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                                                                                                                Score 24; DB 6; Length 1095;
Pred. No. 2.8e+03;
                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                           Mouse phopholipid transporting ATPase, AT2B.
                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Curtis RAJ, Glucksmann MA, Meyers RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; SEQ ID NO 86; 663pp; English.
                                                                                                                                                                                                                                                                        ADD37509 standard; protein; 1095 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-2000; 2000US-0204211P.
29-JUN-2000; 2000US-0221769P.
31-JUL-2000; 2000US-0231769P.
19-SEP-2000; 2000US-0233790P.
25-SEP-2000; 2000US-0238336P.
14-NOV-2000; 2000US-0248364P.
15-NOV-2000; 2000US-0248364P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2000; 2000US-0256588P.
22-JAN-2001; 2000US-025628P.
22-JAN-2001; 2001US-0263169F.
29-JUN-2001; 2001US-008581194.
31-JUL-2001; 2001US-00919781.
19-SEP-2001; 2001US-00957664.
                                                                                                                82.8%;
71.4%;
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2001US-00024623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAY-2002; 2002US-00154419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-00055025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                             5; Conservative
                                                                                                                                                                                                  1016 LMVVAEF 1022
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                                                                                                                                                                         1 VMXVAEF 7
                                                                                                                              Best Local Similarity
                                                                                       Sequence 1095 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003143675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2001;
14-NOV-2001;
17-DEC-2001;
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                                                                                                                                                                                                                                                                                                   ADD37509;
                                                                                                                   Query Match
                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
                                                                                                                                               Matches
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06-APR-2001;
11-APR-2001;
                                      25-APR-2001;
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                                                                                                                                      Curtis RAJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI27988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 79
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                                                                                                                                              encoding a human transporter procein, or its complement, a sequence that its for & identical to the cDNA, or a sequence encoding a fragment of the polypeptide comprising at least 30 nucleotides of the cDNA, or a sequence encoding a fragment of the polypeptide comprising at least 10 contiguous amino acid residues of the cDNA. Also included are a vector comprising the novel nucleic acid molecule, producing the polypeptide, the isolated transporter polypeptide, an isolated artibody that specifically binds to the polypeptide, a kit, identifying a compound that binds to or that modulates the activity of, the polypeptide, and modulating the activity of the polypeptide, and modulating the activity of the polypeptide, and modulating the activity of the reacting polypeptide, and modulating the activity of the recent of its useful for preparing a composition for treating poct-1 fort defined associated disorders e.g. liver tumours, obesity, epilepsy or diabetes. The present sequence represents a novel human transporter protein.
                                                  New isolated nucleic acid, useful for preparing a composition for treating PGC-1 associated disorders e.g. liver tumors, obesity, epilepsy or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; 67084alt; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective; nootropic; antiparkinsonian; hepatotropic; cardiovascular.
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                   invention relates to an isolated nucleic acid comprising a cDNA
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                              82.8%; Score 24; DB 7; Length 1095; 71.4%; Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
  Meyers RE;
                                                                                                            Claim 11; SEQ ID NO 76; 663pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI27978 standard; protein; 1095 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-2000; 2000US-0195734P.
11-APR-2000; 2000US-0195993P.
26-APR-2000; 2000US-0199799P.
19-SEP-2000; 2000US-0233537P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEP-2000; 2000US-0235018P.
25-SEP-2000; 2000US-0235059P.
15-DEC-2000; 2000US-025508P.
18-DEC-2000; 2000US-025588P.
21-DEC-2000; 2000US-025688P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0185938P.
2000US-00518866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-2002; 2002US-00146733
 Curtis RAJ, Glucksmann MA,
                        WPI; 2003-851783/79.
N-PSDB; ADD37498, ADD37500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 71.9
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human 67084alt protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1016 LMVVAEF 1022
                                                                                                                                                                                                                                                                                                                                                                                                              1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                       Sequence 1095 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADI27978;
                                                                                                                                                                                                                                                                                                                                                               Query Match
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ADI27978
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The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,

CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel

CC IC47611, ICA7611, ICA7612, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and

CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and

CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and

CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and

CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and

CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and

CC diagnosing and treating ICF-related diseases. The sequences and be used to treat disorders associated with decreased expression by rectifying of contigens of ICF proteins and the activity of patients own production of ICF proteins. The proteins and an in the production of antibodies against ICF proteins and in assays to identify modulators of ICF protein expression and activity. The antibodies may be used to regulate ICF protein antibodies, agonists and antagonists may be used to regulate ICF protein antibodies, agonists and activity. The antibodies may be used to prevent, diagnose and treat a wide variety of disorders, e.g. cancers and leukaemia, Alzheimer's disease, Parkinson's disease, multiple and leukaemia, Alzheimer's disease, Parkinson's disease, multiple contents the human 67084alt protein of the invention. Note:

The sequence data for this patent is also available in electronic format from USPFO at segdata.uspto-gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective; nootropic; antiparkinsonian; hepatotropic; cardiovascular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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71.4%; Pred. No. 2.8e+03;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Glucksmann MA, Silos-Santiago I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 71; 638pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI27988 standard; protein; 1095 AA.
2001US-00828035.
2001US-00833081.
2001US-00843128.
                                                                                                                           19-SEP-2001; 2001US-00957683.
25-SEP-2001; 2001US-00964252.
25-SEP-2001; 2001US-00964256.
17-DEC-2001; 2001US-000246256.
                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-069000/07.
N-PSDB; ADI27977, ADI27979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1016 LMVVAEF 1022
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine protein #4.
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RESULT 80
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[1647615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel
family (ICF) mucleic acids and proteins. The TWIK-6, IC23927,

[277615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
[27 TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
[27 TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
[27 TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
[28 33763 ICF nucleic acids and proteins may be used for creat disorders associated with decreased expression by rectifying
[27 TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
[28 TWIK-9, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
[28 TWIK-18, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
[29 TWIK-18, IC47611], IC47615, IC47611, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, apphazdelta-4, 54414, or 53763 nucleic acids and proteins, useful for preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.8%; Score 24; DB 8; Length 1095; 71.4%; Pred. No. 2.8e+03; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Silos-Santiago I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 81; 638pp; English
                                                                                                                                                                                                                                       19-SEP-2000; 2000US-0233537P.
25-SEP-2000; 2000US-0235018P.
25-SEP-2000; 2000US-0235059P.
                                                                                                                                                                                                                                                                                                                                21-DEC-2000; 2000US-0258028P.
28-FEB-2001; 2001US-00796720.
06-APR-2001; 2001US-00828035.
11-APR-2001; 2001US-00843128.
                                                                                                                                                              03-WAR-2000; 2000US-00518866.
07-APR-2000; 2000US-0195734P.
11-APR-2000; 2000US-0195993P.
26-APR-2000; 2000US-0199799P.
                                                                                                                                                                                                                                                                                             15-DEC-2000; 2000US-0256240P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-2001; 2001US-00964252
25-SEP-2001; 2001US-00964256
                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2001; 2001US-00957683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-00024623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Curtis RAJ, Glucksmann MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-069000/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1095 AA;
               US2003165891-A1
                                                                                                                                                                                                                                                          25-SEP-2000;
25-SEP-2000;
                                                                                        15-MAY-2002;
                                                    04-SEP-2003
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The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                        transcription regulatory element; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #13661
                                                                                                                               Klebsiella pneumoniae polypeptide segid 8879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 8879; 932pp; English.
ABO62362 standard; protein; 1176 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU28134 standard; protein; 1225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                          expression vector;
                                                                                                                                                                                            Klebsiella pneumoniae protein;
                                                                                                                                                                                                                                                                                                                                                                       27-JAN-2000; 2000US-00489039
                                                                                                                                                                                                                                                                                                                                                                                                                99US-0117747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.8%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-2003 (first entry)
                                                                                    (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                                                        Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Breton GL, Osborne M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             779 VMKVAQF 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-895346/82.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VMXVAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-895346
N-PSDB; ACH95913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-1999;
                                                                                                                                                                                                                                                                                   US6610836-B1.
                                                                                    29-JUL-2004
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                                           ABO62362;
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Conservative

Local Similarity ses 5; Conserv

Matches

1016 LMVVAEF 1022

1 VMXVAEF 7

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21-MAR-2001; 06-SEP-2001; 25-OCT-2001; 08-FEB-2002;

Wang L, Wall D,

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The present sequence represents a Staphylococcus aureus protein, that, based on homology with a Bacillus subtilis protein, is believed to be a probable UDP-N-acetylglucosamine 1-carboxyvinyltransferase (enoylpyruvate transferase, UDP-N-acetylglucosamine enoylpyruvyl transferase). The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of staphylococcal genes. The DNA sequence to control the expression of staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host appaint invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome
                                                                        Staphylococcus aureus protein, ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - us
isolate antimicrobial compounds, and in vaccines against S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Knowles DJC, Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.3%; Score 23; DB 2; Length 36; 83.3%; Pred. No. 1.3e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor protein tyrosine kinase (PTK) subtype tyro-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTK; receptor; protein tyrosine kinase; brain tissue.
                          UDP-N-acetylglucosamine 1-carboxyvinyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ward JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hodgson JE, Ku
Rosenberg M,
                                                                                                                                                                                                                                                                                                                                    /note= "not specified"
                                                                                                                                                                                                                                                             hey Location/Qualifiers Misc-difference 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW79151 standard; protein; 54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 272; 989pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US002318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0011888P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burnham MK,
Reichard RW,
                                                                                                                                                                                                                        Staphylococcus aureus
                                                                                                                                                                   toxic shock syndrome.
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N-PSDB; AAT83751.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 MXVAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                           WO9730070-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Black
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 83
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ID AAW
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention relates to an increte act completely any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(i) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated nutisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway cequired for that has an activity against a biological pathway cequired for that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sactivity; (11) a culture comprising strains in which the estent compound that inhibits the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the control of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation of an organism. The antisense modeled are useful for dence of the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                         Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                         Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 56058; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                         Malone C,
Carr GJ,
                                                                                                      2001US-00948993.
2001US-0342923P.
2002US-00072851.
                          21-MAR-2002; 2002WO-US009107.
                                                                              2001US-00815242
                                                                                                                                                                                          06-MAR-2002; 2002US-0362699P
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                                                                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.8
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       945 VMEVAQF 951
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AAW27782;

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RESULT 82 AAW27782

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This represents a receptor protein tyrosine kinase (PTK) subtype tyro-9.

The invention provides sequences AAV65308 to AAV65313, AAV65315, and
AAV65317 to AAV65319 that encode proteins having a tyrosine kinase domain
and a tissue expression pattern of a receptor PTK subtype selected from
and a tissue expression pattern of a receptor PTK subtype selected from
tyro-1, tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10, tyro-11,
and tyro-12, respectively. The polymaclecides are useful for the
certion of tyrosine kinase domain sequences and detection of tissue
certion patterns of PTK subtypes. The cDNAs can also be injected into
cocytes, the protein expressed, and expression products screened for
using antibodies against tyrosine kinase epitopes. These subtypes
cocytes, the protein expressed, and expression products screened for
using antibodies against tyrosine kinase epitopes. These
certion protocols are used in the diagnosis of diseases associated with
(receptor) PTKS. Recombinant vectors expressing the subtypes can be used
to treat related diseases e.g. tumours, by introduction of the vectors
into skin transplants, then grafting these into the connective tissue of
the dermis, thus specifically targetting tumours as the proteins are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a substantially pure protein(s) or their fragments, comprising a tyrosine kinase domain and a tissue expression pattern having at least one receptor protein-tyrosine kinase subtype. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel pure protein-tyrosine kinase receptor subtypes useful in assays to screen various compositions which modulate these receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein tyrosine kinase; PTK receptor; PTK receptor modulation assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.3%; Score 23; DB 2; Length 54; 57.1%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse receptor protein tyrosine kinase bek.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                     2; Col 51-52; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU83035 standard; protein; 54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 12; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-00884486.
94US-00237401.
95US-00456647.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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9 VMKIADF 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003013848-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JJN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lemke GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU83035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                     Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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ABU83035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding protein tyrosine kinase sub:types - for identification of new sub:types and treatment of diseases associated with the kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTK; receptor; protein tyrosine kinase; recombinant; grafting; diagnosis; tumour; skin transplant; connective tissue; tyro-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This represents a novel receptor protein tyrosine kinase (PTK) polypeptide subtype tyro-9. The invention provides polynucleotide sequences encoding novel PTK polypeptide subtypes tyro-1 to tyro-13. The PTK subtypes are found expressed predominantly in the brain tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                            Receptor protein tyrosine kinase polypeptide, tyro-3 - preferably expressed in brain tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.3%; Score 23; DB 2; Length 54; 57.1%; Pred. No. 2e+02; 1; Indels iive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor protein tyrosine kinase (PTK) subtype tyro-9.
                                                                                                                                                                                                                                          (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Col 51-52; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW81408 standard; protein; 54 AA.
                                                                                                                                         95US-00456647.
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                                                                                                                                                                                 92US-00884486
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N-PSDB; AAV65316.
                                                                                                                                                                                                                                                                                                                          WPI; 1998-530939/45
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                                                                                                                                                                                                                                                                                  Lai CHC, Lemke GE;
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                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV55894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 54 AA;
                                                                                                                                         02-JUN-1995;
                                                                                                                                                                                 15-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JAN-1999
                                                        US5811516-A
                                                                                                 22-SEP-1998
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RESULT 84 AAW81408

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Matches

SX C C C C C X SX X B B X X B X B

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1 VMXVAEF
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                                                                                                                                                                                                                                                                                                             02-MAY-1994;
                                                                                                                                     27-JUN-2003
                                                                                                                                                                                                                                                      16-JAN-2003
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                                                                                                              ABU83034;
                                                                                                                                                                                                                                                                                                                                                 (LEMK/)
                                                                                                                                                                                                                                                                                                                                                            (LAIC/)
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Matches
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                                                                  RESULT 87
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                                                                              ABU8303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a substantially pure protein(s) or their fragments, comprising a tyrosine kinase domain and a tissue expression pattern having at least one receptor protein-tyrosine kinase subtype. The protein(s) comprises a tyrosine kinase domain and a tissue expression pattern having at least one receptor protein-tyrosine kinase subtype selected from tyro-1, tyro-2, tyro-4, tyro-5, tyro-6, tyro-7, tyro-8, tyro-10, tyro-11 and tyro-12. The protein is useful in assays to screen various compositions which modulate these protein-tyrosine kinase receptors. The presents sequence represents the amino acid sequence of a receptor protein tyrosine kinase tyro subtype
      pattern having at least one receptor protein-tyrosine kinase subtype selected from tyro-1, tyro-2, tyro-4, tyro-5, tyro-6, tyro-7, tyro-8, tyro-10, tyro-11 and tyro- 12. The protein is useful in assays to screen various compositions which modulate these protein-tyrosine kinase receptors. The presents sequence represents the amino acid sequence of a receptor protein tyrosine kinase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel pure protein-tyrosine kinase receptor subtypes useful in assays to screen various compositions which modulate these receptors.
protein(s) comprises a tyrosine kinase domain and a tissue expression
                                                                                                                                                                                                                                                                                                                                      Protein tyrosine kinase; PTK receptor; PTK receptor modulation assay;
                                                                                                                                     Gaps
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                                                                                                              Length 54;
                                                                                                                                     1; Indels
                                                                                                              79.3%; Score 23; DB 6; 57.1%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                Rat receptor protein tyrosine kinase tyro-9.
                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 12; 49pp; English.
                                                                                                                                                                                                                                          ABU83019 standard; protein; 54 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-00884486.
94US-00237401.
95US-00456647.
                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00158722,
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-401606/38
N-PSDB; ACA69713.
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VMKIADF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lai CHC;
                                                                                                                                                            1 VMXVAEF 7
                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LEMK/) LEMKE G E. (LAIC/) LAI C H C.
                                                                                                                                                                                                                                                                                                                                                                                               US2003013848-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54 AA;
                                                                                        Sequence 54 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-1998;
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                                                                                                                                                                                                                                                                                         27-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                         Rattus sp.
                                                                                                                                                                                                                                                                  ABU83019;
                                                                                                              Query Match
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88333333388
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Gaps

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Query Match Best Local Similarity Matches 4; Conserva

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel pure protein-tyrosine kinase receptor subtypes useful in assays to screen various compositions which modulate these receptors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Protein tyrosine kinase; PTK receptor; PTK receptor modulation assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a substantially pure protein(s) or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 6;
Pred. No. 2e+02;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                               Receptor protein tyrosine kinase bFGF-R.
                                                                                                                                                           ABU83034 standard; protein; 54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 12; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU78556 standard; protein; 56 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92US-00884486.
94US-00237401.
95US-00456647.
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57.1%;
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                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-401606/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lemke GE, Lai CHC;
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Best Local Similarity
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|| :|:|
9 VMKIADF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003013848-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 54 AA;
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vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic;

09730329-60ed.rag

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Composition for the design or screening of a cytoplasmic Tie2 receptor tyrosine kinase domain modulator, comprises a monoclinic or orthorhombic crystalline form of a cytoplasmic Tie2 receptor tyrosine kinase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human Tiez receptor tyrosine kinase domain polypeptide in a monoclinic, receptor tyrosine kinase domain polypeptide in a monoclinic, receptor tyrosine kinase thought to be involved in vascular development. Naturally occuring R849% and R8978 mutations in the Tiez protein have been identified in human s and have been shown to segregate with the autosomal dominant condition vascular dysmorphogenesis. The invention also comprises methods for designing modulators of the biological activity of the cytoplasmic Tiez receptor tyrosine kinase domain. The Tiez receptor tyrosine kinase domain is used to design or screen for a modulator of the kinase by rational drug design, using computer models. The present sequence represents residues 592-647 of human fibroblast growth factor receptor 1 (FGFR1). The catalytic domain of FGFR1 closely resembles that of Tie 2 and they share 45 percent sequence identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to the 3 dimensional crystal structure of the
               Tie2; Tie2K; human; crystal structure; vascular dysmorphogenesis; protein co-ordinate data; receptor tyrosine kinase; FGFR1; vascular development; fibroblast growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                             Hassell AM, Holmes WD, Shewchuk LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 579; 581pp; English.
                                                                                                                                                                                                                                  06-SEP-2001; 2001WO-US027486.
                                                                                                                                                                                                                                                                            08-SEP-2000; 2000US-0231398P.
                                                                                                                                                                                                                                                                                                                 (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                           Davis RG, Ellis BP,
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-292263/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 56 AA;
                                                                                                                                               WO200220734-A2
                                                                                                                                                                                        14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide
                                                                                                         Homo
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                                                                                                                                                                                                                                                                                                                                                                    Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; heemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovescular disorder; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; disbetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary;
                                      Gaps
                                      ö
79.3%; Score 23; DB 5; Length 56; 57.1%; Pred. No. 2.1e+02;
                                  1; Indels
                Pred. No. 2.1e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                   Human ORF20 protein, SEQ ID NO:40.
                                                                                                                                                                                                                ABP31047 standard; protein; 68 AA.
                                                                                                                                                                                                                                                                                             (first entry)
                Local Similarity 57.1
les 4; Conservative
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45 VMKIADF 51
                                                                          1 VMXVAEF 7
                                                                                                                                                                                                                                                                                             08-JUL-2002
                                                                                                                                                                                                                                                        ABP31047;
Query Match
                                      Matches
                                                                                                                                                                       RESULT 8:
ABP31047
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Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-C designated ORF (open reading frame) 1-4534, and sequences ABN75054-BBN75837 represent cDNAs encoding them. The invention also encompasses CC polypeptides at least 80% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX ct the ORFX nucleic acid sequences, vectors and host cells comprising ORFX ct the ORFX nucleic acid sequences, vectors and host cells comprising ORFX copypeptides, the recombinant production of ORFX potential, antibodies of specific for ORFX proteins, antibodies of polypeptides, methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide cartivity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide cargo of biological activities, such as cytokine, cell proteins and collisers and call proteins activity, hasmostatic activity, hasmostatic activity, hasmostatic activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, thrombolytic activity, company and antiinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins of bodily characteristics, fertility and behaviour. ORFX proteins of the proliferative disorders such as epilepsy and Alzheimer's disorders active and antibodies may be used in the treatment of cancers, corgan transplantation, disorders of tissue growth and regeneration, disorders and processes caused by viral, bacterial, corgan transplantation, disorders such as epilepsy and Alzheimer's disorders and prodens. Of tissue growth and regeneration, corgan transplantation, disorders such as epilepsy and Alzheimer's disorders and probes, in the detection of ORFX genomic sequences in genetic diagnosis, and in forensic biology. The ORFX proteins, and in drug screening. The ORFX proteins an
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                neuroprotective, antiatherosclerotic, anticoagulant, thrombolytic, cardiant, hypotensive, antithyroid, antiinflammatory, immunomodulator, dermatological, analgesic, virucide, antibacterial, fungicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis, treatment and monitoring of ORFX-associated diseases
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Pred. No. 2.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 280; 2508pp; English.
                                                                                                                                                                                                                                           24-MAY-2001; 2001WO-US017076.
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                                                                                                                                                                                                                                                                                                                                                                            Leach MD, Shimkets RA;
                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                       2002-106200/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABN75073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 MXVAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 68 AA;
                                                                                                                                                     WO200190366-A2.
                                                                                                          Homo sapiens.
                                                                                                                                                                                               29-NOV-2001
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ABM37932 standard; protein; 84 AA

ABM37932

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a cares. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. Pracnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies and downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as therefore treat P. acnes infections. The antibodies may also be used as
                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enrayme linked immunosorbent assay; dermatological; osteopathic; neuroprotectent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BIISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 4; Length 84;
Pred. No. 3.2e+02;
1; Mismatches 2; Indels
                                                                                                                                                                Propionibacterium acnes immunogenic protein #2309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitcham JL, Wang SS, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 2608; 1069pp; English
                                        AAU41413 standard; protein; 84 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                             Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS59515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 84 AA;
                                                                                                                                                                                                                                                                                                                                                    WO200181581-A2
                                                                                                                       13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-2001.
                                                                               AAU41413;
RESULT 90
                     AAU41413
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The invention relates to an isolated polymucleotide (ACF64435-ACF64733)

cucoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a comprision, antibodies against polypeptides of the invention; antibodies against polypeptide of the invention; and an isolated T cell population comprising T cells prepared to invention; and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising T cells prepared via this method; a vaccine composition (comprising T cells populations, or antigen-presenting cells that express the polypeptide; antibodies, fusion proteins, T cell populations, or carding the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a complete presenting cells that express the polypeptides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne polypeptides are useful for diagnosing, preventing or treating acne controlly protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the estimalistion of an immune response against process of the reading frame) contained within the P. acnes polymentic assay. The present candithe kit is useful for performing a diagnostic assay. The present canding frame) contained within the P. acnes polymentice date for this patent did not form part of invention. Note: The sequence data for this patent did not form part of invention. Note: The sequence data for this patent did not form part of free processions and the printed specification, but was obtained in electronic format directly free fromes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                      Propionibacterium acnes predicted ORF-encoded polypeptide #2608.
                                                                                                                                                                                   Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Persing DH, Bhatia A,
Lodes MJ, Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 2608; 1481pp; English.
                                                                                                                                                                                                              immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitcham JL, Skeiky YAW, Persi
Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-2001; 2001US-00978825.
                                                                                        (first entry)
                                                                                                                                                                                                                                                          Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-381789/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ACF64444
                                                                                                                                                                                                                                                                                                      WO2003033515-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 84 AA;
                                                                                          20-0CT-2003
                                                                                                                                                                                                                                                                                                                                                     24-APR-2003
                                            ABM37932;
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Gaps

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DB 6; Length 84; 2; Indels

Score 23; DB 6; I Pred. No. 3.2e+02; 1; Mismatches 2,

h 79.3%; Similarity 57.1%; 4; Conservative

Query Match Best Local Similarity Matches 4; Conserv

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Gaps

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4; Conservative

72 VMAIGEF 78

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1 VMXVAEF

ADJ84523

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AAF92502 to AAF92572 represent nucleic acids which encode taste transduction G-protein coupled receptors designated T2R proteins.

AAB87731 to AAB8784 represent T2R proteins, and AAB87825 to AAB87830 represent T2R proteins, and AAB87825 to AAB87830 represent T2R family consensus sequences from the present invention. The T2R proteins are taste modulators. The nucleic acids are useful as probes for the identification of taste cells, as the nucleic acids are specifically expressed in taste cells. They also serve as tools for the generation of taste topographic maps that elucidate the relationship between the taste cells of the tongue and taste sensory neurons leading to taste centres in the brain. The taste modulators are useful for pharmacological and genetic modulation of taste signalling pathways. Modulatory compounds comprising T2R proteins can therefore be used in food and pharmacoulogical industries to customise taste, for e.g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding the T2R family of G-protein coupled taste receptors, useful for identifying taste modulators that can be used in food and pharmaceutical industries to customize taste, for e.g. to decrease the bitter taste of food.
                                                                                                                                                                                                                                                                               Human, rat, mouse, T2R, taste receptor, G-protein coupled receptor, taste transduction G-protein coupled receptor; identification, tongue, taste sensory neuron, taste cell; taste modulator, food, taste signalling pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 23; DB 4; Length 90; 42.9%; Pred. No. 3.5e+02; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adler JE, Ryba N, Mueller K, Hoon M;
                                                                                                                                                                                                                                            Human T2R22 amino acid sequence SEQ ID NO:40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the bitter taste of food or drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Page 177; 249pp; English.
                                                                                                                                   Ş
                                                                                                                             AAB87752 standard; protein; 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-SEP-2000; 2000WO-US024821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-1999; 99US-00393634
22-FEB-2000; 2000US-00510332
                                                                                                                                                                                                       (first entry)
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VMAIGEF 78
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VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             WO200118050-A2.
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                       16-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zuker CS,
                                    72
                                                                                                                                                                    AAB87752;
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                                                                                                            AAB87752
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The invention describes an isolated taste transduction G-protein coupled receptor (1) e.g., T2R which is expressed in a taste cell, comprises greater than 60% sequence identity to a fully defined sequence of 335 (S1), 333 (S2), 299 (S3), 310 (S4), 224 (S5), 77 (S6), 209 (S7), 266 (S16), 165 (S10), 155 (S11), 173 (S12), 94 (S13), 115 (S14), 68 (S15), 300 (S10), 155 (S11), 173 (S12), 94 (S13), 115 (S14), 68 (S16), 300 (S10), 160 (S10), 300 (S10), 155 (S11), 173 (S12), 94 (S13), 115 (S14), 68 (S16), 300 (S10), 160 (S10), 300 (S10), 150 (S11), 170 (S4), 266 (S16), 160 (S16), 160 (S10), 160 (S10), 160 (S10), 160 (S10), 160 (S10), 160 (S11), 170 (S11), 160 (S10), 160 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated taste transduction G-protein coupled receptor e.g., T2R useful for identifying compound that modulates taste signaling in taste
                                                                                                                                                                                    taste transduction; G-protein coupled receptor; T2R; taste signaling; CAMP level; cGMP level; IP3 level; Ca(2+) level; electrical activity; human; G-protein coupled receptor; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoon M, Ryba N, Mueller K;
                                                                                                                                            Human T2R G-protein coupled receptor seg id 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; SEQ ID NO 76; 121pp; English.
ADJ84523 standard; protein; 90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               LO-FEB-2003; 2003US-00364861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00393634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zuker CS, Adler JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2004-203221/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZUKER C S.
ADLER J E.
HOON M.
RYBA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RYBA/) RYBA N. (MUEL/) MUELLER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADJ84524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VMXVAEF
                                                                                                                                                                                                                                                                                                                                 US2004038312-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-1999;
                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                           20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2004
                                              ADJ84523;
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(HOON/)
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Local Similarity

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human.

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The invention relates to a novel enterohaemorragic Bscherichia coli 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection and/or treatment of 057:H7 infection. The nucleotide sequence of the genome of Enterohaemorragic E coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterohemorragic Escherichia coli O157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell.
                                                                                                       Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyperthermophile Methanopyrus kandleri protein #431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperthermophile, protein stability enhancement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 7; I
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; SEQ ID NO 1692; 2067pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM25825 standard; protein; 123 AA.
                                                                                                                                            enterohaemorragic; anti-bacterial
                                                                                                                                                                                                                                                                                                          24-JAN-2002; 2002JP-00015959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.3%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAR-2003; 2003WO-US006664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-2002; 2002US-0380423P.
16-SEP-2002; 2002US-0410974P.
                                                                                                                                                                                                                                                                                                                                                 24-JAN-2001; 2001JP-00112010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein activity enhancement
                                                                                                                                                                                      Escherichia coli, 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 71.4.
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                                                                                                                                                                                                                                                                                                                                                                                      (UYTS-) UNIV TSUKUBA
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-451640/43
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66 VMYVAKF 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003076575-A2.
                                                                                                                                                                                                                           JP2002355074-A.
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14-MAY-2002;
                                                                  04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-2004
                                                                                                                                                                                                                                                                  10-DEC-2002
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                          ADC01644;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention is related to a novel method of identifying a compound that modulates the activity of a TIR or T2R taste receptor. The method comprises providing a eukaryotic cell that expresses a functional TIR or T2R taste receptor and a G protein that couples to it, contacting the eukaryotic cell with a compound and identifying whether the compound modulates the activity of TIR or T2R expressed by the eukaryotic cell based on its effect on MARK activity, CAMP accumulation or adenylyl cyclase activity. The method is used to identify a compound that blocks or bitter taste associated with a particular T2R activator or that blocks or chances unami taste elicited by a compound that activates the TIRZ/TIR3 (umani) taste receptor or sweet taste elicited by a compound that activates the TIRZ/TIR3 (sweet) taste receptor. The method is useful in identifying a compound that modulates the activity of a TIR or T2R taste receptor. The present sequence is that of a human T2R taste receptor creceptor. The present sequence is that of a human T2R taste receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a compound that modulates the activity of a T1R or T2R taste receptor by assaying the effect of the putative modulatory compound on MAPK activation, cAMP accumulation or adenylyl cyclase activity in the
                                                                                                                                                                                                                                                                                   12R, taste receptor; G protein; modulatory compound; MAPK activity; accumulation; adenylyl cyclase; bitter; taste; umami; sweet; T2R22;
                                                                                                                                                                                                                                         Taste receptor modulation-related human T2R22 protein sequence SeqID40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.3%; Score 23; DB 8; Length 90; 42.9%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 40; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu H;
                                                                                                                   ADR29101 standard; protein; 90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brust P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-FEB-2003; 2003US-0444172P.
26-MAR-2003; 2003US-0457318P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-2004; 2004WO-US002987
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                   TIR; T2R; taste receptor; cAMP accumulation; adenyly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ozeck M,
        :::|||
11 ILAIAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-604341/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SENO-) SENOMYX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILAIAEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                       WO2004069191-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eukaryotic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 90 AA;
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                    04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Servant G,
                                                                                                                                                               ADR29101;
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ADR29101
LID ADR3
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Gaps

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(FIDE-) FIDELITY SYSTEMS INC

ADC01644 standard; protein; 112 AA.

RESULT 95 ADC01644 ID ADC01

Matches

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Length 112; 1; Indels

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                                                                                                                                                                                                             hyperthermophile Methanopyrus kandleri, the invention also comprises the complete genome from Methanopyrus kandleri. The Methanopyrus kandleri proteins of the invention are useful for enhancing the stability and/or activity of other proteins. The Methanopyrus kandleri genome is useful in a variety of diagnostic and analytical methods. The present amino acid sequence represents a Methanopyrus kandleri protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to Enterococcus faecalis polynucleotides and bolypetides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for
                                                                                                New isolated nucleic acids encoding any of about 1700 Methanopyrus kandleri proteins, and the encoded proteins, useful as a medicaments or as diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid comprising a sequence encoding an Enterococcus fecalis polypeptide, useful for preparing a composition for diagnosing or treating E. fecalis infection.
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                invention comprises the amino acid sequence of proteins from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis infection; transcription regulatory element;
                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                  79.3%; Score 23; DB 7; Length 123; 66.7%; Pred. No. 4.9e+02; ive 1; Mismatches 1; Indels
                              Pavlova N, Kozyavkin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 3642; 193pp; English.
                                                                                                                                                                  Claim 31; SEQ ID NO 431; 1023pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               faecalis polypeptide #237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH85757 standard; protein; 132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00134000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                              Pavlov A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis.
                                                        WPI; 2003-748383/70.
N-PSDB; ADM27081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-895394/82.
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                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                                                                               2 MXVAEF 7
(MALY/) MALYKH A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADH82352
                                                                                                                                                                                                                                                                                                                       Sequence 123 AA;
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MTIAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibacterial
                            Slesarev AI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                The
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ADH85757
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This invention describes a novel protein conjugate (I) comprising at least 1 functional region (FR) at any position in the sequence of a carrier protein (II) to form a capsid three-dimensional structure of the Lumazine synthase (LS) type, such that the outer periphery is covalently invention also describes (I) a hetero-oligomeric protein conjugate (Ia) comprising either a mixture of at least 2 comprising either a mixture of at least 1 comprising either a mixture of at least 1 configuration of the components optionally covalently linked by chemical treatment; configuration of (I) or of at least 1 (I) that lacks FR, with the components optionally covalently linked by chemical treatment; configuration of (I); (4) a DNA (III) that encodes (I); (5) LS from preparation of (I); (4) a DNA (III) that encodes (I); (5) LS from Bacillus subtilis with Cys 33 and/or Cys139 replaced by Ser; (6) DNA (III) encoding LS from Aquifex aeolius which is codon-optimized for expression in a recombinant Escherichia coli strain; (7) a chimeric protein (CP) comprising amino acids (aa) 1-60 from LS of B. subtilis and can = 61-154 from LS of A. aeolius for use as (II); and (B) pharmaceutical compositions and vaccines containing (I) and (Ia). The products of the invention have cycostatic, antiviral and antibacterial activity and can be used in a vaccine or for gene therapy. (I) are used as pharmaceuticals
                                                                                                                                                                                                                                                                   ö
producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector comprising the nucleic acid and a call comprising the recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Enterococcus faecalis infection. This sequence represents an E. faecalis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lumazine synthase; capsid; cytostatic; antiviral; antibacterial; vaccine; gene therapy; immunotherapy; biosensor; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein conjugate based on lumazine synthase as carrier, useful e.g. for vaccination and immunotherapy, contains many functional molecules attached to outside of the carrier.
                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                          Length 132;
                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaeoglobus fulgidus lumazine synthase protein.
                                                                                                                                                                                                                      79.3%; Score 23; DB 7; I 57.1%; Pred. No. 5.2e+02; ive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB10816 standard; protein; 143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 8; 180pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-2000; 2000WO-EP001899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fischer M, Bacher A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-572230/53.
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9 LMDIAEF 15
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                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACH/) BACHER A.
                                                                                                                                                                                                                                                                                                                 1 VMXVAEF
                                                                                                                                                                                 Sequence 132 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-1999;
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                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                   Matches
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AAB10816
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              tumors) and in vaccine, including multivalent vaccines, against bacterial or viral infections, to produce diagnostic or therapeutic antibodies, for selections, to produce diagnostic or therapeutic antibodies, and for preparation of protein libraries. (I) may also be used as blosensors and for diagnosis, e.g. of tumors. Genes that encode (I) are useful in DNA vaccines and for preparation of plant-based oral vaccines. (I) can contain many FR (same or different) at the surface of a spherical particle (LS comprises 60 subunits that assemble into an icosahedron). The large number of FR may increase sensitivity in immunoassays and the efficiency of immunotherapy agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Bseudomonas aeruginosa and Enterococcus facalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify
 for immunotherapy of human immune deficiency virus infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr GJ;
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prokaryotic cellular proliferation protein; antibiotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotides for the identification and development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                             79.3%; Score 23; DB 3; Length 143; 83.3%; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis cellular proliferation protein #39.
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                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU33403 standard; protein; 150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0191078P.
2000US-0206848P.
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27-NOV-2000; 2000US-0253625P.
22-DEC-000; 2000US-025731P.
16-FEB-2001; 2001US-0269308P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen KL,
                                                                                                                                                                                                                                                            Local Similarity 83.3
hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu HH;
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                                                                                                                                                                                                                                                                                                                                                 MVVAEF 13
                                                                                                                                                                                                                                                                                                               2 MXVAEF 7
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                                                                                                                                                                                                           Sequence 143 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2000;
23-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001.
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                                                                                                                                                                                                                                                                                Matches
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AAU33403
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              antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antiense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
 to express these proteins, and to obtain
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention is related to a Lactococcus lactis nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
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                                                                                                                                                                                                                          Length 150;
                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                       Score 23; DB 4;
Pred. No. 6e+02;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; SEQ ID NO 1794; 2504pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                 ABB55092 standard; protein; 162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis protein aroK.
proteins used in proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                          79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lactis and related species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis; IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
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                                                                                                                                                                                                                                                                                                                           LMDIAEF 46
                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                             1 VMXVAEF 7
                                                                                                                                                                                          Sequence 150 AA;
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16-MAY-2002
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Matches
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 8X888888888X8
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DB 5; Length 162;

Score 23; DB 5; I Pred. No. 6.5e+02;

79.3%;

Query Match Best Local Similarity

0;

0; Gaps

Matches 4; Conservative 1; Mismatches 1; Indels

Qy 2 MXVABF 7

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Db 37 MTIAEF 42

Search completed: June 13, 2005, 13:56:04
Job time: 126 secs

Sequence:

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S-08-885-418-4
(S-09-252-991A-28422
(S-09-270-767-43247
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S-09-134-001C-4257
S-09-252-991A-31250
S-08-673-789-11
US-09-270-767-47506
US-08-701-191A-13
US-09-664-526-13
US-08-701-191A-31
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-09-134-001C-5567
-08-701-191A-3
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APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Doane, Minh Tam
APPLICANT: Power, Michael
APPLICANT: Tatsuno, Gwen
APPLICANT: Tatsuno, Gwen
APPLICANT: Mang, Jaw
APPLICANT: Mang, Shuwen
APPLICANT: Mang, Shuwen
APPLICANT: Michael
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OTHER INFORMATION: Description of Artificial Sequence: Peptide
OTHER INFORMATION: inhibitor P3-P4' XD-V
PEATURE:
                                   ATTLE OF INVENTION: Beta-Secretase Enzyme Compositions and TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and TITLE OF INVENTION: Methods; FILE REPERENCE: 228-US-NEWG2; CURRENT FILING DATE: 2000-11-28; PRIOR APPLICATION NUMBER: US/99/71-28; PRIOR APPLICATION NUMBER: 60/119,571
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR APPLICATION NUMBER: 60/119,172
PRIOR PELLING DATE: 1999-02-10
PRIOR PELLING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
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CTHER INFORMATION: Xaa is hydroxyethylene or statine US-09-724-566A-78
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PCT-US95-04681-19
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US-09-908-855-15
US-07-821-716-2
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US-08-855-910-2
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US-08-924-376-2
US-08-685-212-2
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Patent No. 6627739
GENERAL INPORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Gurigbal
APPLICANT: Boane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tateuno, Gwen
APPLICANT: Tateuno, Gwen
APPLICANT: Tateuno, Gwen
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US-09-724-566A-78
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Gaps

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APPLICANT: Tung, Jay
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: WacConloque, Lisa
APPLICANT: WacConloque, Lisa
TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
TURRENT APPLICATION NUMBER: US 60/114,408
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: US 60/119,571
PRIOR APPLICATION NUMBER: US 60/119,571
PRIOR APPLICATION NUMBER: US 60/119,571
PRIOR PILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 81
LENGTH: 8
"WUNE: DPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Bliot
APPLICANT: Adler, Jon Bliot
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the United States of America
APPLICANT: Department of the United States of America
APPLICANT: Department of Health and Human Services
FILLE REFERENCE: 02307E-098000US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Xaa is hydroxyethylene or statine US-09-471-669A-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 02307E-098000US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 80
LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 80, Application US/09393634
Patent No. 6558910
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US-09-393-634-80
  Power, Michael
Sinha, Sukanto
Tatsuno, Gwen
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Best Local Similarity 100.
Matches 7; Conservative
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NAME/KEY: MOD_RES
LOCATION: (4)
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US-09-393-634-80
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APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: WacConlogue, Lista
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NENC2
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-06-15
NUMBER OF SOI IN NOS: 104
SOUTHARE: FRAUSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.1%; Score 27; DB 4; Length 8; 100.0%; Pred. No. 4.1e+05; rive 0; Mismatches 0; Indels
                                                                                                                                                      0; Indels
                                                                                                        Length 7;
LOCATION: (3) 7. OTHER INFORMATION: Xaa is hydroxyethylene or statine US-09-471-669A-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa is hydroxyethylene or statine
US-09-724-566A-81
                                                                                                  93.1%; Score 27; DB 4; L. 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Peptide inhibitor P4-P4' XD-V
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Anderson, John P.
APPLICANT: Basi, Guriqbal
APPLICANT: Boane, Mith Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 81, Application US/09471669A
Patent No. 6830918
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6830918mand
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; Patent No. 6627739
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ORGANISM: Artificial Sequence
                                                                                   Query Match
Best Local Similarity 100.°
"...hes 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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VMXVAEF 7
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US-09-471-669A-81
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LENGTH: 8
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DEPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REPRENCE: PATHOD-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 1090-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR PLING DATE: 1998-06-30
PRIOR PLING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1999-0-12
PRIOR FILING DATE: 1999-07-02
SEQ ID NOS: 5322
SEQ ID NOS: 5322
LENGTH: 335
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            TITLE OF INVENTION: WXXCOCCUS xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
LENGTH: 188
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Patent No. 6413521
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: Helminth Parasite Antigen with
TITLE OF INVENTION: Aminopeptidase-like Activity
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEB: Barbara G. Ernst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-583-110-5099
; Sequence 5099, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                               h 82.8%;
Similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                      ; ORGANISM: Myxococcus xanthus US-09-902-540-14932
Wiegand, Roger C.
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Best Local Similarity 71.4
Thes 5; Conservative
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APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7260
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Patent No. 6617156

GENERAL INFORMATION:
FILL GRINGHATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILLE DEPERENCE: 032796-032

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR PILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PATENTIN Version 3.1
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89;
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69;
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Pred. No. 69;
0; Mismatches
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Pred. No. 8
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Patent No. 683347
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
                                                                                                                                                   ; Sequence 7260, Application US/09543681A ; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.2%;
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85.7%;
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US-09-543-681A-7260
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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286 VMVVAEF 292
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112 VLSVAEF 118
                                     1 VMXVAEF 7
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                VMXVAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM:
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JOANNA JANE
SUSAN ELIZABETH
RECOMBINANT DNA MOLECULES ENCODING
AMINOPEPTIOASE ENZYMES AND THEIR USE IN THE PREPARATION OF
VACCINES AGAINST HELMINTH INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECOMBINANT DNA MOLECULES ENCODING
AMINOPEPTIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
VACCINES AGAINST HELMINTH INFECTIONS
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Pred. No. 8.8e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,844A
FILING DATE: 09-JAN-1995
CLASSIFICATION NUMBER: US/08/335,844A
FILING APPLICATION NUMBER: US/08/345,844A
FILING DATE: 06-JAN-1995
FILING DATE: 06-MAY-1993
PROR APPLICATION NUMBER: GB 9209936
FILING DATE: 08-MAY-1992
ATTONNEY/AGENT INFORMATION:
NAME: WALKER, BALDARA W.
REGISTRATION NUMBER: 35,400
                                                                                                                                                                     ADDRESSEE: Rothwell, Figg, Ernst & Kurz STREET: Suite 701-E, 555 Thirteenth St., N.W CITY: Washington CATAE: D. C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/09129366

Sequence 24, Application US/09129366

Patent No. 6534638

GENERAL INFORMATION:
APPLICANT: GRAPHAM, MARGARET
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: MUNN, SUGAN ALBERT
APPLICANT: MUNN, SUGAN ELIZABETH
TITLE OF INVENTION: RECOMBINANT DNA MY
TITLE OF INVENTION: AMINOPEPTIDASE ENZ
TITLE OF INVENTION: VACINES AGAINST H
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROthwell, Figg. Front
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1181-223A
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET UNBER: 11
TELECOMMUNICATION:
TELEPHONE: (202)783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 972 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (202) 783-6031
                      APPLICANT: NEWTON, SUSARITILE OF INVENTION: AMINITLE OF INVENTION: AMINITLE OF INVENTION: VACCINUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-335-844A-24
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: ||||
542 VISVAEF 548
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Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION UNMER: US/09/134,001C
CURRENT PELING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4831
LENGTH: 927
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83.3%; Pred. No. 8.4e+02;
.ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.8%; Score 24; DB 4; Length 620; 71.4%; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,670
FILING DATE: 26-UN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Errek Barbara G.
REGISTRATION NUMBER: 1811-0232
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-335-844A-24

Sequence 24, Application US/08335844A

Fatent No. 6066533

GENERAL INFORMATION:
APPLICANT: GRAHAM, MARGARET
APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MINN, EDWARD ALBERT
APPLICANT: MINN, EDWARD ALBERT
APPLICANT: KNOX, DAVID PATRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                          40:
     Floppy disk
                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 620 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83...
S. Conservative
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: [|[|
203 VISVAEF 209
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US-09-134-001C-4831
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        Sequence 18, Application US/08456647B
Patent No. 5811516
GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/456,647B
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-456-647B-46

Sequence 46, Application US/08456647B

Sequence 10. 5811516

GENERAL INFORMATION:
APPLICANT: Lemke Ph.D et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 2;
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla
                                                                                                                                                               E: Fish & Richardson P.C.
4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
FRICK THORE DATE: 02-MAY-1994
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REGISTRATION NUMBER: 31,678
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 54 amino acids
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                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 VMKIADF 15
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Best Local Similarity
                                                                                                                                                                                                              La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VMXVAEF
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                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                       ð
US-08-456-647B-18
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                                                                                                                                                                                                                                     STATE:
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Facence 8879, Application US/09489039A
Facence 8879, Application US/09489039A
Facence 8879, Application US/09489039A
GENERAL INFORMATION:
APPLICANT: Gary Brecon et. al
APPLICANT: Gary Brecon et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 4; Length 972;
Pred. No. 8.8e+02;
1; Mismatches 1; Indels
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 05-AUG-1998
CLASSIFICATION: 435
                                                                                                                                                                                               PULABSLIFLATION
PULABSLIFLATION
PULABLE
APPLICATION NUMBER: US 08/335,844
FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB93/00943
FILING DATE: 06-MAY-1993
PRIOR APPLICATION NUMBER: GB 920936
FILING DATE: 08-MAY-1992
APPLICATION NUMBER: GB 920936
FILING DATE: 08-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BATBATA G.
REFERENCE/DOCKET NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1181-241A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 24:
SEQUENÇE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 972 amino acids
amino acid
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Best Local Similarity 72.3.
اتاب 5، Conservative
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Best Local Similarity 71.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542 VISVAEF 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            779 VMKVAQF 785
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US-09-489-039A-8879
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Patentin Release #1.0, Version #1.25

SOFTWARE:

RESULT 15

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79.3%; Score 23; DB 2; Length 54; 57.1%; Pred. No. 72; 1; Indels ive 2; Mismatches 1; Indels
                                                                                                                                                                                  Score 23; DB 2; Length 54;
Pred. No. 72;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 18, Application US/08237401A
; Patent No. 5837448
; GENERAL INFORMATION:
; APPLICANT: Lember Ph.D. et al., Greg E.
; TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNIE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN BRIESE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,401A
FILING DATE: 02-MAY-1994
CLASSIFICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A.
REFERENCE/DOCKET NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
RELECHOME: (619) 678-5099
INFORMATION FOR SEQ ID NO: 18:
SEQUIENCE CHARACTERISTICS:
LENGRACIENCE CHARACTERISTICS:
LENGRACIAN CALLERING SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 19
US-08-237-401A-46
; Sequence 46, Application US/08237401A
; Setnent No. 5837448
; GENERAL INFORMATION:
                             LENGTH: 54 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                      79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 amino acids
                                                                                                                                                                                    Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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             SEQUENCE CHARACTERISTICS
                                                                                                ) TOPOLOGY: linear
) MOLECULE TYPE: protein
US-08-456-647B-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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9 VMKIADF 15
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9 VMKIADF 15
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Best Local Similarity
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US-08-237-401A-18
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Pred. No. 72;
2; Mismatches 1; Indels
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US-08-456-647B-47

is Sequence 47, Application US/08456647B

is Patent No. 5811516

is GENERAL INFORMATION:

APPLICANT: Lemke Ph.D. et al., Greg E.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: La Jolla

CITY: La Jolla

STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT: 02-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/POCKET NUMBER: 31,678
REFERENCE/COMMUNICATION INFORMATION:
TELEBEHONE: 6199 678-5070
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,647B
FILING DATE: 0.2-UN-1995
CLASSIFTCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/237,401
FILING DATE: 0.2-MAY-1994
PRIOR APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 07251/007002
TELEPHONE: (619) 678-5079
TELEPHONE: (619) 678-5079
TELEPHONE: (619) 678-5099
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ATTORNEY ELEVANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || :|:|
9 VMKIADF 15
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Gaps

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Sequence 1355, Application US/09248796A

Sequence 16156, Application US/09248796A

Patent No. 6747137

GRNERAL INFORMATION:

APPLICANT: Keith Meinstock et al

APPLICANT: Keith Meinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR PEPLION NUMBER: US 60/074,725

PRIOR PELING DATE: 1998-02-13

PRIOR PELING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16636

LENGTH: 74
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The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services
VENTION: SF. a No. 6558910el Family of Taste Receptors
NCE: 02307E-098000US
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Pred. No. 72;
2; Mismatches 1; Indels
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Pred. No. 1e+02;
0; Mismatches 2; Indels
                                           NAME: Haile Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REPERENCE/DOCKET NUMBER: 07251/007001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEPAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 76, Application US/09393634
; Patent No. 6558910
                                                                                                                                                                                                                                                                 not relevant
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Adler, Jon Elliot
Ryba, Nick
Mueller, Ken
Hoon, Mark
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
    FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: not
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9 VMKIADF 15
                                                                                                                                                                                                                                                                                          linear
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FILE REFERENCE: 023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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Pred. No. 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESCEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,401A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              APPLICATION UNBER: US/08/237,401A
PILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PLING APPLICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Halle Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 38,347
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 20
US-08-237-401A-47
; Sequence 47, Application US/08237401A
; Patent No. 5837448
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 54 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.1
....hes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-237-401A-46
                                                                                                                                                                                               ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || :|:|
9 VMKIADF 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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ZIP: 92037
                                                                                                                                                                               COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1999-08-13
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PAtentin version 3.1
SEQ ID NO 3642
LENGTH: 132
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Patent No. 6703491

GENERAL INFORMATION

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 41416

LENGTH: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.3%; Score 23; DB 4; Length 132; 57.1%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                          79.3%; Score 23; DB 4; Length 90;
42.9%; Pred. No. 1.2e+02;
tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SEQ ID NO 76
LENGTH: 90
                                                                                                                                                                                                                                                                     i LOCATION: (1)...(90)
i OTHER INFORMATION: Xaa = any amino acid
US-09-393-634-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3642, Application US/09134000C; Patent No. 6617156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                      OTHER INFORMATION: human GR22
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.3
Best Local Similarity 42.9
Matches 3; Conservative
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Matches 4; Conservative
                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: :|||
11 ILAIAEF 17
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9 LMDIAEF 15
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US-09-134-000C-3642
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US-09-270-767-41416
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DB 4;

Score 23;

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Sequence 34950, Application US/09270767

Sequence 34950, Application US/09270767

Sequence 34950, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

FITUE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 34950

LENGTH: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50167, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 50167
LENGTH: 203
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; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.3%; Score 23; DB 4; Length 203; 83.3%; Pred. No. 2.9e+02; ive 0; Mismatches 1; Indels
                        Indels
57.1%; Pred. No. 2.8e+02; ative 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-34950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-50167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.3
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                      :| ||:|
99 IMDVADF 105
Best Local Similarity
                                                           1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 MHVAEF 21
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US-09-270-767-50167
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                      Matches
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Sequence 15, Application 05/0303250

| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: MOHAMMADI, MOCSA
| APPLICANT: MOHAMMADI, MOCSA
| APPLICANT: MOHAMMADI, MOCSA
| APPLICANT: HUBBARD, STEVAN R. |
| TITLE OF INVENTION: CRYSTALES OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN TITLE OF INVENTION: RECEPTOR TYROSINE KINASES |
| FILE REFERENCE: 038602/0847 |
| CURRENT APPLICATION NUMBER: 09/188, 809 |
| PRIOR FILING DATE: 1996-11-09 |
| PRIOR FILING DATE: 1996-11-09 |
| PRIOR FILING DATE: 1996-11-09 |
| PRIOR FILING DATE: 1996-08-21 |
| NUMBER OF SEQ ID NOS: 41 |
| SEQ ID NO 13 |
| LENGTH: 299 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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19.08-701-191A-31
Sequence 31, Application US/08701191A
Sequence 31, Application US/08701191A
Sequence 31, Application US/08701191A
APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
ITILE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 4; Length 299;
Pred. No. 4.5e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.3%; Score 23; DB 2; I 57.1%; Pred. No. 4.5e+02; iive 2; Mismatches 1;
                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 227/088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFA: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09664526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                        LENGTH: 299 amino acids
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Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                          CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 VMKIADF 178
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172 VMKIADF 178
                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: siz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VMXVAEF 7
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Best Local Similarity
Matches 4; Conserv
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Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
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US-00-701-191A-13

iSequence 13, Application US/08701191A

iPatent No. 5943428

GENERAL INFORMATION:

APPLICANT: Moosa Mohammadi, Joseph Schlessinger,

APPLICANT: Low Normania Normania Library

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon

STREET: Suite 4700

CITY: Los Angeles

STREET: Suite 4700

CITY: Los Angeles

STREET: Suite 4700

CITY: Los Angeles

STREET: Suite 8700

CITY: Los Angeles

STREET: Suite 8700

MEDIUM TYPE: S. Diskette, 1.44 Mb

MEDIUM TYPE: S. Polskette, 1.44 Mb
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Pred. No. 4.2e+02;
2; Mismatches 1; Indels
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Pred. No. 4.2e+02
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FILE REFERENCE: File Reference: 7326-094 CURRENT APPLICATION NUMBER: US/09/270,767 UNERRY FILING DATE: 1999-03-17 NUMBER OF SEQ ID NOS: 62517 SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: PESSESS for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
                                                                                                                                                                 TYPE: PRT; ORGANISM: Drosophila melanogaster
US-09-270-767-32289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
, ORGANISM: Drosophila melanogaster
US-09-270-767-47506
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57.1%;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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US-09-270-767-47506
                                                                                                                  SEQ ID NO 32289
LENGTH: 285
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LENGTH: 285
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Similarity 57.1%;
4; Conservative
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181 VMKIADF 187
                 Query Match
Best Local Similarity
Matches 4; Conserv
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STRANDEDNESS: 813
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GENERAL INFORMATION:
APPLICANT: WOHADMADI, MOCSA
APPLICANT: WOHADMADI, MOCSA
TAPLICANT: WOHADBARD: CYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: CYSTALS OF THE TYROSINE KINASES
FILE REPERENCE: 038602/0847
CURRENT APPLICATION WOMBER: US/09/664,526
CURRENT FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR APPLICATION NUMBER: 09/189,809
PRIOR APPLICATION NUMBER: 09/101,191
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 31
LENGTH: 300
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    OF NON-INSULIN RECEPTOR TYROSINE KINASE
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Pred. No. 4.5e+02;
                                                   CORRESPUNDENCE ADMINISTREET

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BCACAGE
COMPUTER: PREAESEQ for Windows 2.0
SOFTWARE: FastESEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
FILING DATE: AUGUST 21, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 227/088
FILING DATE: RICHARD J.
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
RELEPHONE: (213) 955-0440
FILEPHONE: (213) 955-0440
FILEPHONE CHARACTERISTICS:
FUNDTH: 900 SEQUENCE CHARACTERISTICS:
FUNDTH: 900 SEGUENCE CHARACTERISTICS:
FUNDTH: 900 SEGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 32
US-09-664-526-31
; Sequence 31, Application US/09664526
; Detent No. 6682921
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.3%;
57.1%;
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
TITLE OF INVENTION: OF NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-09-664-526-31
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172 VMKIADF 178
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| Decey
| Decey Watch
| Decey
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Length 310;

Score 23; DB 2; I Pred. No. 4.6e+02; 2; Mismatches 1;

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Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative ;
      h MOLECULE TYPE: protein
h HYPOTHETICAL: NO
US-08-701-191A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                          181 VMKIADF 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
APPLICANT: SCHLESSINGER, JOSEPH
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847
CURRENT APPLICATION NUMBER: US/09/664,526
CURRENT FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR PILING DATE: 1998-11-09
PRIOR FILING DATE: 1996-08-21
RINBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN VOICE: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
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Patent No. 5942428
CENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: Moose Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOWAIN
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 4; Length 309;
Pred. No. 4.6e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPACTABLE
COMPUTER: IBM COMPACTABLE
COPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASESE (FOR WINDOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
FILING DATE: AUGUST 21, 1996
CLASSIFICATION S30
PR.OR APPLICATION DATA:
- APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/088
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                            79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.1
Best Local 4; Conservative
                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VMKIADF 187
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US-08-701-191A-1
                                                                                                                                                                                                                                                                                                         LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                      US-09-664-526-9
                                                                                                                                                                                                                                                                                   SEQ ID NO 9
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BESULT 36

US-08-701-191A-6

US-08-701-191A-6

SEQUENCE (A PAPA)Cation US/08701191A

Patent No. 5942A-6

GENERAL INFORMATION:

JAPLICANT: and Stevan R. Habbard

JITLE OF INVERTION: CRYSTALS OF THE TYROSINE KINASE DOWAIN

TITLE OF INVERTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE

NONESCEE: Lyon & Lyon

STREET: 613 West Fifth Street

STREET: 614 West Fifth Street

STREET: 614 West Fifth Street

STREET: 615 West Fifth Street

STREET: 614 West Fifth Street

STREET: 615 West Fifth Street

STREET: 614 West Fifth Street

STREET: 615 West Fifth Street

STREE
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GENERAL INFORMATION:
APPLICANT: MCTIGUE, MICHELE A.
APPLICANT: MCTIGUE, MICHELE A.
APPLICANT: MCKERSHAM, JOHN A.
APPLICANT: SHOWALTER, RICHARD
APPLICANT: PRASST, CAWRAN V.
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: GENERICK, BARBARA
APPLICANT: GENERICK, BARBARA
APPLICANT: KAN, CHEN-CHEN
APPLICANT: WROCZKOWSKI, BARBARA
APPLICANT: WILAFRANCA, J. BRNEST
APPLICANT: VILLAFRANCA, J. BRNEST
APPLICANT: VILLAFRANCA, J. BRNEST
APPLICANT: WINSHITON: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND
TITLE OF INVENTION: MODIFICATIONS OF USE
TITLE OF INVENTION: WETHODS OF USE
TITLE OF INVENTION: WETHODS OF USE
CURRENT APPLICATION NUMBER: US/09/390,326
CURRENT APPLICATION NUMBER: US/09/390,226
SOFTWARE: PLEING DATE: 1999-09-07
SOFTWARE: PLEING DATE: 100S: 12
SOFTWARE: PAEGIL NOS: 12
SOFTWARE: PAEGIL NOS: 12
SOFTWARE: PAEGIL NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.3%; Score 23; DB 2; Length 310 Best Local Similarity 57.1%; Pred. No. 4.6e+02; Matches 4; Conservative 2; Mismatches 1; Indels
MEDIUM TYPE: 3.5 CONTROLL
MEDIUM TYPE: 4.5 COMPUTER: BENDEREL
COMPUTER: IBM Compactible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASSES for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
FILING DATE: AUGUST 21, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/088
TELEPHONE: (213) 489-1600
TELEPHONE: CAAACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEBNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09390326 Patent No. 6316603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || :|:|
181 VMKIADF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VMXVAEF 7
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-390-326-7
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           GENERAL INFORMATION:

APPLICANT: MOOSA MOHAMMADI, JOSEPH SCHIESSINGER,

APPLICANT: MOOSA MOHAMMADI, JOSEPH SCHIESSINGER,

APPLICANT: MOOSA MOHAMMADI, JOSEPH SCHIESSINGER,

TITLE OF INVENTION: CRYSTALS OF THAT

TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: LyON & LyON

STREET: SAIN WEST FIFTH Street

STREET: SAIN WEST FIFTH STREET

STREET: SAIN WEST FIRM

CONDITY: LOS Angels

STATE: California

CONDITY: LOS Angels

STATE: 3.A. Angels

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: STORM:

MEDIUM TYPE: STORM:

MEDIUM TYPE: STORM:

MEDIUM TYPE: ANGELS

COMPUTER: IBM Compatible

OPERATIOS SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: RABABLE FORM:

APPLICATION NUMBER: US/08/701,191A

FILING DATE: AUGUST 21, 1996

FILING DATE:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/701,191A

FILING DATE:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/701,191A
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US-08-701-191A-8
; Sequence 8, Application US/08701191A
; Patent No. 5542428
; CENERAL INFORMATION:
; APPLICANT: moosa Mohammadi, Joseph Schlessinger,
APPLICANT: moosa Mohammadi, Joseph Schlessinger,
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE
; INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
; UNMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: Saite 4700
; STREET: Suite 4700
; STREET: Suite 4700
; STREET: California
; COUNTRY: U.S. Angelse
; ZIP: 90071-2066
; ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
NAME: Warburg, Richard J.
REGISTRATION UNMBER: 327/088
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFX: (7-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRAEL ANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-701-191A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || :|:|
181 VMKIADF 187
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  ; Patent No. 5942428
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MOHAWMADI, MOOSA
APPLICANT: MCHARMADI, MCNSTALLS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
CURRENT APPLICATION NUMBER: US/09/664,526
CURRENT APPLICATION NUMBER: 09/188,809
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATCHIN VEY: 2.1
SOFTWARE: PATCHIN VEY: 2.1
                    Patent NO. 6882921
GENERAL INFORMATION:
APPLICANT: MCHAMMADI, MCOSA
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALES OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847
CURRENT APPLICATION NUMBER: 08/0864,526
CURRENT FILING DATE: 1200-09-18
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: 08/701,191
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 7: 2.1
LENGTH: 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.3%; Score 23; DB 4; Length 310; Best Local Similarity 57.1%; Pred. No. 4.6e+02; Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.3%; Score 23; DB 4; Best Local Similarity 57.1%; Pred. No. 4.6e+02 Matches 4; Conservative 2; Mismatches
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Sequence 7, Application US/09664526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09664526
Patent No. 6682921
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Homo sapiens
US-09-664-526-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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181 VMKIADF 187
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US-09-939-833-7
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                                                                                          Sequence 1, Application US/09664526

Sequence 1, Application US/09664526

Sequence 1, Application US/09664526

GENERAL INFORMATION:
APPLICANT: MOLHAMADI.
TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
TITLE OF INVENTION: DATE: 198602.0847

CURRENT APPLICATION NUMBER: US/09/664,526

CURRENT APPLICATION NUMBER: 09/189,809

PRIOR PILING DATE: 1998-11-09

PRIOR FILING DATE: 1998-11-09

PRIOR FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 41

SOFTWARE: PATENTING NOS: 41

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Patent No. 6682921

GENERAL INFORMATION:
APPLICANT: MONDAMATION:
APPLICANT: MONDAMATION:
APPLICANT: MONDAMATION:
APPLICANT: MONDAMATION:
APPLICANT: HOUBARD, STEVAN R.
TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847

CURRENT PAPLICATION NUMBER: 09/98,809
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR APPLICATION NUMBER: 09/189
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 6
LENGTH: 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-664-526-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || :|:|
181 VMKIADF 187
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181 VMKIADF 187
181 VMKIADF 187
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US-09-664-526-6
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US-09-664-526-7
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Matches

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Gaps

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RESULT 47
US-08-278-089A-17
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| Sequence 7, Application US/09506906
| Patent No. 6784285
| GENERAL INFORMATION:
| APPLICANT: MCIGUE, MICHELE A. APPLICANT: WICKERSHAM, JOHN A. APPLICANT: WICKERSHAM, JOHN A. APPLICANT: PRARST, CAMEAN V. APPLICANT: PRARST, CAMEAN V. APPLICANT: PRARST, CAMEAN V. APPLICANT: PRARST, CAMEAN V. APPLICANT: TEMPCYZK-RUSSEL, ANNA APPLICANT: TEMPCYZK-RUSSEL, ANNA APPLICANT: TEMPCYZK-RUSSEL, ANNA APPLICANT: APPLICANT: WICKERST, MICHAEL R. APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: WICKERST, APPLICANT: APPLICANT: WICKERST, APPLICANT: APPLICANT: NUMBER: US/09/506,906
| TILLE REFERENCE: 1012-0016US
| TILLE REFERENCE: 1020-02-18
| PRIOR PILING DATE: 2000-02-18
| PRIOR PILING DATE: 1999-09-07
| SOFTWARE: PATENTIN VET: 2.0
| SSOFTWARE: PATENTIN VET: 2.0
| SSOFTWARE: PATENTIN VET: 2.0
| SSOFTWARE: PATENTIN VET: 2.0
APPLICANT: BINKO, CHRIS
APPLICANT: SHOWALTER, RICHARD
APPLICANT: PARAST, CAMANAN V.
APPLICANT: PARAST, CANNAN V.
APPLICANT: TEMPOCZK-GUSSEL, ANNA
APPLICANT: GEHRING, MICHAEL R.
APPLICANT: MRCHAEL R.
APPLICANT: MRCHAEL R.
APPLICANT: MANACKOWSKT, BARBARA
APPLICANT: WILLAFRANCA, J. ERNEST
APPLICANT: APPELT, KGZYSZTOF
TITLE OF INVENTION: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 0125-0016US
CURRENT FILING DATE: 1099-09-07
FUNDRENT APPLICATION NUMBER: US/09/390,326
PRIOR PILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PARENTIN VET: 2.0
SSOFTWARE: PARENTIN VET: 2.0
SSOFTWARE: PARENTIN VET: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 57.3
Matches 4; Conservative
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CRGANISM: Homo sapiens
US-09-506-906-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :|:|
181 VMKIADF 187
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181 VMKIADF 187
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US-09-506-906-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-939-833-7
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Sequence 2, Application US/09664526
Patent No. 6668291
GENERAL INFORMATION:
APPLICANT: MOHAMMADI, MOCSA
APPLICANT: SCHLESSINGER, JOSEPH
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REPERENCE: 038602/0847
CURRENT APPLICATION NUMBER: US/09/664,526
CURRENT FILING DATE: 2000-09-18
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                                                                                 Sequence 2, Application US/08701191A
Patent No. 5942428
GENERAL INFORMATION:
APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.3%; Score 23; DB 2; Length 315; 57.1%; Pred. No. 4.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BEOFRAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOCTUMARE: FASTESQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
FILING DATE: AUGUST 21, 1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATCHER WALDICY, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/088
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids STRANDEDNESS: sincl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || :|:|
186 VMKIADF 192
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Breitman, Martin L.
APPLICANT: Rossant, Janet
APPLICANT: Dumont, Daniel J.
APPLICANT: Vamaguchi, Terry P.
TITLE OF INVENTION: No. 5998187el Receptor Tyrosine Kinase
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West
CITY: Coronto
                                                                                                                                                                                                                                                        Score 23; DB 1; Length 313;
Pred. No. 4.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/0818,957A
FILING DATE: 23-APR-1997
CLASSIFICATION: 435
ATTOMNEY/AGENT INFORMATION:
NAME: KURCHOW, Linda M.
REGISTRATION NUMBER: 34,911
REFERENCE/DOCKET NUMBER: 3153-212
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 361-1398
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 2; I
Pred. No. 4.7e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08838957A Patent No. 5998187 GENERAL INFORMATION:
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                          79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 313 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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159 VMKIADF 165
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Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 VMKIADF 165
                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDN
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                                                                                                                                                                     i IMMEDIATE SOURCE:
CLONE: FlgM
US-08-278-089A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: FlgM
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USO-13-3001C-5567

Sequence 5567, Application US/09134001C

Sequence 5567, Application US/09134001C

Sequence 5567, Application US/09134001C

Sequence 5567, Application US/09134001C

SEQUENCE OF THE OF INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: UNMERR: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

SEQ ID NO 5567

LENGTH: 344
                                                                                                                                                                                                      Sequence 10, Application US/09664526;
Patent No. 6682921
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MOHAMMADI, MOCSA
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847
CURRENT APPLICATION UNMBER: 09/188,809
FRIOR APPLICATION NUMBER: 09/188,809
FRIOR APPLICATION NUMBER: 09/188,809
FRIOR APPLICATION NUMBER: 09/189-11-09
FRIOR APPLICATION NUMBER: 08/701,191
FRIOR FILING DATE: 1996-08-21
NUMBER: O SEQ ID NOS: 41
SCOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
SEQ
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Pred. No. 5.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h Similarity 57.1%; Pred. No. 4.8e+02; 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 54
US-08-701-191A-3
; Sequence 3, Application US/08701191A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.3%;
Best Local Similarity 57.1%;
Matches 4; Conservative
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188 VMKIADF 194
                                                               188 VMKIADF 194
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Best Local Similarity
Matches 4; Conserv
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      1 VMXVAEF 7
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US-09-664-526-10
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US-00-701-191A-10
; Sequence 10, Application US/08701191A
; Patent No. 5942428
; GENERAL INFORMATION:
; APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: AND STATION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
STREET: California
COUNTRY: US.A.
ZIP: DOOTLESSED
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Pred. No. 4.7e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: IEM P.C. DOS 5.0
SOFTWARE: FASTSCA for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,191A
FILING DATE: AUGUST 21, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
PRIOR APPLICATION NUMBER: 09/188,809
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: 08/701,191
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 318 amino acids
                                                                                                                                                                                                                                                                                                                                                                                            79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 VMKIADF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VMXVAEF 7
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                                                                                                                                                                                                                                        LENGTH: 315
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                                                                                                               FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: protein encoded by recombinant baculovirus
US-09-664-526-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: $2052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Sequence 8, Application US/08885418
'Patent No. 5925528
'GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
'APPLICANT: Poulin, Matthew L
'TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 79.3%; Score 23; DB 1; Length 378; Similarity 57.1%; Pred. No. 5.7e+02; 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                  Length 351;
                                                                                                                                                                                                                                  Score 23; DB 4; Length 351
Pred. No. 5.3e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08070165F
Patent No. 5750365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378 amino acids
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 43210
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                            222 VMKIADF 228
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Columbus
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 56
US-08-070-165F-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-885-418-8
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APPLICANT: MCHAMALI, MCOSA
APPLICANT: MCHAMALI, MCOSA
APPLICANT: MCHAMALI, MCOSA
APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRESTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REPERENCE: 038602/0847
CURRENT PILING DATE: 1000-09-18
PRIOR PELICATION NUMBER: 09/188, 809
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
              GENERAL INFORMATION:

APPLICANT: Moosa Mohammadi, Joseph Schlessinger,
APPLICANT: and Stevan R. Hubbard
ITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
TITLE OF INVENTION: OF NON-INSULIN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 23; DB 2; Length 351; 57.1%; Pred. No. 5.3e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                           CITY: Los Augeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/701,191A FILING DATE: August 21, 1996 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327(
REFERENCE/DOCKET NUMBER: 227/(
TELECPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEFRX: (7-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/09664526
; Patent No. 6682921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 VMKIADF 228
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US-08-070-165F-4
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US-08-885-418-4
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Squence 4, Application US/08070165F

Squence 10. 5750365

GENERAL INFORMATION:

APPLICANT: Chiu, Ing-Ming

APPLICANT: Poulin, Matthew L

TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSPEN: Ing-Ming Chiu

STREET: $2052 Davis Medical Research Center, 480 West

STREET: SLOBA Avenue

CITY: Columbus

STATE: Ohio

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23, DB 2; Length 378;
Pred. No. 5.7e+02;
2; Mismatches 1; Indels
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: $2052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
CITY: Columbus
                                                                                                                                                   COMPUTER READBLE FORM:

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
FILING DATE:
CLASSIFICATION: 435
TELEPHONE: (614)-293-8093
TELEPHONE: (614)-293-8631
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 annino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAK: (614)-293-5631
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 388 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1°
Thea 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-885-418-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :|:|
197 VMKIADF 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43210
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US-08-070-165F-4
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                                                                                                                                     COUNTRY:
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RESULT 60

US-09-252-991A-28422

Sequence 28422, Application US/09252991A

Fatent No. 6551795

GENERAL INFORMATION:

APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196,136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                     Sequence 17. Application US/08885418
Fatent No. 592558
GENERAL INFORMATION:
TITUE OF INVENTION: Matthew L
TITUE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: 9th Avenue
STREET: 9th Avenue
CITY: Columbus
STATE: Olimbus
STATE: Olimbus
STATE: Olimbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.3%; Score 23; DB 2; Length 388; 57.1%; Pred. No. 5.9e+02; ive 2; Mismatches 1; Indels
79.3%; Score 23; DB 1; Length 388; 57.1%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 43210

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 388 amino acids TYPE: amino acid
Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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MOLECULE TYPE: protein
                                                                                                                         || :|:|
204 VMKIADF 210
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204 VMKIADF 210
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GENERAL INVORVATION:

GENERAL INVORVATION:

GENERAL INVORVATION:

TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides

FILE REFERENCE: P8484

CURRENT APPLICATION NUMBER: US/10/138,701

CURRENT FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: US 60/098,964

PRIOR APPLICATION NUMBER: US 60/099,861

PRIOR FILING DATE: 1998-09-01

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1998-01-05

PRIOR FILING DATE: 1999-01-05

PRIOR FILING DATE: 1999-01-05

PRIOR FILING DATE: 1997-10-20

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PATENTIN NUMBER: US 08/956,171

PRIOR FILING DATE: 1997-10-20

SEQ ID NO 22

LENGTH: 421
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Pred. No. 6.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23; DB 4; I
Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-138-701-22; Sequence 22, Application US/10138701 Patent No. 6753149; GENERAL INFORMATION:
                                                                                       Sequence 8, Application US/10138701
Patent No. 6753149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Staphylococcus aureus US-10-138-701-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Staphylococcus aureus US-10-138-701-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.5.
Local Similarity 83.5.
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 336 MHVAEF 341
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                                                                      US-10-138-701-8
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Sequence 43247, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REPRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT APPLICATION DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFUMARE: PatentIN Ver. 2.0

SEQ ID NO 43247

LENGTH: 412
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Sequence 1818, Application US/09710279

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFREENCE: PU3480US

CURRENT APPLICATION NUMBER: 06/09/710,279

CURRENT FILING DATE: 2000-11-09

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SEQ ID NO 1818
                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence
US-09-710-279-1818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.3%; Score 23; DB 4; Length 412; 71.4%; Pred. No. 6.3e+02; tive 0; Mismatches 2; Indels
                                                                                                      DB 4; Length 397;
6e+02;
                                                                                                                                            1; Indels
                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Xaa means any amino acid US-09-270-767-43247
                                                                                                        Score 23;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Drosophila melanogaster
                  LENGTH: 397
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                         Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity
The 5; Conserv?
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259 MAIAEF 264
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                                                          ; OKGAN15M: FBEUGO:
US-09-252-991A-28422
                                                                                                                                                                                                                                                                     RESULT 61
US-09-270-767-43247
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US-09-710-279-1818
SEQ ID NO 28422
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Gaps

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Gaps

2 MXVAEF 7

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Sequence 7991, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: GAIT L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DATE: 1999-0.03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7991

LENGTH: 613
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Pred. No. 9.6e+02;
2; Mismatches 1; Indels
                                           TYROSINE KINASE AND LIGAND AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 612;
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                     BSK RECEPTOR LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
             TITLE OF INVENTION: BSK RECEPTOR TITLE OF INVENTION: TYROSINE KIN TITLE OF INVENTION: USE IN DIAGNOTITLE OF INVENTION: USE IN DIAGNOTITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Acinetobacter baumannii
US-09-328-352-7991
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Best Local Similarity 57.1%;
Matches 4; Conservative
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TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.3
Best Local Similarity 71.4
Matches 5; Conservative
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USA
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Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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TITLE OF INVENTION:
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TITLE OF INVENTION:
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57.1%; Pred. No. 7.4e+02;
ive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23; DB 3; I
Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Patent No. 5814479
GENERAL INFORMATION:
APPLICANT: ZHOU, RENPING; SCHULZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31250
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 83.2
Matches 5; Conservative
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| ||||
336 MHVAEF 341
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                                                                                                       RESULT 65
US-09-134-001C-4257
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Sequence 6, Application US/08070165F

Patent No. 2750365

GENERAL INFORMATION:

APPLICANT: Chiu, Ing-Ming

APPLICANT: Poulin, Matchew L

TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Ing-Ming Chiu
STREET: $2052 Davis Medical Research Center, 480 West
STREET: 9th Avenue
CITY: Columbus
STATE: Ohio
                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Tab PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/640,029
FILING DATE: 19910111
CLASSIFICATION: 530
ATTORNEY/AGBNT INFORMATION:
NAMME: McClung, Barbara G.
ATTORNEY/AGBNT INFORMATION:
TELEPHONE: 33,113
REFERENCE/DOCKET NUMBER: CH-165
TELEPHONE: 510-601-2708
TELEPHONE: 510-601-2708
TELEPHONE: 510-601-2708
TELEPHONE: 510-655-3342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
1.FNGTH: 729 amino acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 1; I
Pred. No. 1.2e+03;
2; Mismatches 1;
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIPETCATION: 435
TELECOMUNICATION: 1070-293-8093
TELEPAN: (614)-293-5631
                       4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.3%;
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 729 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 729 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1"
....hes 4; Conservative
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      Abus...
STRET: 4500 CTTY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543 VMKIADF 549
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  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-640-029-3
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                                                                                                     US-08-471-570-10

Sequence 10, Application US/08471570

Patent No. 5750371

GENERAL INFORMATION:
APPLICANT: IGARASHI, Koichi
APPLICANT: SENCO, Masaharu
APPLICANT: WATNANAE, Tatsuya
ITITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kiefer, Michael C.
APPLICANT: Kiefer, Michael C.
APPLICANT: Valenzuela, Pablo D.T.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Growth Factor Receptor
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 1; Length 652;
Pred. No. 1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ERAPPY disk
COMPUTER: ERAPPY disk
COMPUTER: ERAPPY disk
COMPUTER: ERAPPY disk
COMPUTER: ERAPPE COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FLING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US/08/149,664
FILING DATE: 16-AUG-1991
ATFORNEY/AGENT INPORMATION:
FILING DATE: 16-AUG-1991
ATFORNEY/AGENT INPORMATION:
NAME: LINEK, ETHOST U
REGISTRATION NUMBER: 29822
REFERRENCE/DOCKET NUMBER: 29822
REFERRENCE/DOCKET NUMBER: 29822
REFERRENCE/DOCKET NUMBER: 29822
REFERRENCE/DOCKET NUMBER: 29822
RELEPHAN: (617)523-3400
TELEFPAX: (617)523-3400
TELEFRAX: (617)523-3400
TELEFRAX: CAPACTERISTICS:
SEQUINCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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US-07-640-029-3
; Sequence 3, Application US/07640029
; Patent No. 5229501
; GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 652 amino acids TYPE: amino acid
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Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-471-570-10
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523 VMKIADF 529
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53 IMELAEF 59
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RESULT 74
US-08-070-165F-10
is Sequence 10, Application US/08070165F
j Patent No. 5750365
j GENERAL INFORMATION:
j APPLICANT: Chiu, Ing-Ming
j APPLICANT: Chiu, Ing-Ming
j APPLICANT: Chiu, Ing-Ming
j APPLICANT: Chiu, Ing-Ming
j TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
i CORRESSEDNDECS: 12
j CORRESSED Ing-Ming Chiu
j STREET: S2052 Davis Medical Research Center, 480 West
j STREET: 9th Avenue
j CITY: Columbus
j STREE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.3%; Score 23; DB 1; Length 731; 57.1%; Pred. No. 1.2e+03; ive 2; Mismatches 1; Indels
                                                                                                              OPERATION SYSTEM: C-LOS/MS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,807B
FILING DATE: 29-SEP-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BARBAA G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0209.001
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 655-3542
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 731 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
                ZIP: 94608-2916
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-8093
TELEFAX: (614)-293-5631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 731 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-070-165F-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 43210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
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545 VMKIADF 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-921-807B-5
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US-08-885-418-6

i Sequence 6, Application US/08885418

i Parent No. 525528

i GENERAL INFORMATION:

APPLICANT: Chiu, Ing-Ming

ITTLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ing-Ming Chiu

STREET: S2052 Davis Medical Research Center, 480 West

STREET: S21 Avenue

STREET: Olumbus

STREET: Olumbus
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                                                                                   Length 729;
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                                                                                 79.3%; Score 23; DB 1; Length 725
57.1%; Pred. No. 1.2e+03;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.3%; Score 23; DB 2; Length 729
57.1%; Pred. No. 1.2e+03;
tive 2; Mismatches 1; Indels
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Pacent No. 5474914
GENERAL INFORMATION:
APPLICANT: SPAETE, RICHARD
TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
TITLE OF INVENTION: OF VIRAL PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
STREET: PAGE HOLLON Street - R440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (614)-293-5631
TELEPAX: (614)-293-5631
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 729 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-885-418-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                   Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-070-165F-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [|:|:|
547 VMKIADF 553
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547 VMKIADF 553
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                                                                                                                                                                    1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 73
US-07-921-807B-5
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Patent No. 6255454
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Philip, Barr J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23; DB 2; Length 731;
Pred. No. 1.2e+03;
2; Mismatches 1; Indels
   S2052 Davis Medical Research Center, 480 West
                                                                    STATE: Ohio

COUNTRY: USA

ZIP: 42310

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/885,418
FILING DATE:
CLASSIFICATION: 435

TELEPHONE: (614)-293-803

TELEPHONE: (614)-293-803

INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

**REMETH: 731 amino acids
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/439,992A
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Ling-Fong
REGISTRATION NUMBER: 36,482
REFERENCE/DOCKET NUMBER: 0165.004
TELEPHONE: 510-923-2704
TELEPHONE: 510-923-2704
TELEPHONE: 510-923-2704
TELEPHONE: 510-923-2704
TELEPHONE: 510-923-2704
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 731 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || :|:|
549 VMKIADF 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4560 Horl
CITY: Emeryville
STATE: CA
      STREET: 91...
CITY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VMXVAEF 7
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Patent No. 522528
GENERAL INFORMATION:
APPLICANT: Chiu, Ing-Ming
APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 731;
79.3%; Score 23; DB 1; Length 731; 57.1%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08441944A

Patent No. 5767250

GENERAL INFORMATION:
PAPLICANT: SPAETE, RICHARD

TITLE OF INVENTION:
TITLE OF INVENTION:
OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION

STREET: 4560 Horton Street - R440

STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUUNTER: USA

ZIP: 94608-2916

COUNTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM:

PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,944A

FILING DATE: 16-MAY-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/921,807

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: MCCLOMUNG, BARBARA G.

REGISFRATION NUMBER: 33,113

REFERENCE/DOCKET NUMBER: 0209.001

TELECOMMUNICATION INFORMATION:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.3%; Score 23; DB 1; I
57.1%; Pred. No. 1.2e+03;
                                                       2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ 1D NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 731 amino acids
TYPE: amino acid
                        Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                    || :|:|
549 VMKIADF 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545 VMKIADF 551
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                                                                                                               1 VMXVAEF 7
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                                                                                                                                                                                                                                                                RESULT 75
US-08-441-944A-5
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US-08-885-418-10
Query Match
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,944A
FILING DATE: 16-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/921,807
FILING DATE: 29-SED-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BARBARA G.
                                                                              STREET: 4560 Horton Street - R440 CITY: Emeryville STATE: CA
                                                                                                                                             COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TITLE OF INVENTION: OF VIRAL PRO
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (510) 655-3542
INPORMATION POR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 733 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: siz
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USA
                                                                                                      CITY: Eme
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-921-807B-6
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kiefer, Michael C.
APPLICANT: Kiefer, Michael C.
APPLICANT: Valenzuela, Pablo D.T.
APPLICANT: Valenzuela, Pablo D.T.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OP SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: Emeryville
CITY: Emeryville
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.3%; Score 23; DB 1; Length 733; 57.1%; Pred. No. 1.2e+03; ive 2; Mismatches 1; Indels
                                                                                                        Length 731;
                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONDITAT: U.S.

ZIP: 94608

COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/640,029
FILING DATE: 19910111
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: CH-165
TELEPHONE: 510-601-2708
TELEPHONE: 510-601-2708
TELEPHONE: 510-655-3542
INFORMATION FOR SEQ ID NO: 4:
CROMMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 6, Application US/07921807B
; Patent No. 5474914
; GENERAL INFORMATION:
APPLICATE SPAETE, RICHARD
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
                                                                                                    Query Match 79.3%; Score 23; DB 3; I Best Local Similarity 57.1%; Pred. No. 1.2e+03; Matches 4; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                           RESULT 78
US-07-640-029-4
; Sequence 4, Application US/07640029
; Patent No. 5229501
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 733 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-640-029-4
                 TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-439-992A-3
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545 VMKIADF 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08441944A

Patent No. 5767250

GENERAL INFORMATION:
TILLE OF INVENTION: METHOD OF INCERASING EXPRESSION
TITLE OF INVENTION: OF VIRAL PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
STREET: 4560 Horton Street - R440
CITY: Emeryville
SOFTWARE PATENTIN STILL SOFTWARE #1.0, Version #1.25
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,807B
FILING DATE: 29-SEP-1992
CLASSIFICATION: 435
ATTONREY/AGERT INFORMATION:
NAME: MCCLUNG, BARBARA G.
REGISTRATION NUMBER: 33,113
REFRENCE/DOCKET UNMBER: 0209.001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (510) 601-2708
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REGISTRATION NUMBER: 33,113

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Sequence 7119, Application US/09949016

Batent No. 6812339

GADREAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL107
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.3%; Score 23; DB 1; Length 769; 57.1%; Pred. No. 1.2e+03; ive 2; Mismatches 1; Indels
                                                          Sequence 8, Application US/08471570
Patent No. 5750371
GENERAL INFORMATION:
APPLICANT: SENCO, Macharu
APPLICANT: WATANABE, Tatsuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-JUN-1995
CLASSIPICATION: 435
PRIOR ADDITATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 06-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/149,664
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, ETHERE V
REGISTRATION NUMBER: 29822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                   130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     769 amino acids
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TELBEA: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                     STREET: 130 Water Str
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
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640 VMKIADF 646
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US-09-949-016-7119
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APPLICANT: Rablo, Valenzuela D.T.
APPLICANT: Pablo, Valenzuela D.T.
APPLICANT: Philip, Barr J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Receptor
NUMBER OP SEQUENCES: 12
CORRESPONDENCE S: 12
ADDRESSE: Chiron Corporation
                                                                                                                                                                                                                                                              79.3%; Score 23; DB 1; Length 733; 57.1%; Pred. No. 1.2e+03; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 3; Length 733; Pred. No. 1.2e+03; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USAN
ZIP: 9460B
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,992A
FILING DATE: 12-MAY-1995
CLASSIFICATION 15-30
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Ling-Fong
REGISTRATION NUMBER: 36,482
REFERENCY/DOCKET INFORMATION:
TELEPHONE: 510-923-2704
TELEPHONE: 510-923-2704
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER: 0209.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4, Application US/08439992A; Patent No. 6255454; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Chiron Corporation
4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.3%;
                                                                                                                     LENGTH: 733 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 733 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.15
The A, Conservative
                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                 single
                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         || :|:|
547 VMKIADF 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        547 VMKIADP 553
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CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                              1 VMXVAEF 7
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US-08-439-992A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: C. COUNTRY:
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APPLICANT: Timans, Jacqueline C.
APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Antonius
APPLICANT: Bazan, Theodore R.
APPLICANT: Rastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 1.3e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: U-0CT-1998
CLASSIFICATION: 435
PRIOR APPLICATION TABER: US 60/065,776
PRIOR APPLICATION NUMBER: US 60/065,776
PRIOR APPLICATION NUMBER: US 60/078,008
FILING DATE: 17-NOV-1997
PRIOR APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION NUMBER: US 60/062,066
FILING DATE: 18-MAR-1998
PRIOR APPLICATION NUMBER: US 60/062,066
FILING DATE: 18-MAR-1998
PRIOR APPLICATION NUMBER: US 60/062,066
FILING DATE: 18-MAR-1997
ATTONENEY/AGENT INPORMATION:
NUMBER: US 60/062,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34,090
BER: DX0767X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1104
COMPUTER READABLE FORM:
RDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              US-09-173-151A-33
; Sequence 33, Application US/09173151A
; Patent No. 6326472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXOT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEPAX: (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.3%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   802 amino acids
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
                     624 VMKIADF 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-173-151A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
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APPLICATION NUMBER: US/09/383,630A FILING DATE: 26-Aug-1999
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 84
US-09-383-630-6
; Sequence 6, Application US/09383630A
; Patent No. 6265632
; GENERAL INFORMATION:
; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
CHONDRODYSPLASIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Mark M. Friedman c/o Anthony Castorina STREET: 2001 Jefferson Davis Highway, Suite 207 CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 801;
                                                                                                                                                                                                                                                           Length 795;
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                                                                                                                                                                                                                                                         79.3%; Score 23; DB 4; I 57.1%; Pred. No. 1.3e+03; iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 1402/2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7119
LENGTH: 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
TOPOLGGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-383-630-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 972-3-5625553
TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1.
4; Conservative
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619 VMKIADF 625
                                                                                                                                                                                                                                                                                                                                                      1 VMXVAEF 7
                                                                                                                                                                TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                              US-09-949-016-7119
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1 VMXVAEF 7

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Sequence 10904, Application US/09949016

Sequence 10904, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CLOOD1307

CURRENT APPLICATION NUMBER: US/99/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREAESEQ for Windows Version 4.0

SEQ ID NO 10904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.3%; Score 23; DB 4; Length 816; 57.1%; Pred. No. 1.3e+03; cive 2; Mismatches 1; Indels
                                                                            COUNTRI: USAN ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMDATIBLE
COMPUTER: IBM PC COMDATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/640,029
FILING DATE: 19910111
CLASSIFTCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET 133,113
REFERENCE/DOCKET 133,113
REFERENCE/DOCKET NUMBER: CH-165
TELEPHONE: 510-601-2708
TELEPHONE: 510-601-2708
TELEPAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.3%; Score 23; DB 1; I Best Local Similarity 57.1%; Pred. No. 1.3e+03; Matches 4; Conservative 2; Mismatches 1;
     4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 816 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-07-640-029-1
                         CITY: Emeryville
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || :|:|
639 VMKIADF 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-10904
                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
COMPUTER: Twinhead* Slimnote-890TX
COMPUTER: Twinhead* Slimnote-890TX
COMPUTER: Twinhead* Slimnote-890TX
COPERATING SYSTEM: Windows version 3.1
SOFTWARE: Word for Windows version 2.0 converted
to an ASCI file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,630A
FILING DATE: 26-Aug-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: CURNOWN>
FILING DATE: VUNKNOWN>
FILING DATE: VUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Friedmam, Mark M.
REGISTRATION NUMBER: 33,883
REGISTRATION NUMBER: 1402/2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-640-029-1

Sequence 1, Application US/07640029

Patent No. 5229501

GENERAL INFORMATION:

APPLICANT: Kiefer, Michael C.

APPLICANT: Walenzuela, Pablo D.T.

APPLICANT: Barr, Philip J.

TITLE OF INVENTION: Expression and Use of Human Fibroblast

TITLE OF INVENTION: Growth Factor Receptor

NUMBER OP SQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation
                                                                         ESSUL: 8-50-3

1S-09-383-630-3

1 Sequence 3, Application US/09383630A

2 Patent No. 6256532

2 GENERAL INFORMATION:

APPLICANT: ATNET YAYON et al.

TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH

CHONDRODYSPLASIA
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.3%; Score 23; DB 3; I 57.1%; Pred. No. 1.3e+03; tive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear sEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-383-630-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 972-3-5625553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 57.1
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630 VMKIADF 636
625 VMKIADF 631
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                                                                       RESULT 86
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Gaps

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Gaps

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ADDRESSEE: CHIRON CORPORATION
STREET: 4560 Horton Street - R440
CITY: Emeryville
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COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08441944A Patent No. 5767250
                                                                                                                                                                                                                                                                                                                          TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 820 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1
Matches 4; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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634 VMKIADF 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 91
US-08-441-944A-3
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             US-07-61 05

US-07-61 05

Sequence 2, Application US/07640029

Sequence 2, Application US/07640029

Patent No. 5229501

GREPAL INFORMATION:
APPLICANT: Wicher, Michael C.
APPLICANT: Valenzuela, Pablo D.T.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Patent No. 5474914

GENERAL INFORMATION:
APPLICANT: STRETE, RICHARD
ITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
ITLE OF INVENTION: OF VIRAL PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
STREET: 4560 Horton Street - R440
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER FRADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/640,029
FILING DATE: 19910111
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/POCKET UMBER: 33,113
REFERENCE/POCKET UMBER: 31,103
TELEFAX: 510-601-2708
TELEFAX: 510-65-3542
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERIFICS:
LENGTH: 817 amino acids
TYPE: AMINO ACID
STRANDENESS: single
TYPE: AMINO ACID
STRANDENESS: single
TYPE: AMINO ACID
TYPE: A
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ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: peptide US-07-640-029-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emeryville
: California
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || :|:|
632 VMKIADF 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-921-807B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATION SYSTEM: VC-LUCS/MS-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,944A
FILING DATE: 16-MAY-1995
CLASSIFICATION NUMBER: US 07/921,807
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,807
FILING DATE: 29-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BARBARA G.
FEGISTRATION NUMBER: 0209.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTER STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: SPAETE, RICHARD
TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
TITLE OF INVENTION: OF VIRAL PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/07/921,807B
FILING DATE: 29-SEP-1992
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BARBARA G.
REGISTRATION NUMBER: 33,113
REFRENCE/DOCKET NUMBER: 0209.001
TELEPHONE: (510) 601-2708
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                    TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08451822A

Sequence 13, Application US/08451822A

Patent No. 586388

GENERAL INFORMATION:
APPLICANT: Diome, Craig A
APPLICANT: Jaye, Michael C
APPLICANT: Jaye, Michael C
APPLICANT: Jaye, Michael C
APPLICANT: Johnston C
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 19
CORRESPONDENCES: 19

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.3%; Score 23; DB 3; Length 820; 57.1%; Pred. No. 1.3e+03; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Date IDMS PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,992A
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Ling-Fong
REFERENCE/DOCKET NUMBER: 0165.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-923-2704
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-923-2704
TELEFRAX (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TEMPTER: REPERENCE/DOCKET NUMBER: 0165-0364
TELEFRAX (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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26-MAY-1995
      Philip, Barr J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 57.1
Matches 4; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || :|:|
634 VMKIADF 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 94608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-439-992A-1
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          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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79.3%; Score 23; DB 1; Length 820; 57.1%; Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yayon, Avner
APPLICANT: Ornitz, David M.
APPLICANT: Klagbrun, Michael
APPLICANT: Leder, Philip
TITLE OF INVENTION: SYSTEM FOR ASSAYING BINDING
TITLE OF INVENTION: TO A HEPARIN-BINDING GROWTH
TITLE OF INVENTION: 6
NUMBER OF SEQUENCES: 6
                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: Wordberfect (Version 7.0)
CURRENT APPLICATION DATA:
APPLICATION WHEBE: US/08/166,717D
FILING DATE: 12/14/93
CLASSIPICATION 1435
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 07/631,717
FILING DATE: 12/20/90
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kristina Bieker-Brady
REGISTRATION WINBER: 39,109
REFERENCE/DOCKET NUMBER: 00383/017002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08439992A
Patent No. 6255454
GENERAL INFORMATION:
APPLICANT: Fablo, Valenzuela D.T.
                                                                                                                                                                                                                                                                                                                                  US-08-166-717D-6
; Sequence 6, Application US/08166717D
Patent No. 5789182
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENČE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 723-8962
Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-166-717D-6
                                                                                                                                                                      || :|:|
634 VMKIADF 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               634 VMKIADF 640
                                                                                                                                   1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 93
US-08-439-992A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Gaps

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ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia ZIP: 2200.

COMPUTER: Virginia ZEADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPUTER: PROSPER FORM: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PAPLICATION DATA: APPLICATION NUMBER: US/07/997,133 FILING DATE: 28-DEC-1992 CLASSIFICIATION SATION SATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.3%; Score 23; DB 1; Length 822; Best Local Similarity 57.1%; Pred. No. 1.30+03; Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                   Score 23; DB 3; Length 821; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bargonzoni, Laura
APPLICANT: Barcochi, Annonella
APPLICANT: Isacchi, Annonella
APPLICANT: Sarmientos, Romeo
APPLICANT: Sarmientos, Paolo
TITLE OF INVENTION: Extracellular Form of the Human
TITLE OF INVENTION: Pibroblast Growth Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA

APPLICATION NUMBER: US/07/642,755

FILING DATE: 18-JAN-1991

ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5288855man F.

REGISTRATION NUMBER: 24,618

REPERNICE/DOCKET NUMBER: 769-226-0

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)486-2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07997133
Patent No. 5288855
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                     LENGTH: 821 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-323-430-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 822 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || :|:|
639 VMKIADF 645
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636 VMKIADF 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-997-133-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Crumley, Graig A
APPLICANT: Crumley, Greg
APPLICANT: Jaye, Michael C
APPLICANT: Schlessinger, Joseph
IITLE OF INVENTION: Fibroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RElease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,430
FILING DATE: VS/08/323,430
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US to be assigned
PILING DATE: 05-010-1990
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-010-1990
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32,534
REPERBENCE/DOCKET NUMBER: 32,534
REPERBENCE/DOCKET NUMBER: A64-3817
TELECOMMUNICATION INFORMATION:
TELEBERHONE: (215) 454-3817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhone-Poulenc Rorer Legal Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
APPLICATION NUMBER: US 08/323,430
FILING DATE: 14-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-UUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: 28/12/2ky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A0496E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3808
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 821 amino acids
TYPE: Innear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 13, Application US/08323430; Patent No. 6344546; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Rhone-Poulenc
STREET: 500 Arcola Road
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || :|:|
639 VMKIADF 645
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US-08-323-430-13
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-441-944A-4

INCORMITION:

Sequence 4, Application US/0844194A

Sequence 4, Application US/0844194A

Sequence 4, Application US/0844194A

SEQUENCE 1 INTORMATION:

ITLE OF INVENTION:

MUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

STREET: 4560 Horton Street - R440

CITY: Emeryvile

STATE: CA

COUNTRY: USA

ZIP: 94608-2916

COMPUTER: IBMP COMPABLIBE

COMPUTER: IBMP COM
                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,296
FILING DATE: 02-UN-1995
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                               7573-024
                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Lealie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7573-
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-790-9090
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 822 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   822 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636 VMKIADF 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-459-296-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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US-08-459-296-2
; Sequence 2, Application US/08459296
; Sequence 2, Application US/08459296
; Patent No. 5670323
; GENERAL INFORMATION:
; APPLICANT: No. 5670323a, Michael
; APPLICANT: Gonzalez, Ana-Maria
APPLICANT: Garalez, And-waria
; TITLE OF INVENTION: PROCESS FOR DETECTION OF NEOPLASTIC
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STRRET: 1155 Avenue of the Americas
; CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.3%; Score 23; DB 1; Length 822; 57.1%; Pred. No. 1.36+03; tive 2; Mismatches 1; Indels
                                                                        Sequence 4, Application US/07921807B

Sequence 4, Application US/07921807B

Patent NO. 5474914

GENERAL INFORMATION:

APPLICANT: SPATE: RICHARD

TITLE OF INVENTION: OF VIRAL PROTEINS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION

STREET: 4560 HOLON Street - R440

CITY: Emeryville

COUNTRY: USA

ZIP: 94608-2916

CONPUTER: Floppy disk

COMPUTER: Ploppy disk

CURRENT APPLICATION DATA:

REFERENCE/DOCKET NUMBER: 0209.001

FELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (10) 655-3542

INFORMATION FOR SEQ ID NO: 4:

LENGCTH. RAPERISTICS:

LENGCH. RAPERISTICS:

LENGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 822 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                              RESULT 100
US-08-451-822A-12
; Sequence 12, Application US/08451822A
; Patent No. 5863888
; GENERAL INFORMATION:
; APPLICANT: Dionne, Craig A
; APPLICANT: Cruley, Greg
; APPLICANT: Schlessinger, Joseph
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors
; VUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department
; GITTY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.3%; Score 23; DB 2; Length 822; 57.1%; Pred. No. 1.3e+03; ive 2; Mismatches 1; Indels
                                                                 79.3%; Score 23; DB 1; Length 822; 57.1%; Pred. No. 1.3e+03; Live 2; Mismatches 1; Indels
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ZIP: 19426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,822A
FILING DATE: 26-MAY-1995
CIASSIFICATION DATA:
APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-MG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-MG-1992
PRIOR APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUL-1990
ATPORNEY/AGENT INFORMATION:
ANNE: SAVIZEX, MARTIN
REGISTRATION NUMBER: 29,699
REFERENCE/DOKET NUMBER: 29,699
REGISTRATION NUMBER: A0496E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELECOMMUNICATION INFORMATION:
TELEPHONE: G10) 454-3816
TELEFAX: (610) 454-3816
TELEFAX: (610) 454-3816
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TELEPHONE: G10 454-3816
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TELECOMMUNICATION INFORMATION
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Best Local Similarity 57.1
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Best Local Similarity 57.1
Matches 4; Conservative
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MOLECULE TYPE: peptide
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STATE: PA
COUNTRY:
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Search completed: June 13, 2005, 14:00:49

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Sequence 46060, A Sequence 142919, Sequence 5367, A P Sequence 5367, A P Sequence 24, Appl Sequence 73, Appl Sequence 26, Appl Sequence 36, Appl Sequence 76, Appl

68, Appl 26, Appl 36, Appl 76, Appl 71, Appl 81, Appl 56058, A

Sequence 8 Sequence 7 Sequence 8

Sequence 20 Sequence 18 Sequence 46

Title: Perfect score:

Sequence:

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Scoring table:

Searched:

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                                             June 13, 2005, 14:00:08; Search time 109 Seconds (without alignments) 24.618 Million cell updates/sec
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US-10-364-861-80

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US-10-283-172A-64091

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Maximum Match 100%
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Score

Result õ

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16 US-10-664-421-27 Sequence US-10-763-418-1 Sequence US-10-763-418-6 Sequence US-10-763-418-7 Sequence US-10-763-418-7 Sequence US-10-763-418-8 Sequence US-10-763-418-8 Sequence US-10-774-155A-2526 Sequence US-10-91-10-13-4 Sequence US-10-10-11-19-4 Sequence US-10-10-11-19-4 Sequence US-10-10-11-19-4 Sequence US-10-292-798-1478 Sequenc	15 US-10-343-650A-672 Sequenc 16 US-10-70-127-44 Sequenc 16 US-10-770-127-71 Sequenc 17 US-10-962-365-44 Sequenc 17 US-10-962-365-71 Sequenc 16 US-10-763-418-10 Sequenc 16 US-10-763-418-10 Sequenc 15 US-10-763-418-10 Sequenc 15 US-10-763-418-10 Sequenc 17 US-10-763-418-10 Sequenc 1	14 US-10-763-418-3 Sequence US-10-763-418-3 Sequence US-10-437-963-184025 Sequence US-10-437-963-184025 Sequence US-10-282-122A-43999 Sequence US-10-857-625-727 Sequence US-10-857-625-727 Sequence US-10-857-123-13-13-13-13-13-13-13-13-13-13-13-13-13	9 US-09-815-242-5303 Sequence US-09-815-242-1238 Sequence US-09-815-242-1238 Sequence US-09-815-242-1238 Sequence US-09-815-242-1238 Sequence US-09-815-242-1239 Sequence US-08-123-135-123-123-123-123-123-123-123-123-123-123	Sequence 238 Sequence 238 Sequence 208 Sequence 208 Sequence 208 Sequence 208 Sequence 208 Sequence 208 Sequence 338 Sequence 338 Sequence 338 Sequence 338 Sequence 255	9 US-09-805-020-47 Sequence 47, 28-03-03-037-817-6 Sequence 15, 28-10-437-963-134076 Sequence 15, 28-10-437-963-134076 Sequence 16, 28-10-441-486-9 Sequence 23, 215-23-14 Sequence 23, 215-23-14 Sequence 74, 216-29-255-302-714 Sequence 714, 216-10-222-122A-58722 Sequence 715, 216-10-235-977-7240 Sequence 72, 217, 216-29-004-40 Sequence 72, 217, 216-29-004-40 Sequence 72, 217, 216-29-004-40 Sequence 98, 218-242-844-96 Sequence 98, 218-243-243-241-241, 218-241, 218
9.3 310 16 US-10-664-421-27 Sequence 9.3 310 16 US-10-763-418-1 Sequence 9.3 310 16 US-10-763-418-6 Sequence 9.3 310 16 US-10-763-418-7 Sequence 9.3 310 16 US-10-763-418-8 Sequence 9.3 312 10 US-10-763-418-8 Sequence 9.3 312 17 US-10-774-355A-2526 Sequence 9.3 314 10 US-10-510-332-44 Sequence 9.3 314 14 US-10-017-161-1934 Sequence 9.3 314 15 US-10-292-798-1478	3 314 15 US-10-343-650A-672 Sequences 3 314 16 US-10-770-127-44 Sequences 3 314 16 US-10-770-127-71 Sequences 3 314 17 US-10-962-365-44 Sequences 3 315 16 US-10-962-365-71 Sequences 3 315 16 US-10-763-418-10 Sequences 3 318 16 US-10-763-418-10 Sequences 3 318 15 US-10-763-418-10 Sequences 3 318 15 US-10-763-418-10 Sequences 3 319 15 US-10-763-114-55531 Sequences 3 319 US-10-763-114-55531 Sequences 3	9.3 351 16 US-10-763-418-3 Sequence 9.3 378 16 US-10-64-421-45 Sequence 9.3 378 16 US-10-64-421-45 Sequence 9.3 378 15 US-10-68-421-45 Sequence 9.3 383 15 US-10-282-122A-43999 Sequence 9.3 387 15 US-10-857-625-727 Sequence 9.3 387 15 US-10-857-625-727 Sequence 9.3 387 15 US-10-369-439-21613 Sequence 9.3 393 15 US-10-369-439-21613 Sequence 9.3 394 13 US-10-087-192-1131 Sequence 9.3 394 13 US-10-087-192-1131 Sequence	9.3 421 9 US-09-815-242-5303 Sequence 9.3 421 9 US-09-815-242-12388 Sequence 9.3 421 9 US-09-815-242-12388 Sequence 9.3 421 9 US-09-815-242-12828 Sequence 9.3 421 14 US-10-138-701-8 Sequence 9.3 421 15 US-10-282-122A-71223 Sequence 9.3 421 15 US-10-282-122A-71223 Sequence 9.3 421 15 US-10-282-122A-71239 Sequence 9.3 447 15 US-10-282-125A-5239 Sequence 9.3 447 15 US-10-425-115-239771 Sequence 9.3 447 15 US-10-425-115-335184 Sequence 9.3 477 15	9.3 480 15 US-10-732-923-238 Sequence 259 9.3 484 15 US-10-732-923-2782 Sequence 259 9.3 484 15 US-10-732-923-2782 Sequence 618 9.3 484 15 US-10-732-923-2782 Sequence 618 9.3 501 16 US-10-425-115-205773 Sequence 279 9.3 515 15 US-10-425-9146129 Sequence 146 9.3 526 16 US-10-430-859-2 Sequence 146 9.3 530 15 US-10-430-830 Sequence 176 9.3 530 15 US-10-425-114-60637 Sequence 178 9.3 591 15 US-10-425-114-47187 Sequence 178 9.3 591 15 US-10-425-114-47187 Sequence 178 9.3 650 14 US-10-732-923-13660 Sequence 119 9.3 650 14 US-10-193-477-119 Sequence 116 9.3 681 15 US-10-885-784-21 Sequence 116 9.3 682 17 US-10-885-778-21 Sequence 216	3 702 9 US-U9-805-020-47 Sequence 47, 3 735 15 US-10-307-6 Sequence 61, 3 735 16 US-10-307-817-6 Sequence 61, 3 752 16 US-10-437-963-134076 Sequence 13, 3 759 17 US-10-441-486-9 Sequence 23, 3 759 17 US-10-941-486-9 Sequence 71, 3 764 10 US-09-925-302-714 Sequence 71, 3 773 15 US-10-282-122A-58722 Sequence 71, 3 773 15 US-10-282-122A-58722 Sequence 71, 3 773 15 US-10-35-977-7240 Sequence 72, 3 773 15 US-10-659-004-40 Sequence 72, 3 788 17 US-10-659-004-40 Sequence 96, 3 789 15 US-10-342-844-96 Sequence 99

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APPLICANT: Zuker, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Ryba, Nick
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Barepartment of Health and Human Services
ITILE OF INVENTION: SF, a No. US20020051997Alel Family of Taste Receptors
FILE REFERENCE: 02307E-098000US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
                                                                                                                                                                                                                                                                                                                Query Match 93.1%; Score 27; DB 9; Length 68; Best Local Similarity 71.4%; Pred. No. 30; Matches 5; Conservative 1; Mismatches 1; Indels
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US-09-393-634-80
Second BO, Application US/09393634
Patent No. US20020051997A1
GENERAL INFORMATION:
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US-09-393-634-80
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                 SEQ ID NO 80
LENGTH: 68
                                                                                                                                                                                                                                                                           FEATURE:
                                                                                  Sequence 1303, Ap Sequence 276785, Sequence 567, App Sequence 267, App Sequence 267, App Sequence 262081, Sequence 366041, Sequence 209172, Sequence 2558, Ap Sequence 62544, A Sequence 193330, Sequence 193330,
                                                                                                                                                                                                                              Sequence 110, App
Sequence 110, App
Sequence 2636, App
Sequence 2636, App
Sequence 21568, App
Sequence 21568, Appl
Sequence 60512, A
Sequence 60512, A
Sequence 511, Appl
Sequence 51, Appli
Sequence 7310, A
Sequence 7310, A
Sequence 7310, A
Sequence 7310, A
Sequence 27174, Sequence 27174, Appl
Sequence 27174, Appl
Sequence 27174, Appl
Sequence 27174, Appl
Sequence 10345, A
Sequence 6922, Appl
Sequence 7323, Appl
Sequence 7323, Appl
Sequence 7324, Appl
Sequence 6946, A
Sequence 7324, Appl
Sequence 72509, A
Sequence 72509, A
Sequence 72509, A
                                Sequence 29320, A
Sequence 247856,
Sequence 119522,
Sequence 236103,
Sequence 190652,
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Sequence 311273,
Sequence 18824, A
Sequence 3394, Ap
Sequence 8394, Ap
   Sequence 19, Appl
Sequence 212734,
Sequence 152970,
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| US-10-227-646-110
| US-10-431-467A-686
| US-10-431-467A-686
| US-10-431-467A-686
| US-10-432-115-298003
| US-10-369-493-11568
| US-10-369-493-21568
| US-10-377-268-32
| US-10-377-268-32
| US-10-377-268-32
| US-10-794-493-4
| US-10-794-493-5
| US-10-794-493-5
| US-10-794-493-6
| US-10-794-493-8
| US-10-794-493-8
| US-10-794-493-8
| US-10-794-493-1034-5
| US-10-794-493-1034-5
| US-10-785-115-243901
7 US-10-915-017-19
5 US-10-425-115-212734
6 US-10-437-963-152970
6 US-10-029-386-29320
7 US-10-424-599-247856
7 US-10-425-115-238103
7 US-10-425-115-238103
7 US-10-425-115-190652
7 US-10-424-599-276785
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7 US-10-429-205-65
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US-10-425-115-311273
US-10-369-493-18824
US-10-128-714-3394
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US-09-769-744A-152
US-10-282-122A-74248
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US-10-282-122A-57497
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US-10-437-963-127004
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US-10-739-930-7324
US-10-732-923-13448
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JAPPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Ryba, Nick
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the United States of America
APPLICANT: The Regents of the United States of America
APPLICANT: Bepartment of Health and Human Services
TITLE OF INVENTION: SF, a No. US20030157568Aiel Family of Taste Receptors
FILE REFERENCE: 023078-09800US
CURRENT FILICATION NUMBER: US/10/383,982
CURRENT FILICATION NUMBER: US/09/393,634
PRIOR FILICATION NUMBER: US/09/393,634
PRIOR FILICATION NUMBER: US/09/393,634
SPIOR PLICATION NUMBER: US/09/393,634
PRIOR FILICATION NUMBER: US/09/393,634 ö ö Gaps ö ; 0 Query Match 93.1%; Score 27; DB 14; Length 68; Best Local Similarity ,71.4%; Pred. No. 30; Matches 5; Conservative 1; Mismatches 1; Indels

ALIGNMENTS

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CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191, 078

PRIOR APPLICATION NUMBER: 60/191, 078

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/230, 335

PRIOR APPLICATION NUMBER: 60/230, 335

PRIOR APPLICATION NUMBER: 60/230, 347

PRIOR APPLICATION NUMBER: 60/230, 347

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-23

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/257, 931

PRIOR APPLICATION NUMBER: 60/257, 931

PRIOR APPLICATION NUMBER: 60/267, 636

PRIOR APPLICATION NUMBER: 60/267, 636

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06
                  PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-12-22

PRIOR PILING DATE: 2001-12-09

PRIOR PILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PALENTH VARIED: 78614

SOFTWARE: PALENTH VARIED: 3.1

SEQ ID NO 63416
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
FILE REFERENCE: ELITRA.0340
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 15; Length 223;
Pred. No. 1.8e+02;
1; Mismatches 1; Indels
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APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mycoplasma genitalium
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71.48;
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || :|||
93 VMNIAEF 99
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APPLICANT:
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APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: The Government of Health and Human Services
TITLE OF INVENTION: T2R, a No. US20040038312Alel Family of Taste Receptors
FILE REFERENCE: 02307E-09802008
CURRENT APPLICATION NUMBER: US/10/364,861
CURRENT FILING DATE: 2003-06-30
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn Ver. 2.1
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE OF INVENTION: Identification of Essential Genes in Microorganisms FILE EXPERSION: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 050191,078
PRIOR APPLICATION NUMBER: 60/191,078
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Pred. No. 30;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: human T2R24, GR24 or SF24 US-10-364-861-80
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PRIOR APPLICATION WINBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                                  ; Sequence 80, Application US/10364861; Publication No. US20040038312A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zawudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zydkind, Judith
APPLICANT: Yanick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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ORGANISM: Homo sapiens
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11 IMAVAEF 17
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VMXVAEF 7
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US-10-364-861-80
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LENGTH: 68
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rovalic, David K.
APPLICANT: Zhou, Yihus
APPLICANT: Zhou, Yihus
APPLICANT: Con, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 187006
SEQ ID NO 187006
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                                             PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-24
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-16
PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-16
PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-16
PRIOR PRI
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US-10-425-115-187006
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NAME/KEX: unsure
LOCATION: (1). (118)
OTHER INFORMATION: unsure at all xaa locations
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ORGANISM: Zea mays
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APPLICANT: Wu, wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT PLIJOR DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 170879
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                   89.7%; Score 26; DB 15; Length 224; 71.4%; Pred. No. 1.8e+02;
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US-10-437-963-170879
                                                                                                                                                                                                                                                                                1; Mismatches
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 170879, Application US/10437963; Publication No. US20040123343A1
                                                                                          TYPE: PRT
ORGANISM: Mycoplasma pneumoniae
SOFTWARE: PatentIn version 3.1
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
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APPLICANT: Samudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                             Conservative
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Matches 5; Conservative
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ORGANISM: Oryza sativa
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93 VMNIAEF 99
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                     US-10-282-122A-64091
                             SEQ ID NO 64091
LENGTH: 224
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APPLICANT:
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APPLICANT: Lancaster, Laura
APPLICANT: Dallas, Anne
TITLE OF INVENTION: COMPLEXES OF THE BACTERIAL RIBOSOME CONTAINING TRANSFER RNA
TITLE OF INVENTION: AND MODEL MESSENGER RNAS
TITLE OF INVENTION: AND MODEL MESSENGER RNAS
FILE REFERENCE: 19629-7010
CURRENT APPLICATION NUMBER: US 60/254,603
PRIOR APPLICATION NUMBER: US 60/254,603
PRIOR APPLICATION NUMBER: US 60/278,013
PRIOR APPLICATION NUMBER: US 60/294,394
PRIOR PILING DATE: 2001-03-22
PRIOR PILING DATE: 2001-03-22
PRIOR PILING DATE: 2001-03-23
PRIOR PILING DATE: 2001-03-60
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 170244, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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Pred. No. 3.7e+02;
                                                                                                                                       Length 134;
                                                                                                                                           Score 24; DB 15; Length 13
Pred. No. 3.4e+02;
1; Mismatches 1; Indels
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(134)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; CHER INFORMATION: Clone ID: PAT_MRT3847_4685C.1.pep
US-10-424-599-226832
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OTHER INFORMATION: 50S ribosomal protein L13
OTHER INFORMATION: 191yM
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Publication No. US20020188108A1
GENERAL INFORMATION:
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ORGANISM: Haloarcula marismortui
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APPLICANT: Baucom, Albion
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                                                                                                                                           Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TTILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(52323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 226832
LENGTH: 134
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Matches 5, Conservative
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ORGANISM: Homo sapiens
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64 LMVVAEF 70
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US-10-424-599-226832
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Sequence 540, Application US/10389566

Publication No. US20040025202A1

GENERAL INFORMATION:

APPLICANT: Monsanto Technology, LLC

APPLICANT: Laurie, Cathy C

TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants

FILE REFERENCE: 38-77(22900) D

CURRENT APPLICATION NUMBER: US/10/389,566

CURRENT FILING DATE: 2003-03-31

PRIOR APPLICATION NUMBER: US 60/365,301

PRIOR APPLICATION NUMBER: US 60/391,786

PRIOR APPLICATION NUMBER: US 60/392,018

PRIOR PILING DATE: 2002-06-25

PRIOR PILING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 2459

SEQ ID NO 540

LENGTH: 195
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-32
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-05-36
            Gaps
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ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc feature
LOCATION: (132)...(132)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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            Indels
            ä
            Mismatches
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Zyskind, Judith
Wall, Daniel
Trawick, John
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Yamamoto, Robert
Forsyth, R.
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Matches 5; Conservative
            4; Conservative
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131 LMAIAEF 137
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                                                                1 VMXVAEF
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PLING DATE: 2000-19-09

PRIOR PLING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/253,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PLING DATE: 2001-12-22

PRIOR PLING DATE: 2001-12-22

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-09

PRIOR
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Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                      Score 24; DB 15; Length 180;
Pred. No. 4.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_124745C.1.pep
US-10-424-599-170244
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 170244
LENGTH: 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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57.1%;
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 83.3
Matches 5; Conservative
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Trawick, Joh
                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
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US-10-282-122A-52538
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LENGTH: 191
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SOFTWARE: Patentin version 3.1
SEQ ID NO 54190
LENGTH: 238
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Best Local Similarity 57.1%;
Matches 4; Conservative
           NUMBER OF SEQ ID NOS: 78614
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72 VLSIAEF 78
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US-09-815-242-13346
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ORGANISM:
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FILE REFERENCE: ELITTAA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/204,848

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-24

PRIOR PLILNG DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-06

PRIOR PLILNG DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/204,347

PRIOR APPLICATION NUMBER: 60/204,377

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-11-23

PRIOR FILING DATE: 2000-11-23

PRIOR FILING DATE: 2000-11-27

PRIOR PLILNG DATE: 2000-12-22

PRIOR PLILNG DATE: 2000-12-22

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-0/25

PRIOR PLING DATE: 2000-11-0/25

PRIOR PLING DATE: 2000-11-0/25

PRIOR PLING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 57.1%,
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131 LMAIAEF 137
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US-10-282-122A-54190
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LENGTH: 195
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GENERAL INVORMATION:
GENERAL INVORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wall, Baniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yammoro, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-28
PRIOR FILING DATE: 2000-05-28
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/25,565
PRIOR FILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2000-10-21
PRIOR FILING DATE: 2001-20-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PARSENCE LEAST AND ADDERTY HANDER: COLLORS ADDERTY APPLICATION NUMBER: COLLORS ADDERTY APPLICATION ADDERTY APPLICATION ADDER
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82.8%; Score 24; DB 9; Length 335;
Best Local Similarity 71.4%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                        Score 24; DB 15;
Pred. No. 6.2e+02;
2; Mismatches 1.
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13346, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
; TYPE: PRT
; ORGANISM: Cornyebacterium diptheriae
US-10-282-122A-54190
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Sequence 1738, Application US/10472928
; Sequence 1738, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INPORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; TITLE REFERENCE: P026926W0
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SEQWIN99, version 1.03
; SEQ ID NO 1738
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION UMBER: 105/10/282,122A
CURRENT FILING DATE: 2003-02-20
     Gaps
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OTHER INFORMATION: Cellular location: cytoplasm
OTHER INFORMATION: Similar to strain R6 sequence 15902840 (0.E+01)
US-10-472-928-1738
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  Indels
  5
  Mismatches
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Sequence 51530, Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Applicant: Zamudio, Carlos
APPLICANT: Applicant: Zamudio, Carlos
APPLICANT: Applicant: Zyskind, Judith
APPLICANT: Applicant: Zyskind, Judith
APPLICANT: Mall, Daniel
APPLICANT: Trawick, John
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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PRIOR APPLICATION NUMBER: 60/230,347
PRIOR ALING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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Yamamoto, Robert
Forsyth, R.
  5; Conservative
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Best Local Similarity
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US-10-282-122A-51530
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APPLICANT:
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  Matches
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Publication No. US20040110181A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REFERENCE: AM100649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER: OF SEQ ID NOS: 752
SOFTWARE: Patentin version 3.1
SEQ ID NO 654
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Pred. No. 8.9e+02;
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                                                                                                                                                                                                                                                                         CURRENT APPLICATION: IGENITICALION OF ESSENTIAL CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR FILING DATE: 2000-03-21 PRIOR PILING DATE: 2000-03-21 PRIOR PILING DATE: 2000-05-23 PRIOR PLING DATE: 2000-05-23 PRIOR PILING DATE: 2000-05-24 PRIOR PILING DATE: 2000-05-26 PRIOR PILING DATE: 2000-05-26 PRIOR PRIOR DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 60/230,335 PRIOR PILING DATE: 2000-09-09 PRIOR APPLICATION NUMBER: 60/230,335 PRIOR PILING DATE: 2000-10-23 PRIOR APPLICATION NUMBER: 60/242,578 PRIOR PILING DATE: 2000-110-23 PRIOR APPLICATION NUMBER: 60/253,625 PRIOR PILING DATE: 2000-112-27 PRIOR PILING DATE: 2000-112-27 PRIOR PILING DATE: 2000-112-22 PRIOR PILING DATE: 2000-12-22 PRIOR PILING DATE: 2000-12-22 PRIOR PILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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TYPE: PRT
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-282-122A-73914
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
                                                                                                                            Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                           Zyskind, Judith
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Matches 5; Conservative
                                                                                                       Wall, Daniel
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Best Local Similarity
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LENGTH: 335
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US-10-474-776-654
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US-10-739-930-5878
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Sequence 5878, Application US/10739930

Sequence 5878, Application US/10739930

Publication No. US20040216190A1

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(5337) B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

SEQ ID NOS: 11088

LENGTH: 378
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PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR SPLING APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-16

SOFTWARE OF SEQ ID NOS: 78614

SOFTWARE PATENTIN PERSION 3.1

SEQ ID NO 51530

LENGTH: 367
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; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TANSGENIC
; FILE REFERENCE: 38-15(52796)C
; CURRENT FILING NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; RUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 14226
; LANGTH: 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Anopheles gambiae str. PEST
US-10-732-923-14226
                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51530
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ORGANISM: Arabidopsis thaliana
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29 VMEVAEY 35
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RESULT 24

US-10-081-816-14

Sequence 14, Application US/10081816

Publication No. US20030045472A1

GENERAL INFORMATION:

APPLICANT: AREL, Richard

APPLICANT: Scott, Kristin

TITLE OF INVENTION: Uses Thereof

FILE REFERENCE: 0575/64019-A/DFW/ADM

CURRENT APPLICATION NUMBER: US/10/081,816

CURRENT APPLICATION NUMBER: 05/271,319

PRIOR APPLICATION NUMBER: 60/271,319

PRIOR PILING DATE: 2001-02-23

PRIOR FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 116

SOFTWARE: PatentIn version 3.1

SEQ ID NO 14
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US-10-437-963-131765
is Sequence 111765. Application US/10437963
is Publication No. US20040123343A1
is Publication No. US20040123343A1
is RAPLICANT: La Rosa, Thomas J.
is APPLICANT: Zhou, Yihua
is APPLICANT: Zhou, Yihua
is APPLICANT: Applicant Rovalic, David K.
is APPLICANT: Wu, Wei
is APPLICANT: Wu, Wei
is APPLICANT: Boukharov, Andrey A.
is APPLICANT: Li, Ping F.
is APPLICANT: Barbazuk, Brad
is APPLICANT: Li, Ping P.
is APPLICANT: Li, Ping P.
is APPLICANT: Li, Ping P.
is APPLICANT: Li, Ping B.
is
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Score 24; DB 16; Length 378;
Pred. No. 1e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 409;
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Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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US-10-437-963-131765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Drosophila melanogaster US-10-081-816-14
Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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48 VMNMAEF 54
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APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Tyekind, Judith
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 46068
LENGTH: 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 82.8
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
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206 VMTIADF 212
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: BLITRA.034A
CURRENT APPLICATION UMBER: 105/10/282,122A
CURRENT FILING DATE: 2003-02-20
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 46060
LENGTH: 807
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ive 0; Mismatches 1; Indels
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Show, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                      ; Sequence 46060, Application US/10282122A
; Publication No. US20040029129Al
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.8
Best Local Similarity 83.3
Matches 5; Conservative
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94 VMLVAEY 100
1 VMXVAEF 7
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                                                                                                                       RESULT 26
US-10-282-122A-46060
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR PRIOR PRIOR NUMBER: 60/23,625

PRIOR PRIOR PRIOR PRIOR NUMBER: 60/25,931

PRIOR PRIOR PLILING DATE: 2000-10-23

PRIOR PLILING DATE: 2001-10-22

PRIOR PLILING DATE: 2001-12-22

PRIOR PRIOR PLILING DATE: 2001-02-09

PRIOR PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PLILING DATE: 2001-02-09

PRIOR PLILING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_43879C.1.pep
US-10-437-963-142919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 46068, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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09730329-60ed.rapb

NAME/KEY: MISC FEATURE
LOCATION: (30)...(30)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (215)...(215)
OTHER INFORMATION: X=any amino acid FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (222)...(222)
OTHER INFORMATION: X=any amino acid FEATURE: NAME/KEY: MISC_FEATURE LOCATION: (543) .. (543) OTHER INFORMATION: X=any amino acid NAME/KEY: MISC FEATURE LOCATION: (597)..(597) OTHER INFORMATION: X=any amino acid FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (659)
OTHER INFORMATION: X=any amino acid NAME/KEY: MISC FEATURE LOCATION: (732)...(732) OTHER INFORMATION: X=any amino acid NAME/KEY: MISC FEATURE LOCATION: (549)..(549) JTHER INFORMATION: X=any amino acid NAWE/KEY: MISC FEATURE LOCATION: (556)...(556) JTHER INFORMATION: X=any amino acid NAME/KEY: MISC FEATURE LOCATION: (594) OTHER INFORMATION: X=any amino acid NAME/KEY: MISC FEATURE LOCATION: (635)..(635) OTHER INFORMATION: X=any amino acid FEATURE: NAME/KEY: MISC_FEATURE LOCATION: (649) THER INFORMATION: X=any amino acid NAME/KEY: MISC FEATURE LOCATION: (663)..(663) JTHER INFORMATION: X=any amino acid NAME/KEY: MISC FEATURE LOCATION: (687)..(687) JTHER INFORMATION: X=any amino acid FEATURE:
NAME/KEY: MISC FEATURE
COCATION: (693)..(693)

THER INFORMATION: X=any amino acid AMME/KEY: MISC FEATURE
LOCATION: (711).
OTHER INFORMATION: X=any amino acid NAME/KEY: MISC FEATURE LOCATION: (718)..(718) THER INFORMATION: X=any amino acid ORGANISM: Bacillus anthracis FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (737)..(737)

US-10-36-493-5367

i Sequence 5367, Application US/10369493

is Publication No. US20030233675A1

is Publication No. US20030233675A1

is Publication No. US20030233675A1

is APPLICANT: Cao, Yongwei

is APPLICANT: Greeory J.

APPLICANT: Gladman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: USA S. US/10/369, 493

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR PLING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 5367

LENGTH: 919

"LENGTH: 919 ö ö APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVERION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A Gaps Gaps ; 0 ; 0 h 82.8%; Score 24; DB 15; Length 919; Similarity 71.4%; Pred. No. 2.5e+03; 5; Conservative 1; Mismatches 1; Indels Length 902; 1; Indels Query Match
82.8%; Score 24; DB 15;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 0; Mismatches 1. Sequence 70737, Application US/10282122A; Sequence 70737, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos; APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith FEATURE:

NAME/KEY: MISC_FEATURE

COTHER INFORMATION: (809)

COTHER INFORMATION: X=any amino acid
FEATURE:

NAME/KEY: MISC_FEATURE

LOCATION: (810)...(810)

COTHER INFORMATION: X=any amino acid

US-10-282-122A-46068 OTHER INFORMATION: X=any amino acid ; TYPE: PRT ; ORGANISM: Caenorhabditis elegans US-10-369-493-5367 || |||: 592 VMIVAEY 598 113 MTVAEF 118 Query Match Best Local Similarity Matches 5; Conserv 1 VMXVAEF 7 2 MXVAEF 7 g ò

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Sequence 73, Application US/10154419

Publication No. US20030143675A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Gluckeman, Maria Alexandra

APPLICANT: Gluckeman, Maria Alexandra

APPLICANT: Meyers, Rachel B.

TITLE OF INVENTION: 57259, 67118, 67067, 62092, 8099, 46455, 54414, 53763, TITLE OF INVENTION: AND 57255alt MOLECULES AND USES THEREFOR FILE REPERENCE: MNI-249

CURRENT APPLICATION NUMBER: US/10/154,419

CURRENT FILING DATE: 2002-05-22
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Pred. No. 3e+03;
1; Mismatches 1; Indels
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82.8%; Score 24; DB 14; Length 1084;
Best Local Similarity 71.4%; Pred. No. 3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels (
                                           1; Indels
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SOFTWARE: FastSEQ Version 4.0
SEQ ID NO 73
LENGTH: 1084
TYPE: PRT
ORGANIEW: Homo sapiens
       Pred. No. 2.7e+03;
1; Mismatches 1
       71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                           5, Conservative
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CRGANISM: Homo sapiens
US-10-024-623-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| ||||
1016 LMVVAEF 1022
                                                                                                                                                                              542 VISVAEF 548
Best Local Similarity
Matches 5, Conserv
                                                                                                            1 VMXVAEF 7
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| Sequence 24, Application US/10100049
| Publication No. US20030078398A1
| GENERAL INFORMATION:
| APPLICANT: Smith, Trevor
| APPLICANT: Graham, Margaret
| APPLICANT: Now. David
| FILE REFERENCE: 1181-261
| CURRENT FILING DATE: 1998-06-05
| PRIOR APPLICANTION NUMBER: US 09/12936
| PRIOR APPLICANTION NUMBER: CT/CB93/00943
| PRIOR PILING DATE: 1993-06-08
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              PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-21
PRIOR PLING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
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Pred. No. 2.5e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Haemonchus contortus
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.6
Best Local Similarity 83.3
Matches 5; Conservative
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Query Match

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Gaps
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                                                                                                                                                                                                                                                                                                        Score 24; DB 14; Length 1084; Pred. No. 3e+03; 1; Mismatches 1; Indels
                       Sequence 68, Application US/10146733
Publication No. US20030165891A1
                                                                                                                                                                                                                                                                                                         82.8%;
                                                                                                                                                                                                                                                                                                         Query Match 82.8
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-146-733-68
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1016 LMVVAEF 1022
1016 LMVVAEF 1022
                                                                                                                                                                                                                                                                                                                           1 VMXVAEF 7
                                GENERAL INFORMATION:
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US-LU-V44-E45-30
Sequence 36, Application US/10024623
Sequence 36, Application US/10024623
Publication No. US20020187524A1
GENERAL INFORMATION:
GAPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: 8039, 46455, 54414, 53763, 67076, 67102, 44181,
TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
TILLE OF INVENTION: 670812-17
CURRENT APPLICATION NUMBER: US 60/256,240
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH 1095
                                     Sequence 26, Application US/10024623
; Sequence 26, Application US/10024623
; Publication No. US20020187524A1
; GENERAL INFORMATION:
   APPLICANT: Curtis, Rory A.J.;
   APPLICANT: Curtis, Rory A.J.;
   TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF TITLE OF INVENTION: USE THEREOF
   TITLE OF INVENTION: USE THEREOF
   TITLE OF INVENTION: USE THEREOF
   TITLE OF INVENTION: 67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
   TITLE OF INVENTION: 6708THEREOF
   TITLE OF INVENTION: 0708THEREOF
   TITLE OF INVENTION: 0700-12-17
   PRIOR PELICATION NUMBER: US 60/256,240
   PRIOR PELICATION NUMBER: US 60/256,240
   PRIOR PELICATION NUMBER: US 60/256,028
   PRIOR PELICATION NUMBER: US 60/256,028
   PRIOR FILING DATE: 2000-12-21
   NUMBER OF SEQ ID NOS: 40
   SOFTWARE: FastSEQ for Windows Version 4.0
   SEQ ID NO 26
   LENGTH: 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.8%; Score 24; DB 13; Length 1095; 71.4%; Pred. No. 3e+03; ive 1; Mismatches 1; Indels
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CCATION: 801, 1005
COTHER INFORMATION: Xaa = any amino acid
US-10.024-623-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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ORGANISM: Homo sapiens
US-10-024-623-26
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ORGANISM: Mus musculus
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Best Local Similarity
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US-10-024-623-36
RESULT 35
US-10-024-623-26
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| US-10-16-73-71
| Sequence 71, Application US/10146733
| CONTRIGATION UNIVERNITON: US/10146733
| TITLE OF INVENTION: UNMADE: US/101467333
| CURRENT PILICATION NUMBE: US/101467333
| CURRENT PILICATION NUMBE: US/101467333
| PRIOR PELICATION NUMBE: US/101467333
| PRIOR PELICATION NUMBE: US/101467334
| PRIOR PELICATION NUMBE: US/1014674
| PRIOR PELIC
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71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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1016 LMVVAEF 1022
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Sequence 86, Application US/10154419
Sublication No. US20030143675A1
GENERAL INFORMATION.
APPLICANT: Cutris, Rory A.J.
APPLICANT: Cutris, Rachel 1
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Meyers, Rachel 1
TITLE OF INVENTION: 67076, 67102, 44181, 67084FL, 67084ALT, PBH58295FL, 57763,
TITLE OF INVENTION: AND 57255A1 MOLECULES AND USES THERREFOR
FILE REFERENCE: MNI-249
CURRENT APPLICATION NUMBER: US/10/154,419
CURRENT APPLICATION Temoved - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ Version 4.0
FEAST OF TRACE TO THE PARTIES OF THE PA
                                                                                                                                                                                                                         APPLICANT: Curtis, Rory A.J.
APPLICANT: Clucksman, Maria Alexandra
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Meyers, Rachel E.
TITLE OF INVENTION: 57259, 67118, 67067, 62092, 8099, 46455, 54414, 53763,
TITLE OF INVENTION: 67076, 67102, 44181, 67084FL, 67084ALT, FBH58295FL, 57255,
TITLE OF INVENTION: AND 572531t MOLECULES AND USES THEREFOR
TITLE OF MILLARICATION NUMBER: US/10/154,419
CURRENT APPLICATION NUMBER: US/10/154,419
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Pred. No. 3e+03;
1; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ Version 4.0
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CTHER INFORMATION: Xaa = any amino acid
US-10-154-419-86
                                                                                                                                   ; Sequence 76, Application US/10154419; Publication No. US20030143675A1; GENERAL INFORMATION:
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-419-76
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1016 LMVVAEF 1022
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ORGANISM: Mus musculus
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US-10-154-419-86
                                                                                                     10-154-419-76
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RESULT 40 US-10-146-733-81 ; Sequence 81, Application US/10146733

RESULT 39

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FILE FREERENCE: ELITRA, 034A

CURRENT APPLICATION INUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR PLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR PLICATION NUMBER: 60/207,727

PRIOR PLICATION NUMBER: 60/230,335

PRIOR PLILING DATE: 2000-05-06

PRIOR PLILING DATE: 2000-10-23

PRIOR PLILING DATE: 2000-11-27

PRIOR PLILING DATE: 2000-11-2-20

PRIOR PLILING DATE: 2001-12-2-69

PRIOR PLILING DATE: 2001-02-16

PRIOR PLILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PLING DATE: 2001-02-16

PRIOR PRIO
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24; DB 15; Length 1225;
Pred. No. 3.4e+03;
1; Mismatches 1; Indels (
            Sequence 56058, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRGANISM: Enterobacter cloacae US-10-282-122A-56058
                                                                                                                                                     Haselbeck, Robert
Ohlsen, Kari
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.8%;
                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.8
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  945 VMEVAQF 951
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US-10-437-963-200466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 801, 1005
; OTHER INFORMATION: Xaa = any amino acid
US-10-146-733-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.8%;
71.4%;
Publication No. US20030165891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement Sequence 200466, Application US/10437963
Publication No. US20040123343A1
GENERAL INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yihua
APPLICANT: W. Wei
APPLICANT: W. Wei
APPLICANT: Barbazuk, Brad

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Gaps

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                                                                                                            US-09-158-722-46

Sequence 46, Application US/09158722

Publication No. US20030013848A1

GENERAL INFORMATION:

APPLICANT: Lenke Ph.D. et al., Greg B.

TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEB: Fish & Richardson P.C.

STREET: La Jolla

CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-158-722-47

Sequence 47, Application US/09158722

Sequence 47, Application US/09158722

Publication No. US20030013848A1

GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg B.

TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.

STREET: La Jolla

CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23; DB 10;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07251/007002
TELECHMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/456,647
FILING DATE: 02-007-1995
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not relevant
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57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 amino acids
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Best Local Similarity 57.2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
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9 VMKIADF 15
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                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                              RESULT 44
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Pred. No. 5.8e+03;
2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.3%; Score 23; DB 10; Length 54; 57.1%; Pred. No. 2.4e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-158-722-18

Sequence 18, Application US/09158722

Publication No. US20030013848A1

GENERAL INFORMATION:

APPLICANT: Lemke Ph.D. et al., Greg E.

TITLE OF INVENTION:

MUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: La Jolla
                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_95932C.1.pep
US-10-437-963-200466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/158,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/456,647
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NUMBE: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
TELEDGOMINICATION INFORMATION:
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 2059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION
TELEFANOR: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
                                                                                                                                                                                                                                                                      82.8%;
57.1%;
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1
Lagrand 4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                      :: ||||
1869 ILAVAEF 1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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1 VMXVAEF 7

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Wig-09-864-408A-40
Sequence 40, Application US/0964408A
Sequence 40, Application US/0964408A
Sequence 40, Application No. US20040009474A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
FILE REPRENCE: 21402-012
CURRENT FILING DATE: 2001-05-24
CURRENT APPLICATION NUMBER: 60/206,690
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR PILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE PARESE FARESEQ for Windows Version 4.0
SEQ ID NO 40
                                                                     US-10-767-701-50646

i Sequence 50646, Application US/10767701

j Publication No. US20040172684A1

i GENERAL INFORMATION:

APPLICANT: Shou, Yihua

i APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE REFERENCE: 38-21(5535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 50646

LENGTH: 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: LIB3480-021-P1-K1-H3.pep
US-10-767-701-50646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 16;
Pred. No. 2.8e+02;
0; Mismatches 2;
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APPLICANT: Zuker, Charles S.; APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 VMQTAEF 30
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14 MTIAEF 19
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(5323)B
CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

LENGTH: 61

LENGTH: 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.3%; Score 23; DB 10; Length 54; 57.1%; Pred. No. 2.4e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_123941C.1.pep
US-10-424-599-169354
                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,722
                                                                                                                                                                                                                                         FILING WAFE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/456,647
FILING DATE: 02-UNA-1995
APPLICATION NUMBER: US 08/237,401
FILING DATE: 02-MAY-1994
FILING DATE: 02-MAY-1994
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: US 07/884,486
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGESTRANTON NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07251/007002
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION OF 78-5099
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-09-158-722-47
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
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9 VMKIADF 15
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                     COUNTRY: U
ZIP: 92037
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2 MXVAEF 7

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Application US/10383982
No. US20030157568A1
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Best Local Similarity 42.5
Bertage 3; Conservative
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ORGANISM: Homo sapiens
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11 ILAIAEF 17
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NAME/KEY: MOD_RES
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APPLICANT: Ryba, Nick
APPLICANT: Mueller, Ken
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: T2R, a No. US20030022278Alel Family of Taste Receptors
FILE REPERSENCE: 023078-098010US
CURRENT APPLICATION NUMBER: US/09/510,332
CURRENT APPLICATION NUMBER: US 09/393,634
PRIOR APPLICATION NUMBER: US 09/393,634
PRIOR PILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 172
SOFTWARE: Patentin Ver. 2.1
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the University of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. US20020051997Alel Family of Taste Receptors
FILE REPERSINCE: 02307E-088000US
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 23; DB 9; Length 90; 42.9%; Pred. No. 4.1e+02; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                FEATURE:
CTHER INFORMATION: human GR22
NAME/KES: MOD. RES
LOCATION: (1)...(90)
CTHER INFORMATION: Xaa = any amino acid
US-09-393-634-76
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OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: human T2R22 (hGR22)
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-510-332-40
Sequence 40, Application US/09510332
Publication No. US20030022278A1
GENERAL INFORMATION
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
                                                                                                                                                                                                                                                         PatentIn Ver. 2.1
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Best Local Similarity 42.5
Matches 3; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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11 ILAIAEF 17
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11 ILAIAEF 17
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                                                                                                                                                                                                                                                                       SEQ ID NO 76
LENGTH: 90
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LENGTH: 90
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Matches
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RESULT 51 US-10-383-982-76

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RESULT 56
US-10-385-415-119
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Publication No. US20040214239A1

GENERAL INFORMATION:
APPLICANT: SERVANT: GUY
APPLICANT: OZECK, MARK
APPLICANT: OZECK, MARK
APPLICANT: XU, HONG
TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF TIR
TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF TIR
TITLE OF INVENTION: AND TER MODULATORS
TITLE OF INVENTION: AND TER MODULATORS
FILE REFERENCE: 100337.54281US
CURRENT PAPLICATION NUMBER: 60/44,172

PRIOR PELING DATE: 2004-02-03
PRIOR FILING DATE: 2003-02-03
PRIOR FILING DATE: 2003-02-03
PRIOR FILING DATE: 2003-03-26
NUMBER OF SEQ ID NOS: 210
SOFTWARE: Patentin version 3.2
SEQ ID NO 40

LENGTH: 20

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79.3%; Score 23; DB 15; Length 90; 42.9%; Pred. No. 4.1e+02;
                                                                       1; Indels
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APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: T2R, a Novel Pamily of Taste Receptors
FILE REFRENCE: 02307E-0980LOUS
CURRENT APPLICATION UNMER: US/10/962,365
CURRENT FILING DATE: 2004-10-07
                                                                       3; Mismatches
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LOCATION: (35)..(35)
OTHER INFORMATION: Variable amino acid
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LOCATION: (397..(39)
OTHER INFORMATION: Variable amino acid
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LOCATION: (82)...(82)
SOTHER INFORMATION: Variable amino acid
US-10-770-127-40
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US-10-962-365-40
; Sequence 40, Application US/10962365
; Publication No. US20050048586A1
; GENERAL INFORMATION:
                                  Local Similarity 42.5
nes 3; Conservative
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11 ILAIAEF 17
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ILAIAEF 17
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Best Local Similarity
Matches 3; Conserv
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US-10-770-127-40
   Query Match
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Sequence 119, Application US/10385415
Publication No. US20040014158A1
GENERAL INFORMATION:
APPLICANT: Bacher, Adelbert
APPLICANT: Fischer, Markus
TITLE OF INVENTION: PRODUCING THEM, THEIR USE AND MEDICAMENTS AND VACCINES CONTAINING
TITLE OF INVENTION: A CERTAIN QUANTITIY OF SAID PROTEIN CONJUGATES
FILE REPERENCE: 9286.6CT
CURRENT APPLICATION NUMBER: US/10/385,415
CURRENT APPLICATION NUMBER: US/0996,028
PRIOR FILING DATE: 2003-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Shou Yihua
APPLICANT: Shou Yihua
APPLICANT: Cano Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT FILIANG DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 173522
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US-10-424-599-173522
                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 23; DB 17; 42.9%; Pred. No. 4.1e+02;
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Pred. No. 5.6e+02;
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; PRIOR APPLICATION NUMBER: US/09/510,332; PRIOR FILING DATE: 2000-02-22; PRIOR APPLICATION NUMBER: US 09/393,634; PRIOR FILING DATE: 1999-09-10; NUMBER OF SEQ ID NOS: 172; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO FILING DATE: 90; LENGTH: 90
                                                                                                                                                                                      TYPE: PRT
ORGANISH: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
I.CCATION: (1) .. (90)
OTHER INFORMATION: human T2R22 (hGR22)
OTHER INFORMATION: Xaa = any amino acid
US-10-962-165-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-424-599-173522
; Sequence 173522, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 42.5.
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ORGANISM: Glycine max
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11 ILAIAEF 17
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Publication No. US20030233675A1
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Matches 5; Conservative
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ORGANISM: Oryza sativa
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Best Local Similarity
Matches 4; Conserv
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37 MTIAEF 42
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US-10-424-599-231564
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Pred. No. 6.6e+02;
0; Mismatches 1; Indels
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Baniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILLE REFERENCE: ELITRA.011A
FILLE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILLING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRENT AFFLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-20-16
PRIOR FILING DATE: 2001-20-16
PRIOR FILING DATE: 2001-20-16
PRIOR FILING DATE: 2001-2-20
PRIOR FILING DATE: 2001-2-16
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PRIOR APPLICATION NUMBER: PCT/ED00/01899
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: DE 19910102.7
PRIOR FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 119
LENGTH: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4899, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                            ORGANISM: Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), ORGANISM: Enterococcus faecalis
US-09-815-242-4899
                                                                                                                                                                                                                                                                                                          79.3%;
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                                                                                                                                                                                                                                                                                                                                                              5; Conservative
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LMDIAEF 46
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Best Local Similarity
Matches 5; Conserv
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US-10-369-493-18481
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US-09-815-242-4899
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LENGTH: 150
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; Sequence 18481, Application US/10369493

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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Garegory J.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: VONDER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION OF SEQ ID NOS: 47374
SEQ ID NO 18481
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APPLICANT: LA KOVALION:
APPLICANT: LA KOVALION:
APPLICANT: LA KOVALION:
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brobandia Randauk, Brad
APPLICANT: Brobandia Randauk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERRNCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 184028
LENGTH: 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.3%; Score 23; DB 15; Length 162; 66.7%; Pred. No. 7.5e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT4530_81060C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Ramamoro, Robert
APPLICANT: Forsyth, R.
APPLICANT: Wi, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE REFREENCE: ELITRA.0348
TITLE REFREENCE: ELITRA.0340.220
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                PRIOR PELLIANG DATE: 2003-02-20
PRIOR PELLIANG NUMBER: 60/191,078
PRIOR PELLIANG NUMBER: 60/206,848
PRIOR PELLING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-09-06
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-22
PRIOR PELLING DATE: 2000-11-22
PRIOR PELLING DATE: 2001-12-22
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-02-06
PRIOR PELLING DATE: 2001-02-16
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Pred. No. 8.8e+02;
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: APPLICANT: Oblsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Oblsen, Kari
APPLICANT: Mall, Daniel
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Best Local Similarity 83.3
Matches 5; Conservative
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## APPLICANT: Zhou Yihua

### APPLICANT: Zhou Yihua

### TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

### TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

### FILE REFERENCE: 38-21(3)223) ### CURRENT APPLICATION NUMBER: US/10/424,599

### CURRENT FILING DATE: 2003-04-28

### NUMBER OF SEQ ID NOS: 285684

### SEQ ID NO 231564

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Publication No. US20030148324A1
GENERAL INFORMATION:
Publication No. US20030148324A1
GENERAL INFORMATION:
APPLICANT: I.M.S.E.R.M.
TITLE OF INVENTION: Polynuclectides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: E.coli, and biological uses of these polynuclectides and of their FILE REFERENCE: B.coli, and biological uses of these polynuclectides and of their FILE REFERENCE: 2002-09-10
FILE REFERENCE: 2002-09-10
FRIOR PRILICATION NUMBER: 0003145
FRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: Patentin version 3.1
SEQ ID NO 1037
LENGTH: 189
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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Pred. No. 8.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.3%; Score 23; DB 15; Length 177; 57.1%; Pred. No. 8.2e+02; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT3847_51123C.1.pep
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57.1%;
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 ILDVAEF 29
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US-10-238-075-1037
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwal
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Dlants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Dlants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Dlants and Uses Thereof For Plant Improvement
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
LENGTH: 237
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Sequence 182, Application US/10334143
Fublication No. US20040009549A1
GENERAL INFORMATION:
APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
TITLE OF INVENTION: UNDERS: US/10/334,143
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: 60/343,169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392Alel full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR PLICATION OFFE:
NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Clone ID: SORBI-28MAY03-C120919_1.pep
US-10-767-701-36898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.3%; Score 23; DB 16;
85.7%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)..(237)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2492, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.74
East Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2492
LENGTH: 244
                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CAGANISM: Homo sapiens
US-10-104-047-2492
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            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      FEATURE: NAME/KEY: unsure
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US-10-104-047-2492
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 72561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.3%; Score 23; DB 9; Length 237; 42.9%; Pred. No. 1.1e+03; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 36898, Application US/10767701
; Publication No. US20040172684A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4458, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Streptococcus mutans
US-10-282-122A-72561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAYASHI, MIKIRO
COCHIAI, KBIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SERVOH, AKKHIRO
IKEDA, MAKATO
OZAKI, AKIO
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Best Local Similarity 42.5.
Best Local 3; Conservative
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64 IISVAEF 70
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74 ILSIAEF 80
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US-10-767-701-36898
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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09730329-60ed.rapb

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Squence 42888 Application US/10767701

Fublication No. US20040172684A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 42888
LENGTH: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C29394_1.pep
US-10-767-701-42888
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Best Local Similarity 57.1.
Best Local 4; Conservative
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ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: homo sapiens
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96 VMSIAKF 102
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150 VMKIADF 156
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  26 MLVAEF 31
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US-09-738-626-4505
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                                                                                                                                                                   ; OTHER INFORMATION: Description of Unknown Organism: 1fgkA protein sequence US-10-334-143-182
                                                                                                                                                                                                                                                                                               Gaps
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Sequence 15615, Application US/10732923

Publication No. US20050108791A1

Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-15 (52796)C

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT APPLICATION NUMBER: 10/310,154

PRIOR FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 15615

LENGTH: 251
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TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 15746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 23; DB 17; Length 249; 83.3%; Pred. No. 1.2e+03; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                              79.3%; Score 23; DB 15; Length 245; 57.1%; Pred. No. 1.1e+03; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-732-923-15746
; Sequence 15746, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
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ORGANISM: Anopheles gambiae str. PEST
PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 182
LENGTH: 245
                                                                                                             TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.3
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Aedes aegypti
                                                                                                                                                                                                                                                                                                                                                                || :|:|
131 VMKIADF 137
                                                                                                                                                                                                                                                                                                                                       1 VMXVAEF 7
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Best Local Similarity
Matches 5; Conserv
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  Length 265;
                                                  1; Indels
Query Match 79.3%; Score 23; DB 16; Best Local Similarity 57.1%; Pred. No. 1.2e+03; Matches 4; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                       WS-10-470-957-23

Sequence 23, Application US/10470957

Publication No. US20040142404A1

GENERAL INFORMATION:
APPLICANT: Wilks, Andrew Frederick
APPLICANT: Wilks, Andrew Frederick
APPLICANT: Fantino, Emmanuelle
TITLE OF INVENTION: Protein kinase signalling
FILE REFERENCE: 529282001000
CURRENT APPLICATION NUMBER: US/10/470,957

CURRENT FILING DATE: 2003-07-30

PRIOR FILING DATE: 2003-07-30

PRIOR FILING DATE: 2002-01-30

PRIOR FILING DATE: 2002-01-30

PRIOR FILING DATE: 2002-01-30

PRIOR FILING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 51

SEQ ID NO 23

LENGTH: 274
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APPLICANT: MILBURN, MICHAEL VANCE

TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
FILE REFRENCE: 03936340303
CURRENT APPLICATION NUMBER: 040437,268
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: 60/437,929
PRIOR PILING DATE: 2003-01-02
PRIOR PILING DATE: 2003-01-02
PRIOR FILING DATE: 2002-09-16
SOFTWARE: PACHLIN VOR: 38
SOFTWARE: PACHLIN VET: 2.1
SEQ ID NO 29
LEMOTH: 290
LEMOTH: 290
LEMOTH: 290
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US-10-377-268-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 1.4e+03;
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR PELING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-28

PRIOR APPLICATION NUMBER: G0/207,727

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-29

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-22

PRIOR PELING DATE: 2000-12-22
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Chery1
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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57.1%;
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Yamamoto, Robert
Forsyth, R.
Xu, H.
                       , KLAUS-PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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165 VMKIADF 171
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APPLICANT:
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Publication No. US20040031072A1
GENERAL INDOMATION:
APPLICANT: LA Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.3%; Score 23; DB 9; Length 280; 71.4%; Pred. No. 1.3e+03; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_103906C.1.pep
US-10-424-599-147161
                                                                                                                                                                                                                                                      TITLE DETERRICE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 4505
LENGTH: 280
                                                                                                                                                                                                APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Corynebacterium glutamicum
US-09-738-626-4505
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US-10-377-268-29
; Sequence 29, Application US/10377268
; Publication No. US20040171062A1
            MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
NAKAGAWA, SATOSHI
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Best Local Similarity 83.3
Matches 5; Conservative
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VVVVAEF 12
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Best Local Similarity
Matches 5; Conserv
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US-10-424-599-147161
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LENGTH: 287
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APPLICANT:
APPLICANT:
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SEQ ID NO 13
LENGTH: 299
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-763-418-31
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US-10-470-957-21
                                                                                                      US-10-763-418-13
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Sequence 13, Application US/10763418

Bublication No. U820040185547A1

GENERAL INFORMATION:

APPLICANT: MOHAMMADI, MOOSA

TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: RECEPTOR TYROSINE KINASES

FILE REFERENCE: 038602/0847

CURRENT FILING DATE: 2004-01-26

PRIOR APPLICATION NUMBER: US/09/664,526

PRIOR APPLICATION NUMBER: 09/188,809

PRIOR PILING DATE: 1998-11-09

PRIOR PILING DATE: 1998-11-09

PRIOR FILING DATE: 1998-11-09

PRIOR FILING DATE: 1998-11-09

PRIOR FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 41

NUMBER OF SEQ ID NOS: 41
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US-10-334-133-203
; Sequence 203, Application US/10334143
; Sequence 203, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRICORNIEV, IGGR VYACHESLAVOVICH
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: 202-12-31
; PRIOR PILING DATE: 2002-12-31
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207-12-31
; SOFTWARE: Patentin Ver. 2.1
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
ERQ ID NO 52955
LENGTH: 293
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                                                                                                                                                                                                                         ; ORGANISM: Clostridium difficile US-10-282-122A-52955
                                                                                                                                                                                                                                                                                               Query Match 79.3
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
US-10-334-143-203
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173 VMKIADF 179
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LENGTH: 299
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APPLICANT: WICKERSHAM JOHN A.
APPLICANT: WICKERSHAM JOHN A.
APPLICANT: PINKO, CHIELE A.
APPLICANT: PINKO, CHIELE A.
APPLICANT: PINKO, CHIELE A.
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: KAN, CHEN-CHEN
APPLICANT: KANSSTOP
TITLE OF INVENTION: MODIFICATION SOF THE VEGF RECEPTOR-2 PROTEIN AND
TITLE OF INVENTION: MODIFICATION WIMBER: US/09/939, 754
CURRENT PELING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/390,326
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VOF: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MICKERSHAW, JOHN A.
APPLICANT: MICKERSHAW, JOHN A.
APPLICANT: SHOWGALTER; RICHARD
APPLICANT: SHOWGALTER; RICHARD
APPLICANT: SHOWGALTER; RICHARD
APPLICANT: TEMPCYZK-RUSSEL, ANNA
APPLICANT: GERRING, MICHAEL R.
APPLICANT: GERRING, MICHAEL R.
APPLICANT: WILLAFRANCA, J. ERNEST
APPLICANT: VILLAFRANCA, J. ERNEST
APPLICANT: VILLAFRANCA, J. ERNEST
APPLICANT: WAN, CHEN, GOILGUS
TITLE OF INVENTION: MODIFICATIONS OF THE VEGF RECEPTOR-2 PROTEIN AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 0.125-0016US
CURRENT APPLICATION NUMBER: 09/390,326
PRIOR FILING DATE: 1099-09-07
NUMBER OF SEQ ID NOS: 1.2
SOFTWARE: PATEUTIN VEV. 2.0
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                          1; Indels
Pred. No. 1.5e+03;
2; Mismatches 1
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Patent No. US200201238381
GENERAL INFORMATION:
APPLICANT: MCTIGUE, MICHELE A.
                                                                                                                                                                                                                      US-09-939-754-7
; Sequence 7, Application US/09939754
; Patent No. US20020051965A1
; GENERAL INFORMATION:
57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
Best Local Similarity 57.1
Matches 4, Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                     181 VMKIADF 187
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181 VMKIADF 187
                                                                         1 VMXVAEF 7
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; Publication No. US20030233675A1
; GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Galer: Kerven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(152052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
; SEQ ID NO 11118
LENGTH: 309
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publication No. US20040185547A1

publication No. US20040185547A1

GRERAL INPORMATION:
APPLICANT: MCHAMMADI, MCOSA

APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: RECEPTOR TYROSINE KINASES

PILE REFERENCE: 038602/0847

CURRENT APPLICATION NUMBER: US/10/763,418

CURRENT FILING DATE: 2004-01-26

PRIOR PILING DATE: 2000-09-18

PRIOR PLICATION NUMBER: US/09/664,526

PRIOR PELICATION NUMBER: 09/188,809

PRIOR PLING DATE: 1996-11-09

PRIOR PLING DATE: 1996-08-21

NUMBER OF SEQ ID NOS: 41

SEQ ID NO 9

LENGTHARE: PARCENTIN OF: 2.1

SEQ ID NO 9

LENGTHARE: 1099
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                                                                      79.3%; Score 23; DB 16; Length 301; 57.1%; Pred. No. 1.4e+03; tive 2; Mismatches 1; Indels
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                                                                 Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
; ORGANISM: homo sapiens
US-10-470-957-21
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176 VMKIADF 182
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Gaps

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Sequence 1, Application US/10763418
; Sequence 1, Application US/10763418
; Publication No. US20040185547A1
; General INFORMATION:
    APPLICANT: MOHAMMADI, MOOSA
; APPLICANT: HUBBARD, STEVAN R.
; TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
; TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOMAIN OF NON-INSULIN
; TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
; FILE REFERENCE: 038602/0847
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US/09/664,526
; PRIOR APPLICATION NUMBER: US/09/664,526
; PRIOR FILING DATE: 1998-11-09
; PRIOR FILING DATE: 1998-11-09
; PRIOR FILING DATE: 1998-11-09
; PRIOR FILING DATE: 1996-08-21
; NUMBER OF SEQ ID NOS: 41
; SOSTWARE: PATENTIN VET. 2.1
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i Sequence 6, Application US/10763418

i Publication No. US20040185547A1

j Publication No. US20040185547A1

j GENERAL INFORMATION:

j APPLICANT: MOHAMMADI, MOOSA

j APPLICANT: HUBBARD, STEVAN R.

TITLE OF INVENTION: RECEPTOR TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: RECEPTOR TYROSINE KINASES

TITLE OF INVENTION: RECEPTOR TYROSINE KINASES

CURRENT APPLICATION NUMBER: US/10/763,418

CURRENT PILING DATE: 2004-01-26

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 1998-11-09

PRIOR APPLICATION NUMBER: 08/711,191

PRIOR APPLICATION NUMBER: 08/701,191

PRIOR PILING DATE: 1996-08-21

NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23; DB 16; Length 310;
Pred. No. 1.5e+03;
2; Mismatches 1; Indels
                                                                                                                                                  Length 310;
                                                                                                                                                Score 23; DB 16; Length 31
Pred. No. 1.5e+03;
2; Mismatches 1; Indels
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Similarity 57.1%;
4; Conservative
                                                                                                                                                  Query Match 79.3%;
Best Local Similarity 57.1%;
Matches 4; Conservative
            SOFTWARE: Patentin Ver. 3.2; SEQ ID NO 27; LENGTH: 310; TYPE: PRT
CORGANISM: Homo sapiens
US-10-664-421-27
NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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181 VMKIADF 187
                                                                                                                                                                                                                                                                     181 VMKIADF 187
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Best Local Similarity
Matches 4; Conserv
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LENGTH: 310
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                                                                                                           Query Match 79.3%; Score 23; DB 9; Length 310; Best Local Similarity 57.1%; Pred. No. 1.5e+03; Matches 4; Conservative 2; Mismatches 1; Indels
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57.1%; Pred. No. 1.5e+03;
tive 2; Mismatches 1; Indels
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US-10-664-421-27

$ Sequence 27, Application US/10664421

$ Publication No. US20040142864A1

$ Publication No. US20040142864A1

$ SENERAL INFORMATION:

$ APPLICANT: BREMER, RYAN

$ APPLICANT: KUMAR, ABHINAV

$ APPLICANT: MILBURN, MICHAEL V.

$ TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE

$ FILE REFERENCE: 039363/0703

$ CURRENT FILING DATE: 2003-09-16

$ PRIOR APPLICATION NUMBER: 60/412,341

$ PRIOR PILING DATE: 2002-09-16

$ PRIOR PELING DATE: 2002-09-16

$ PRIOR FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 310
TYPE: PRT
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Best Local Similarity 57.1
Best Local 4; Conservative
            ; LENCTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-832-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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181 VMKIADF 187
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181 VMKIADF 187
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SEQ ID NO 7
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Gaps

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APPLICANT: Alsobrook II, John F
APPLICANT: Alsobrook II, John F
APPLICANT: Gerlach, Valerie I
APPLICANT: Gerlach, Valerie I
APPLICANT: Gerlach, Valerie I
APPLICANT: MacDougall, John R
APPLICANT: Mishra, Vishnu
ITILE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-070
CURRENT FAPLICATION NUMBER: US/09/912,976
CURRENT FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: 60/221,336
PRIOR PILING DATE: 2000-10-05
PRIOR PELING DATE: 2000-10-05
PRIOR PELING DATE: 2001-01-05
PRIOR PELING DATE: 2001-01-05
PRIOR PILING DATE: 2001-02-22
PRIOR PELING DATE: 2001-02-23
PRIOR PILING DATE: 2001-03-23
PRIOR PILING DATE: 2001-03-23
PRIOR PILING DATE: 2001-04-02
PRIOR PILING DATE: 2001-04-02
PRIOR PILING DATE: 2001-04-02
PRIOR PILING DATE: 2001-04-02
PRIOR FILING DATE: 2001-04-04
PRIOR FILING
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i) Sequence 2526, Application US/10774355A

i) Publication No. US20050043513A1

i) GENERAL INFORMATION:

i) APPLICANT: Firestein, Stuart

i) APPLICANT: Firestein, Stuart

i) APPLICANT: AJANG, Xinmin

i) TITLE OF INVENTION: MOUSE OLFACTORY RECEPTOR GENE SUPERFAMILY

i) FILE REFERENCE: A34570-FCT-USA-A 070050.2520
                                                                                                                                                                                          Score 23; DB 16; Length 310;
Pred. No. 1.5e+03;
2; Mismatches 1; Indels
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Pred. No. 1.5e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 70, Application US/09912976
Publication No. US20030212255A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mezes, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burgess, Catherine
Casman, Stacie
Grosse, William M
Alsobrook II, John P
                                                                                                                                                                                          Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-10-763-418-8
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; ORGANISM: Mus musculus
US-09-912-976-70
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181 VMKIADF 187
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US-09-912-976-70
   SEQ ID NO 8
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APPLICANT: HUBBARD, STEVAN R.
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN
TITLE OF INVENTION: RECEPTOR TYROSINE KINASES
FILE REFERENCE: 038602/0847
CURRENT APPLICATION NUMBER: US/10/763,418
CURRENT PILING DATE: 2004-01-26
PRIOR PILING DATE: 2004-01-26
PRIOR PILING DATE: 1999-11-09
PRIOR PILING DATE: 1996-08-21
PRIOR PILING DATE: 1996-08-21
PRIOR FILING DATE: 1996-08-21
NUMBER OF SEQ ID NOS: 41
SOFTWARR: PATENTION VUMBER: 08/701,191
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 7
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Sequence 10. Sequence 10. US20040185547A1

SEDERAL INFORMATION:
APPLICANT: MCHAMADI, MCOSA

APPLICANT: MCHAMADI, MCOSA

APPLICANT: MCHAMADI, MCOSA

APPLICANT: HUBBARD, STEVAN R.

TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN OF NON-INSULIN

TITLE OF INVENTION: RECEPTOR TYROSINE KINASES

FILE REFERENCE: 038602/0847

CURRENT FAPLICATION NUMBER: US/10/763,418

CURRENT FILING DATE: 2004-01-26

PRIOR PAPLICATION NUMBER: US/09/664,526

PRIOR APPLICATION NUMBER: 09/188,809

PRIOR PILING DATE: 1999-11-09

PRIOR FILING DATE: 1999-11-09

PRIOR FILING DATE: 1999-11

NUMBER OF SEQ ID NOS: 41

NUMBER OF SEQ ID NOS: 41
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79.3%; Score 23; DB 16; Length 310;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MOHAMMADI, MOOSA
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-10-763-418-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-763-418-7
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181 VMKIADF 187
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181 VMKIADF 187
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US-10-763-418-8
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                           SEQ ID NO 6
LENGTH: 33
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TYPE: PRT
CORGANISM: Homo sapiens
US-10-017-161-1934
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ORGANISM: Homo sapiens
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11 ILAIAEF 17
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11 ILAIAEF 17
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APPLICANT: Adler, Jon Elliot
APPLICANT: Adler, Jon Elliot
APPLICANT: APPLICANT: Mack
APPLICANT: Mealler, Ken
APPLICANT: Mealler, Ken
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TILLE OF INVENTION: TEX, a No. US20030022278A1el Family of Taste Receptors
CURRENT TILLED DATE: 2000-02-22
CURRENT APPLICATION NUMBER: US 09/393,634
PRIOR FILLING DATE: 2000-02-22
PRIOR FILLING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 172
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 44
TADES DESCRIPTION OF APPLICATION OF APPLI
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Publication No. US20030022278A1
GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
The Regents of the University of Taste Receptors
TITLE OF INVENTION: T2R, a No. US20030022278A1e1 Family of Taste Receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.3%; Score 23; DB 17; Length 312; 57.1%; Pred. No. 1.5e+03; ive 2; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/774,355A
CURRENT FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: PCT/USO2/25556
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 2596
SOFTWARE: PSELSEQ for Windows Version 4.0
EMOSTH: 312
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US-09-510-332-44
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US-09-510-332-44
Sequence 44, Application US/09510332;
Publication No. US20030022278A1;
GENERAL INFORMATION:
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Matches 4; Conservative
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Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
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11 ILAIAEF 17
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US-09-510-332-71
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Sequence 1478, Application US/10292798
; Sequence 1478, Application No. US20030235833A1
; Bublication No. US20030235833A1
; GENERAL INPORMATION:
; APPLICANT: SANI, KIYOSHI
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: 105/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2001-12-18
; PRIOR FILING DATE: 2001-12-18
; PRIOR FILING DATE: 2001-246789
; PRIOR FILING DATE: 2001-06-18
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Pred. No. 1.5e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SCHALLAND MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
FILE REPERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
FRIOR PEDLICATION NUMBER: JP 2001/246789
FRIOR PELING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PARENTIN Ver: 2.1
SEQ ID NO 1934
CURRENT APPLICATION WUMBER: US/09/510,332
CURRENT APPLICATION WUMBER: US/09/510,332
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION WUMBER: US 09/393,634
PRIOR FILING DATE: 1999-09-10
WUMBER OF SEQ ID NOS: 172
SEQ ID NO 71
LENGTH: 314

LENGTH: 314
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; OTHER INFORMATION: human T2R45 (hGR45)
US-09-510-332-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1934, Application US/10017161; Publication No. US20030143668A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   79.3%;
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Best Local Similarity 42.57
ماء عبار 3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
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Query Match

Best Local Similarity 42.9%;
Matches 3; Conservative
                                         Query Match 79.3
Best Local Similarity 42.9
Matches 3; Conservative
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ORGANISM: Homo sapiens
US-10-770-127-71
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ORGANISM: Homo sapiens
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11 ILAIAEF 17
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11 ILAIAEF 17
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  US-10-770-127-44
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Publication No. US20040214239A1

GENERAL INFORMATION:
APPLICANT: SERVANT, GUY
APPLICANT: SERVANT, GUY
APPLICANT: SERVANT, GUY
APPLICANT: SERVANT, GUY
APPLICANT: WINGTON:
AND T2R MODULATORS
TITLE OF INVENTION: AND T2R MODULATORS
TITLE OF INVENTION: AND T2R MODULATORS
TITLE OF INVENTION: AND T2R MODULATORS
CURRENT APPLICATION NUMBER: US/10/770,127
CURRENT FILING DATE: 2004-02-03
PRIOR PRILING DATE: 2003-02-03
PRIOR RELING DATE: 2003-03-26
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PatentIn version 3.2
SEQ ID NO 44
LIBRICATION 14
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                                                                                                                                                                 79.3%; Score 23; DB 15; Length 314; 42.9%; Pred. No. 1.5e+03; Live 3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 572, Application US/10343650A
| Sequence 572, Application US/10343650A
| Publication No. US20040067499A1
| GENERAL INFORMATION:
| APPLICANT: HAGA, TATURA
| TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
| FILE REFERENCE: 31671-186347
| CURRENT FILING DATE: 2003-07-21
| PRIOR APPLICATION NUMBER: UP 2000/237818
| PRIOR APPLICATION NUMBER: JP 2001/34434
| PRIOR APPLICATION NUMBER: JP 2001/34434
| PRIOR APPLICATION NUMBER: JP 2001/34434
| SEQ ID NOS: 694
| SEQ ID NO 672
| LENGTH: 314
                   SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1478
                                                                                                                                                             Query Match
Best Local Similarity 42.9
Matches 3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
NUMBER OF SEQ ID NOS: 2070
                                                                                                  ORGANISM: Homo sapiens
US-10-292-798-1478
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; ORGANISM: Homo sapiens
US-10-343-650A-672
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ORGANISM: Homo sapiens
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11 ILAIAEF 17
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11 ILAIAEF 17
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US-10-343-650A-672
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US-10-770-127-44
                                                                                TYPE: PRT
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JUSTICATION OF THE SEQUENCE TI, Application US/10770127

Sequence 71, Application US/10770127

Sequence 71, Application US.0040214239A1

GENERAL INFORMATION:

APPLICANT: SERVANT, GUY

APPLICANT: OZECK, MARK

APPLICANT: WINST COUNTION: PAUL

TITLE OF INVENTION: PUNCTIONAL COUPLING OF TIRS AND T2RS BY GI PROTEINS

TITLE OF INVENTION: AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF TIR

TITLE OF INVENTION: AND T2R MODULATORS

FILE REFERENCE: 10033-5428INS

CURRENT FILING DATE: 2004-02-03

PRIOR FILING DATE: 2003-02-03

PRIOR FILING DATE: 2003-02-03

PRIOR FILING DATE: 2003-02-03

PRIOR FILING DATE: 2003-02-03

SOFTWARE: PALENTING NAMBER: 60/457,318

PRIOR FILING DATE: 2003-03-26

SOFTWARE: PALENTIN VERSION 3.2

SEQ ID NO 71

LENGTH: 314

TUBLE OF INVENTION WHICH SEQ ID NO 71

LENGTH: 314
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US-10-962-365-44

Sequence 44, Application US/10962365

Publication No. US20050048586A1

GENERAL INFORMATION:

APPLICANT: Alber, Charles S.

APPLICANT: Alber, Jon Blliot

APPLICANT: Mueller, Ken

APPLICANT: Howen Set the University of California

TITLE OF INVENTION: T2R, a Novel Family of Taste Receptors

TITLE OF INVENTION: T2R, a Novel Family of Taste Receptors

TITLE OF INVENTION: T2R, a Novel Family of Taste Receptors

TITLE OF INVENTION: T2R, a Novel Family of Taste Receptors

TITLE OF INVENTION: UNMBER: US/10/962,365

CURRENT FILING DATE: 2004-10-07

FRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 172

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 44

LENGTH: 314
79.3%; Score 23; DB 16; Length 314; 42.9%; Pred. No. 1.5e+03; ive 3; Mismatches 1; Indels
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Pred. No. 1.5e+03;
3; Mismatches 1;
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US-10-962-365-71

Sequence 71, Application US/10962365

Publication No. US20050048566A1

GENERAL INFORMATION:
APPLICANT: Adler, Charles S.
APPLICANT: Adler, Uon Elliot
APPLICANT: The Regents of the University of California
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: TR, a Novel Family of Taste Receptors
FILE REFERENCE: 02307E-098010US
CURRENT APPLICATION NUMBER: US/10/962,365
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 09/393,634

PRIOR PILING DATE: 1000-02-22
PRIOR APPLICATION NUMBER: US 09/393,634

PRIOR FILING DATE: 1000-02-22

PRIOR APPLICATION NUMBER: US 09/393,634

PRIOR FILING DATE: 1000-02-22

PRIOR APPLICATION NUMBER: US 09/393,634

PRIOR PILING DATE: 1000-02-22

PRIOR APPLICATION NUMBER: US 09/393,634

PRIOR PILING DATE: 1000-02-22

PRIOR APPLICATION NUMBER: US 09/393,634

PRIOR PILING DATE: 1000-02-22

PRIOR APPLICATION NUMBER: US 09/393,634

PRIOR PILING DATE: 1000-02-22

PRIOR PILING PATE: 1000-02-22

PRIOR PILING 
                                                                                                                                               Query Match 79.3%; Score 23; DB 17; Length 314; Best Local Similarity 42.9%; Pred. No. 1.5e+03; Matches 3; Conservative 3; Mismatches 1; Indels
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79.3%; Score 23; DB 17; Length 314;
Best Local Similarity 42.9%; Pred. No. 1.5e+03;
Matches 3; Conservative 3; Mismatches 1; Indels
; OTHER INFORMATION: human T2R24 (hGR24)
US-10-962-365-44
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US-10-962-365-71
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11 ILAIAEF 17
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1 VMXVAEF 7

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79.3 157 2 G00016 79.3 162 2 G86842 79.3 169 2 AB2739 79.3 172 2 S27019 79.3 172 2 S27022	187 2 191 2 3 209 2 3 248 2	3 254 1 3 291 2 3 291 2	3 373 2	3 388 2	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	9.3 415 2	3 467 2 3 484 2 3 500 2	3 594 2 3 598 2 3 604 2	3 609 2 3 612 2 3 618 2	3 650 1 3 662 2 3 662 2	3 676 2	207 C C C C C C C C C C C C C C C C C C C	3 729 2	3 750 2 3 769 2	3 773 2	3 790 2 3 791 2	3 797 2 3 799 2	8000 1	3 801 2 3 802 1	3 806 3 806	3 814 1 816 2	818	820 2	3 821 1 3 821 1	3 822 1 TVHUF 3 822 1 TVMSF	3 822 2 B5484 3 822 2 A4508	3 822 3 822
30 31 31 33 33 34 34 35 35						733	8888							-												660	
5.1.6 Compugen Ltd.	Search time 24 Seconds (without alignments) 28.063 Million cell updates/sec				ers: 283416					predicted by chance to have a score of the result being printed.	core distribution.	Description	enome p	probable potassium deoxyribose-phosph deoxyribose-phosph	probable steroid s hypothetical prote	probable electron ribosomal protein	thymidine kinase (hypothetical prote	hypothetical prote serine/threonine p	6-phosphofructokin 6-phosphofructokin	fusion, chorismate unknown protein, 3	probable type II D hynothetical prote	archaeosine trna-r	hypothetical prote	isoleucine-tRNA 11 isoleucyl-tRNA syn	Eph receptor tyros hypothetical prote	hypothetical prote hypothetical prote	ű c
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hypothetical prote hypothetical prote fibroblast growth phenylalanyl-tRNA anion transporter DNA topoisomerase band 3 anion trans protein-tyrosine k receptor protein-t	receptor tyrosine kenbryo kinase 5 - receptor tyrosine kenbryo kinase 5 - receptor tyrosine keceptor tyrosine hypothetical prote protein-tyrosine kcalium-binding proteine-binding synth grammicidin S synth hypothetical protein hypothetical protein hypothetical protein ribosomal protein	probable IS1016 tr 50S ribosomal prote conserved hypothet H transfer determi H transfer determi hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote intractose-6-phosph galactose-6-phosph galactose-6-phosph galactose-6-phosph chromate transport hypothetical prote intracellular sept hypothetical prote transcription regu resolvase - Escher thymidine kinase (probable resolvase probable resolvase probable resolvase hypothetical prote thymidine kinase (hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote
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ibrol ibrol rote: rote: lbrol ibrol sole:	genome polyprotein protein tyrosine k protein tyrosine k protein tyrosine k protein (09H1).3 [hypothetical protein genome polyprotein genome polyprotein (NS1, nonserved hypothet hypothetical protein homologufA protein hypothetical protein hypothetical protein hypothetical protein ketol-acid reducto ketol-acid reducto	tungsten-containing serine proteinase serine proteinase glycosyl transfera high affinity gluc tetracycline resis clathrin coat asse UTP-glucose glucose protein-tyrosine k protein-component sens probable acid-CoA tyrochetical protein-probable acid-CoA hypothetical protein-tyrothetical prot
03 23 79.3 822 2 04 23 79.3 822 2 05 23 79.3 822 2 06 23 79.3 822 2 07 23 79.3 829 2 09 23 79.3 829 2 11 23 79.3 921 2	113 23 79.3 980 2 114 23 79.3 1065 2 116 23 79.3 1065 2 117 23 79.3 1065 2 118 23 79.3 3412 1 119 23 79.3 3415 1 120 22 75.9 120 2 121 22 75.9 170 2 122 75.9 184 2 123 22 75.9 184 2 124 22 75.9 184 2 125 22 75.9 184 2 126 22 75.9 184 2 127 22 75.9 188 2 128 22 75.9 188 2 139 22 75.9 243 1 130 22 75.9 265 2 131 22 75.9 268 2 132 22 75.9 268 2 133 22 75.9 268 2 134 22 75.9 268 2 135 22 75.9 268 2 136 22 75.9 268 2 137 22 75.9 268 2 138 22 75.9 268 2 140 22 75.9 310 2 141 22 75.9 339 2	143 22 75.9 373 2 D71094 144 22 75.9 373 2 D71094 146 22 75.9 393 2 B95261 148 22 75.9 490 2 B95261 150 22 75.9 440 2 B91342 150 22 75.9 440 2 B41860 150 22 75.9 446 2 S59646 153 22 75.9 446 2 S41860 153 22 75.9 446 2 S41860 153 22 75.9 480 2 A57174 154 22 75.9 480 2 A57174 155 22 75.9 580 2 A53391 156 22 75.9 580 2 B63187 160 22 75.9 590 2 B6311

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R;Guirakhoo, F.; Heinz, P.X.; Mandl, C.W.; Holzmann, H.; Kunz, C.; Gresikova, M.
J. Gen. Virol. 72, 333-338, 1991
A;Title: The relationship between the flaviviruses Skalica and Langat as revealed by mont A;Reference number: A61409; MUID:91132129; PMID:1847173
A;Recension: A61409
A;Status: not compared with conceptual translation
A;Molecule type: genomic RNA
A;Residues: 319-337 <GUIS
A;Status: not compared with conceptual translation
A;Rolecule type: genomic RNA
A;Residues: 319-337 <GUIS
A;Status: not compared with conceptual translation
A;Molecule type: genomic RNA
A;Residues: B77-994 <GUIS
C;Superfamily: yellow fever virus genome polyprotein
C;Keywords: glycoprotein; nonstructural protein; nucleotide binding; P-loop; polyprotein; C;Superfamily: yellow fever virus genome polyprotein
C;Keywords: glycoprotein; nonstructural protein NS2 #status predicted <NS3-
F;35-582/Product: nonstructural protein NS3 #status predicted <NS3-
F;3135-1847Product: nonstructural protein NS4 #status predicted <NS3-
F;3135-1847Product: nonstructural protein NS5 #status predicted <NS3-
F;3135-1847Product: nonstructural protein NS5 #status predicted <NS5-
F;1464-1735/Product: nonstructural protein NS5 #status predicted <NS5-
F;1464-1735/Product: nonstructural protein NS5 #status predicted <NS5-
F;135-1484-1735/Product: nonstructural protein NS5 #status predicted <NS5-
F;85,207,223,873,1212,1671,1950/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Appr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
Ciscession: T05596
Ribevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.)
Air Eference number: Z15419
Air Efer
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Pred. No. 86;
0; Mismatches 1; Indels
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C;Keywords: ion transport
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85.7%;
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Best Local Similarity
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probable gufA prot
signal recognition
prophage pi2 prote
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T23498
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JC5465
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        T13456
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ALIGNMENTS

RESULT 1

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genome polyprotein - Langat virus (strain TP21) (fragment)
N;Contains: nonstructural protein NS1; nonstructural protein NS2a; nonstructural protein
                                                                                                                                                  C;Species: Langat virus
C;Species: Langat virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A42545; A61409; C61409
C;Accession: A42545; A61409; C61409
R;Iacono-Connors, L.C.; Schmaljohn, C.S.
Virology 188, 875-880, 1992
Virology 188, 875-880, 1992
A;Title: Cloning and sequence analysis of the genes encoding the nonstructural proteins
A;Reference number: A42545; MUID:92263794; PMID:1316684
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A,Cross-references: UNIPROT:P29837; GB:S35365; NID:g249315; PIDN:AAB22165.1; PID:g249316 A, Molecule type: genomic RNA A, Residues: 1-2638 <IAC>

deoxyribose-phosphate aldolase (EC 4.1.2.4) - Mycoplasma genitalium Cispecies: Mycoplasma genitalium C; Species: Mycoplasma genitalium C; Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004 C; Accession: E64205 R; Accession: E64205 R; Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; Nayen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.I. Science 270, 397-403, 1995

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Gaps

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Local Similarity 71.4

Query Match

629 VMSIAEF 635

RESULT 3 E64205

1 VMXVAEF 7

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Gaps

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Indels

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <STO>
A;Cross-references: UNIPROT:Q9ZPQ5; GB:AE002093; NID:g4406768; PIDN:AAD20079.1; GSPDB:GN(
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein ytbQ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                        2; Length 324;
      A; Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                                                                     Score 26; DB 2
Pred. No. 36;
1; Mismatches
                                                                                                                                                                                                                  A,Gene: At2g03770
A,Map position: 2
C,Superfamily: alcohol sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 86.2%;
Similarity 57.1%;
4; Conservative ;
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ilarity 71.4%;
Conservative
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233 VMRIAEF 239
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IMDIAEF 29
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Matches 4; Conserv
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A,Title: The minimal gene complement of Mycoplasma genitalium.

A,Reference number: A64200; MUID:96026346; PMID:7569993

A,Accession: E64205

A,Accession: E64205

A,Residues: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-23 < TIGR>
A,Residues: 1-23 < TIGR>
A,Esperimental source: strain G-37
A,Experimental source: strain G-37
A,Genetics:
C,Genetics:
C,Genetics:
C,Superiamily: deoxyribose-phosphate aldolase
C,Keywords: aldehyde-lyase; carbon-carbon lyase
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probable steroid sulforransferase [imported] - Arabidopsis thaliana
probable steroid sulforransferase [imported] - Arabidopsis thaliana
(Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84452
M: Koo, H:; Moffat, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M: Koo, H:; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-766, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A; Reference number: S73327; MUID:97105885; PMID:8948633 A; Accession: S73417 A; Accession: S73417 A; Accession: S73417 A; A; Mulliprian and Sequence not shown; translation not shown A; Residues: 1-224 < HIM>
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A;Molecule type: DNA
A;Residues: 1-224 <LDE>
A;Residues: 1-224 <LDE>
A;Cessereferences: UNIPROT:P09924; EMBL:X13544; NID:g44480; PIDN:CAA31897.1; PID:g44481
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AE000011; GB:U00089; NID:g1673740; PIDN:AAB95739.1; PID:g167374
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geoxythose-phosphate aldolase (EC 4.1.2.4) - Mycoplasma pneumoniae C;Species: Mycoplasma pneumoniae A;Variety: ATC 29342
A;Variety: ATC 29342
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004 C;Accession: S02216; S73417
R;Loechel, S.; Inamine, J.M.; Hu, P.C.
Nucleic Acids Res. 17, 801, 1989
A;Title: Nucleotide sequence of the deoC gene of Mycoplasma pneumoniae.
A;Reference number: S02216; MUID:89128453; PMID:2492658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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C;Superfamily: deoxyribose-phosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase
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Best Local Similarity
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VMNIAEF 99
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Cipacesion: F69988

R;Kunst, F; Ogaswara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Bertero, C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi S; Brouillet, S.; Brouillet, S.; Brouillet, S.; Bruschi, C.V.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Anthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Fuma, S.; Galizzi, A.; Galler, A; Anthors: Foulger, D.; Fritz, C.; Fujita, M.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Anthors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A; Anthors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon, A; Toganon, A.; Toganon, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yate, C.; Yoshida, K.; Yate, C.; Yoshida, K.; Keference number: Asserting Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB14996.1; PID:e1185891; A;Experimental source: strain 168
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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Pred. No. 42;
2; Mismatches 1; Indels
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Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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217 VLDVAEF 223
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Matches
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G81693
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A,Cross-references: UNIPROT:P87111; EMBL:295334; PIDN:CAB08598.1; GSPDB:GN00066; SPDB:SF A;Experimental source: strain 972h-; cosmid c20G8
A;Genetics:
A;Gene: SPDB:SFAC20G8.04c
A;Gene: SPDB:SPAC20G8.04c
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A;Molecule type: DNA
A;Rolecule type: DNA
A;Cross-treferences: UNIPROT:Q97F65; GB:AE001437; PIDN:AAK80830.1; PID:g15025935; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thymidine kinase (EC 2.7.1.21) [similarity] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C; Accession: C97255 R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4823-4838, 2001 A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A; Reference number: A96900; MuID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-145 <KRO>
A;Cross-references: UNIPROT:P29198; GB:M76567; NID:g148775; PIDN:AAA73097.1; PID:g148777
C;Superfamily: ribosomal protein L13
                                                                                                                                                                                                                                                                                                                                                                                            ribosomal protein L13 [aimilarity] - Haloarcula marismortui
C;Species: Haloarcula marismortui
C;Species: Haloarcula marismortui
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: B41715
R;Kroemer, W.J.; Arndt, E.
A;Elol. Chem. 256, 24573-24579, 1991
A;Title: Halobacterial S9 operon. Three ribosomal protein genes are cotranscribed with bacterium) marismortui.
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                                                                                                                                              DB 2; Length 632;
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A;Accession: B41715
A;Ederus: preliminary
A;Molecule type: DNA
                                                                                                                                         86.2%; Score 25; DB 2; I
71.4%; Pred. No. 1.3e+02;
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Pred. No. 56;
0; Mismatches
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Best Local Similarity 83.3%;
Matches 5; Conservative
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C,Superfamily: thymidine kinase
C,Keywords: phosphotransferase
                                                                                                                                                                 Best Local Similarity 71.4
Matches 5; Conservative
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193 VMSLAEF 199
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131 LMAIAEF 137
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MSVAEF 6
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Cipacesion: B0728
Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Coloror, R.; Davish, R.; Perlwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S., Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome the Reference number: A70500; MulD:98295987; PMID:9634230
A; Reference number: A70500; MulD:98295987; PMID:9634230
A; Residues: 1-236 <COL>
A; Residues: 1-236 <COL>
A; Residues: 1-236 <COL>
A; Cross-references: UNIPROT:050740; GB:277250; GB:AL123456; NID:g3261617; PIDN:CAB01046.JA; Experimental Bource: strain H37Rv
A; Experimental Bource: strain H37Rv
A; Genetics:
A; Genetics:
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C.Species: Leishmania major
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T18315
R.Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.; Estonited to the EMBL Data Library, May 1999
A.Reference number: Z18876
A.Accession: T18315
A.Accession: T18315
A.Accession: T18315
A.Molequle type: DNA
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C;Genetics:
A;Note: L7610.5
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Modecule type: DNA
A;Residues: 1-249 cTET>
A;Cross-references: UNIPROT:Q9PKD5; GB:AE002321; GB:AE002160; NID:g7190560; PIDN:AAF3937
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R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Reference number: A81500; MUID:20150255; PMID:10684935
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hypothetical protein Rv2558 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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C,Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C,Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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Pred. No. 95;
1; Mismatches 1; Indels
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C.Species: Clostridium acetobutylicum C.Species: Limporteuy - Clostridium acetobut C.Species: Clostridium acetobutylicum C.Species: Clostridium acetobutylicum C.Species: Clostridium acetobutylicum C.Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C.Accession: F97010 R.Nolling, J.; Barberon, G.; OmelChenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A.Accession: F97010 A.Accession: F97010 A.Accession: F97010 A.Accession: F97010 A.Speques: preliminary A.Molecule type: DNA
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A,Experimental source: Clostridium acetobutylicum ATCC824
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., J., I., J.H.; Li, Y.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Authors: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                  tusion, chorismate mutase and shikimate 5-dehydrogenase [imported] - Clostridium acetobut
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C,Species: Aeropyrum pernix
C,Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86416
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Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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                                                          224 VMSAAEF
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C; Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: F95103
R;Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A, Experimental source: strain Nigg (MoPn)
C, Genetics:
A, Gene: TC0530
C, Superfamily: conserved hypothetical protein ylo0; conserved hypothetical protein ylo0
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A,Gene: SP0896
C,Superfamily: ATP-dependent phosphofructokinase, prokaryotic type; 6-phosphofructokinas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: pfkA
C;Superfamily: ATP-dependent phosphofructokinase, prokaryotic type; 6-phosphofructokinas
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA |
A;Residues: 1-335 «KUR»
A;Cross-references: UNIPROT:097RC6; GB:AE005672; PIDN:AAK75023.1; PID:914972371; GSPDB:
A;Experimental source: strain TIGR4
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                                                                                                                                              Score 24; DB 2; Length 249; Pred. No. 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24; DB 2; Length 335;
Pred. No. 1.30+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                  1; Mismatches
                                                                                                                                              82.8%;
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Best Local Similarity 71.4%;
Matches 5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6-phosphofructokinase [imported]
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Best Local Similarity 71.4.
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A;Molecule type: DNA
A;Residues: 1-335 <KUR>
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A;Residues: 1-754 <JOH>
A;Cross-references: UNIPROT:P91063; EMBL:U80847; PIDN:AAB37983.1; GSPDB:GN00028; CESP:Cl?
A;Experimental source: strain Bristol N2; clone C17H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 8/3; 92/1; 142/1; 404/1; 437/1; 645/3
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
                                                                                                                                                                                                                                                                                                         hypothetical protein C17H11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein MO3A1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: CESP:C17H11.2
A;Map position: X
A;Introns: 155/1; 246/3; 288/3; 631/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C17H11.2
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        Length 584;
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C;Genetics:
     Score 24; DB 2; Length 584
Pred. No. 2.2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.8%; Score 24; DB 2; Length 754
83.3%; Pred. No. 2.9e+02;
ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               RiJohnson, D.
Submitted to the EMBL Data Library, December 1996
Appescription: The sequence of C. elegans cosmid C17H11.
A;Reference number: 220049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Fulton, B.; Marra, M. asta Library, February 1996 submitted to the EMBL Data Library, February 1996 A;Description: The sequence of C. elegans cosmid M03Al. A;Reference number: Z20645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-919 <FUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
     Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Matches 5; Conservative
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440 VMAIAEY 446
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592 VMIVAEY 598
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A;Molecule type: DNA
A;Residues: 1-565 «KAW»
A;Cross-references: UNIPROT:Q9YE64; DDBJ:AP000060; NID:g5104188; PIDN:BAA79682.1; PID:g5
A;Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 18
E971052
hypothetical protein PH1116 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: E71052
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekirr
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: E71052
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Molecule type: DNA
A;Residues: 1-584 <KAW>
A;Residues: 1-584 <KAW>
A;Cross-references: UNIPROT:O9UZNO; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB5002
A;Experimental source: strain Orsay
C;Genetics:
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-582 - CKAW>
A;Cross-references: (KAW>
A;Cross-references: UNIPROT:O58843; GB:AP000005; NID:g3236132; PIDN:BAA30215.1; PID:d103
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
A;Gene:: PH1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Accession: F75090
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Accession: F75090
A;Accession: F75090
                                                                               A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy;
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72660
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A;Gene: AFB0706
C;Superfamily: Archaeoglobus fulgidus probable DNA topoisomerase VI chain B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 2; I
Pred. No. 2.2e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                               82.8%;
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Best Local Similarity 83.3-
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Matches 4; Conservative
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440 VMAIAEY 446
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03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     790 VMIVAEY 796
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A;Genome: plasmid pMT1
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NiAlternate names: isoleucyl-tRNA synthetase
C;Species: Bacillus subtilis
C;Species: bacillus subtilis
C;Species: bacillus subtilis
C;Saccession: H6543
E;Accession: H6543
E;Accession: H65443
E;Accession: H6544431
E;Accession: H65443
E;Accession: H65443
E;Accession: H65443
E;Accession: H65443
E;Accession: H65443
E;Accession: H6544417
E;Accession: H644417
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E;Accession: H644417
E;Accession: H644417
E;Accession: H644417
E;Accession: H644417
E;Accession: H644
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A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-921 <STO>
A, Cross-references: UNIPROT: 09K9V0, GB: AP001515, GB: BA000004, NID:g10174886, PIDN: BAB062
C, Genetics:
A, Seperimental source: strain C-125
C, Genetics:
A, Gene: iles
C, Superfamily: isoleucine-tRNA ligase
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A;Gene: ileS
C;Superfamily: isoleucine-tRNA ligase
C;Superfamily: isoleucine-tRNA synthetase; ligase; protein biosynthesis
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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83.3%; Pred. No. 3.5e+02;
iive 0; Mismatches 1; Indels
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Best Local Similarity
Matches 5; Conserv
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C;Accession: T42400
R;George, S.B.; Simokat, K.; Hardin, J.; Chisholm, A.D.
Cell 92, 633-643, 1998
Cell 92, 633-643, 1998
A;Title: The VAB-1 Eph receptor tyrosine kinase functions in neural and epithelial morphone; T42400
A;Title: The VAB-1 Eph receptor tyrosine kinase functions in neural and epithelial morphone; T61100
A;Reference number: Z22158; MUID:98165343; PMID:9506518
A;Accession: T42400
A;Cestain: T42400
A;Accession: T42400
A;Cestain: T42400
A;Cestain:
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Cispecies: Yersinia pestis
Cispecies: Yersinia pestis
Cispecies: Versinia pestis KIM5 plasmid
Cispecies: Versinia pestis KIM5 plasmid
Airele: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid
Airele: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5 plasmid
Airele: Versinia pestis KIM5 plasmid
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellis clark, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Beter, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB3577; MUID:21608550; PMID:11743193
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A;Residues: 1-96 - KURX-
A;Cross-references: UNIPROT:Q8U8Q1; GB:AE008689; PIDN:AAL44840.1; PID:g17742484; GSPDB:GN
A;Experimental source: strain C58 (Dupont)
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Pred. No. 64;
0; Mismatches 1; Indels
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Genetics:

RESULT 24 T424b receptor tyrosine kinase - Caenorhabditis elegans C;Species: Caenorhabditis elegans

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Cyaccession: H69212, #sequence_revision us-Dec-1997 #text_change 09-Jul-2004
Cyaccession: H69215,
Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J. Clayton, L.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F., Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woses, C.R.; Venter, J.C.
A,Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A,Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:028152; GB:AE000957; GB:AE000782; NID:g2689280; PIDN:AAB8912*
C;Superfamily: riboflavin synthase beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q28332; EMBL:Z68149; NID:g1279349
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote:
F;1-157/Domain: protein kinase homology (fragment) <KIN>
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C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg A;Reference number: A86625; MuID:21235186; PMID:11337471
A;Reference number: A86625; MuID:21235186; PMID:11337471
A;Reference preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-162 <STO>
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   C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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C;Accession: G00016
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C;Superfamily: shikimate kinase; shikimate kinase homology
C;Keywords: phosphotransferase
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A;Molecule type: mRNA
A;Residues: 1-157 <EIN>
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83.3%; Pred. No. 1e+02;
tive 0; Mismatches
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C;Species: Callithrix jacchus (common marmoset)
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Matches 5; Conservative
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Best Local Similarity
Matches 4; Conserv
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A; Residues: 1-143 < KLE>
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G00016
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B9087
hypothetical protein BCs2869 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Accession: B9087
R;Hayashi, T; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, C.G.
Basawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90887
A;Accession: B90887
A;Status: preliminary
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C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C; Accession: H85832
R; Perra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Mature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q8X7L7; GB:BA000007; PIDN:BAB36292.1; PID:g13362338; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Experimental source: strain O157:H7, substrain EDL933
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Pred. No. 80;
1; Mismatches 1; Indels
                                                                                     Length 96;
                                                                                                                                                  1, Indels
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                                                                                  Score 23; DB 2;
Pred. No. 69;
2; Mismatches
                                                                                     79.3%;
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71.4%;
A;Gene: Atu4039
A;Map position: linear chromosome
                                                                            Query Match 79.3
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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Matches 5; Conservative
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52 ILNVAEF 58
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66 VMYVAKF 72
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A;Residues: 1-112 <HAY>
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A; Residues: 1-112 <STO>
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A, Status: preliminary
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A;Gene: ECs2869
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A,Gene: Z3230
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H69515
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fibroblast growth factor receptor - Japanese medaka (fragment)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Orgains latipes (Japanese medaka)
C;Date: 19-Mar.1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C;Accession: S27020
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: ll-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB2739
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. Karp, P.; Romero, P.; Rant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q8UFS5; GB:AE008688; PIDN:AAL42328.1; PID:g17739732; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;163/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193 A;Accession: AB2739
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                 Length 162;
                   Score 23; DB 2; Pred. No. 1.2e+02;
                                                    1; Mismatches
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A,Map position: circular chromosome
                   79.3%;
Best Local Similarity 57.1
Matches 4; Conservative
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Matches 5; Conservative
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37 MTIAEF 42
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A,Molecule type: DNA
A,Residues: 1-169 <KUR>
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A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1.17 < cEMO>
A;Acatus: 1.17 < cEMO>
A;Cross-references: UMPROT:002528; GB:D13552; NID:g222936; PIDN:BAA02751.1; PID:g222937
A;Cross-references: UMPROT:002528; GB:D13552; NID:g222936; PIDN:BAA02751.1; PID:g222937
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; proteis
C;Keywords: alternative splicing; ATP; autophosphorylation; growth factor receptor; magne P:137,0040 and the factor receptor; magne P:23,40,132/Active site: Lys, Glu, Asp #status predicted
F;137,150/Binding site: magnesium (Asn, Asp) #status predicted
F;163/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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N;Contains: protein-tyrosine kinase (EC 2.7.1.112)

C;Specias: Oryzias latipes (Japanese medaka)

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

C;Accession: S27021

R;Emori, Y: Y Sauoka, A.; Saigo, K.

R;Emori, Y: Y Yasuoka, A.; Saigo, K.

A;Title: Identification of four FGF receptor genes in Medaka fish (Oryzias latipes).

A;Reference number: S27019; MUID:93093167; PMID:1459248
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fibroblast growth factor receptor - Japanese medaka (fragment)
N;Contains: protein:-tyrosine kinase (EC 2.7.1.112)
C;Species: Orytias latipes (Japanese medaka)
C;Species: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
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Best Local Similarity
Matches 4; Conserv
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A; Experimental source: serogroup O1; strain N16961; biotype El Tor
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83.3%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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IMMVSEF 53
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Best Local Similarity
Matches 5; Conserv
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                                      C;Genetics:
A;Gene: VCA0999
A;Map position: 2
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                              FEBS Lett. 314, 176-178, 1992

Affile: Identification of four FQF receptor genes in Medaka fish (Oryzias latipes).

Affile: Identification of four FQF receptor genes in Medaka fish (Oryzias latipes).

Affile: Identification of four FQF receptor genes in Medaka fish (Oryzias latipes).

Affile: Oromograe of Mulb: 93093167; PMID: 1459248

Affile: Oromograe of Mulb: 93093167; PMID: 93093167;

Affile: Oromograe of Mulb: 93093167;

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A/Molecule type: DNA
A/Cross-references: UNIPROM: P26278; EMBL:X57597; NID:g43356; PIDN:CAA40820.1; PID:g43361
C/Superfamily: photosynthetic reaction center cytochrome
C/Keywords: chromoprotein; electron transfer; heme; iron; membrane protein; metalloprote
F/127,130/Binding site: heme (Cys) (covalent) #status predicted
F/131/Binding site: heme (Cys) (covalent) #status predicted
F/182/Binding site: heme iron (His) (axial ligand) #status predicted
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C; Stacession: A82392
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; R; Heidelberg, J.F.; Eisen, J.A.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R. Nature 406, 477-483, 2000
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID: 20406833; PMID: 10952301
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Pred. No. 1.2e+02;
2; Mismatches 1;
R; Emori, Y.; Yasuoka, A.; Saigo, K.
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Matches 4; Conserv
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A,Molecule type: DNA
A,Residues: 1-191 <HEI>
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MHVAEF 63
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hypothetical protein AGR_C_2436 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C.Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: H97519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rigoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-209 <KUR>
A;Cross-references: UNIPROT:Q8UFS5; GB:AE007869; PIDN:AAK87113.1; PID:g15156377; GSPDB:G}
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R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin. C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable tonB transport protein Cj0181 [imported] - Campylobacter jejuni (strain NCTC 11 C;Species: Campylobacter jejuni
C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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   Length 191;
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Score 23; DB 2; Length 191
Pred. No. 1.4e+02;
0; Mismatches 1; Indels
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Pred. No. 1.5e+02;
0; Mismatches 1;
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A,Gene: AGR C_2436
A,Map position: circular chromosome
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C; Accession: G69479
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F. Fletschmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Marure 390, 364-370, L1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A; Reference number: A69250; MuID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Rolecule type: DNA
A;Rosidues: 1.291 «KLE»
A;Cross-references: UNIPROT:028438; GB:AE000976; GB:AE000782; NID:g2689299; PIDN:AAB8941:
C;Superfamily: Escherichia coli methionyl aminopeptidase
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R; Strayer, D.S.; Jerng, H.H.; O'Connor, K.
Virology 185, 585-595, 1991
A; Title: Sequence and analysis of a portion of the genomes of Shope fibroma virus and mal A; Reference number: A41700; MUID:92074222; PMID:1660196
A; Accession: F36819
A; Status: translation not shown
A; Molecule type: DNA
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accessionn AC0253
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Iil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E
Nature 413, 253-257, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A,Residues: 1-373 «KUR»
A;Cross-references: UNIPROT:Q8ZESB; GB:AL590842; PIDN:CAC90887.1; PID:g15980086; GSPDB:GP
C;Genetics:
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C;Species: rabbit fibroma virus, Shope fibroma virus
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 17-Nov-2000
C;Accession: F36819
Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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Pred. No. 2.6e+02;
0; Mismatches 2; Indels
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A,Cross-references: GB:M32743
C;Superfamily: vaccinia virus nucleoside-triphosphatase I
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Best Local Similarity 71.4%;
Matches 5; Conservative (
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C;Superfamily: ribonuclease D
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F36819
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A, Cross-references: UNIPROT:P07283; EMBL:X03213; NID:94444; PIDN:CAA26957.1; PID:94445
A, Cross-references: UNIPROT:P07283; EMBL:X03213; NID:94444; PIDN:CAA26957.1; PID:94445
B, Cross-references: United to the EMBL Data Library, May 1958
A, Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces of A, Reference number: $56186
A, Reference number: $56186
A, Accession: $56218
A, Accession: $56218
A, Residues: 1-254 cMUR>
A, Residues: 1-254 cMUR>
A, Residues: 1-254 cMUR>
A, Residues: 1-254 cMUR>
A, Cross-references: EMBL:D50617; NID:9836685; PIDN:BAA09196.1; PID:9836710; GSPDB:GN0006 C, Genetics:
A, Gene: $GD:SEC53; MIPS:YFL045c
A, Genetics:
A, Gene: $GD:SEC53; PIDS: PIDS: FIDS: FIDS:
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828749
NADD2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - blue mussel mitochondrion (fragm c; Species: mitochondrion Mytilus edulis (blue mussel)
C; Species: mitochondrion Mytilus edulis (blue mussel)
C; Date: 22-Nov-1993 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C; Accession: 828749; 82875
R; Hoffmann, R.J.; Boore, J.L.; Brown, W.M.
Genetics 131, 39'-412, 1992
A; Title: A novel mitochondrial genome organization for the blue mussel, Mytilus edulis.
A; Reference number: $28743; MUID:92354892; PMID:1386586
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C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                     phosphomannomutase (EC 5.4.2.8) - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein YFL045c
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: S05874; S56210
S;Bernstein, M.; Hoffman, W.; Ammerer, G.; Schekman, R.
J. Cell Biol. 101, 2374-2382, 1985
A;Title: Characterization of a gene product (sec53p) required for protein assembly in A;Reference number: S05874; MUID:86059690; PMID:3905826
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methionyl aminopeptidase (map) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
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A;Residues: 1-104;105-275 <BRO>
A;Cross-references: UNIPROT:Q00860; EMBL:M83758; EMBL:M83759
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Best Local Similarity 66.,
4, Conservative
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196 VMFIAEY 202
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MSIAEF 6
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A; Molecule type: DNA
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Best Local S
Matches 4
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R;Poulin, M.L.; Patrie, K.M.; Botelho, M.J.; Tassava, R.A.; Chiu, I.
Development 119, 333-361, 1993
A;Fitle: Heterogeneity in the expression of fibroblast growth factor receptors during lin
A;Reference number: I51023; MUID:94116439; PMID:8287792
                                                                                                                                                                                                                                                                                                                                  C, Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protest C; Reywords: AFP; growth factor receptor F; 44-329/Domain: protein kinase homology < KIN> F; 54-329/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Pyrococcus anysis:
C;Date: 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H75137
R;Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Accession: H75137
A;Reference number: A75001
A,Accession: H75137
A;Status: preliminary
A;Residues: 1-393 «KAW»
A;Residues: 1-393 «KAW»
A;Residues: 1-393 «KAW»
A;Cross_references: UNIPROT:Q9V088; GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49817;
A;Conetics:
G;Genetics:
G;Genetics:
G;Superfamily: O-succinylhomoserine (thiol)-lyase
C;Superfamily: O-succinylhomoserine (thiol)-lyase
C;Superfamily: O-succinylhomoserine (thiol)-lyase
C;Keywords: carbon-oxygen lyase; carbon-sulfur lyase
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C;Date: 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Datesion: Al1302
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Jones, L.M.; Karst, U.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, J. C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pantothenate metabolism flavoprotein homolog homolog lmo1825 [imported] - Listeria monocy
                                                                                                                  A;Accession: IS1023
A;Atatus: prelimary; translated from GB/EMBL/DDBJ
A;Atatus: prelimary; translated from GB/EMBL/DDBJ
A;Residues: 1-388 <POU>
A;Cross-references: UNIPROT:Q91146; GB:L19868; NID:g476726; PIDN:AAA49384.1; PID:g476727
C;Genetics:
A;Gene: FGFR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable carbon-sulfur lyase (EC 4.4.1.-) PAB0605 - Pyrococcus abyssi (strain Orsay)
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Pred. No. 2.8e+02;
2; Mismatches 1; Indels
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Pred. No. 2.8e+02;
1; Mismatches 1; Indels
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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204 VMKIADF 210
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-399 <GLA>
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                                                                                                                                                                                                                                                                                                                        Groce polyprotein - tick-borne encephalitis virus (strain K23) (fragment)
N.Contains: membrane protein M; nonstructural protein NS1
S.Gescise: tick-borne encephalitis virus
C.Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C.Accession: A48352; S18104
R.Jacobs, S.C.; Stephenson, J.R.; Wilkinson, G.W.
Arch. Virol. 129, 279-285, 1993
A.Title: Sequence of the NS 1 gene of the K 23 isolate of tick-borne encephalitis virus
A.Reference number: A48352; MUD: 9328450; PMID: 8470955
A.Accession: A48352
A.Accession: A48352
A.Accession: A88352
A.Accession: A88352
A.Accession: A88352
A.Grose-references: UNISOT: O88482; EMBL: X62886; NID: G62032; PIDN: CAA44678.1; PID: G62033
A.Crose-reference extracted from NCBI backbone (NCBIP: 129078)
C.Superfamily: yellow fever virus genome polyprotein
C.Superfamily: yellow fever virus genome polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conserved hypothetical protein PA3374 [imported] - Pseudomonas aeruginosa (strain PA01) (Species: Pseudomonas aeruginosa (CiSpecies: Pseudomonas aeruginosa (CiSpecies: Pseudomonas aeruginosa (CiSpecies: Pseudomonas aeruginosa (CiSpecies: Basep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 (CiSpecies: CiSpecies: CiSpecies: Pseudomonas aeruginos (CiSpecies: Pseudomonas aeruginos (CiSpecies: Pseudomonas aeruginosa PA01, an opportunistic pathors, CiSpecies: Aseference number: Aseference of Pseudomonas aeruginosa PA01, an opportunistic pathors, Asecession: H83223
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A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9HYM7; GB:AE004759; GB:AE004091; NID:g9949500; PIDN:AAG0676
A;Experimental source: strain PAO1
A;Genetics:
A;Gene: PA3374
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fibroblast growth factor receptor 1 - eastern newt (fragment)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51023
                                                               Gaps
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79.3%; Score 23; DB 2; Length 373; 83.3%; Pred. No. 2.6e+02; ive 0; Mismatches 1; Indels
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                                                            Conservative
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                                                                                                                                                                               120 MLVAEF 125
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                         Best Local Similarity
Matches 5; Conser
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Matches 5; Conser
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Matches 4; Conser
                                                                                                                  2 MXVAEF 7
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   Query Match
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A48352
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Length 415;

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h 79.3%;
Similarity 57.1%;
4; Conservative
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233 VMKIADF 239
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        Query Match
Best Local Similarity
Matches 4; Conserv
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Al1674
pantochenate metabolism flavoprotein homolog homolog lin1939 [imported] - Listeria innoc
C,Species: Listeria innocua
C,Species: Jourea Listeria innocua
C,Species: Jourea Listeria innocua
C,Accession: Al1674
R,Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-882, 2001
A,Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A,Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A,Reference number: AB1077; MUID:21537279; PMID:11679669
A,Rocession: Al1674
A,Residues: L-399 «GLA»
A,Residues: 1-399 «GLA»
A,Gross-references: UNIPROT:Q92Al3; GB:AL592022; PIDN:CAC97169.1; PID:g16414440; GSPDB:C
C,Genetics:
A,Gene: lin1939
C;Superfamily: pantothenate metabolism flavoprotein dfp
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C,Species: Rattus norvegicus (Norway rat)
C,Species: Rattus norvegicus (Norway rat)
C,Species: Rattus norvegicus (Norway rat)
C,Accession: 165223; 165226
R;Yan, G.; McBride, G.; McKeehan, W.L.
Biochem. Biophys. Res. Commun. 194, 512-518, 1993
A;Title: Exon skipping causes alteration of the COOH-terminus and deletion of the phosph A;Reference number: 152281; MUID:93326167; PMID:8333865
A;Accession: 16523
A;Accession: 16523
A;Accession: 16523
A;Accession: 16523
A;Accession: 16528
A;Accession: 16528
A;Molecule type: mRNA
A;Residues: 1-415 - RES>
A;Cession: 16528
A;Accession: 16528
A;Acc
A;Cross-references: UNIPROT:Q8Y674; GB:NC_003210; PIDN:CAC99903.1; PID:g16411279; GSPDB:A;Experimental source: strain EGD-e C;Genetics c: school: A;Gene: Imo1825 C;Superfamily: pantothenate metabolism flavoprotein dfp
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                                                                                                                                                                                                                                  Query Match 79.3%; Score 23; DB 2; Length 399; Best Local Similarity 57.1%; Pred. No. 2.8e+02; Matches 4; Conservative 2; Mismatches 1; Indels
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171 VLRIAEF 177
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171 VLRIAEF 177
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C;Accession: A90003
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogucha, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Dancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T28015

R;Harris, B
submitted to the EMBL Data Library, May 1996

A;Reference number: 220456

A;Reference number: 220456

A;Reference number: 220456

A;Reference number: preliminary; translated from GB/EMBL/DDBJ

A;Rolecule type: DNA

A;Residues: 1-445 < WIL>
A;Residues: 1-445 < WIL>
A;Residues: 1-45 < CESP:ZKE

A;Experimental source: clone ZK822
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28015
                                                                                                                                                                                                                                                                                                                                                          C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                          Gaps
                                                                                                                                                                                                                                                                                                                               hypothetical protein murA [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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fAD/FMN-containing dehydrogenase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
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A;Introns: 20/2; 56/2; 69/2; 87/2; 105/2; 123/2; 254/3; 272/3; 350/3
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C;Superfamily: UDP-N-acetylglucosamine 1-carboxyvinyltransferase
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                                                          1; Indels
Score 23; DB 2;
Pred. No. 2.9e+02;
2; Mismatches 1
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09730329-60ed.rpr

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A,Gene: BMEI1382
A,Map position: I
C.Superfamily: NaD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C,Keywords: oxidoreductase
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57.1%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity
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les 5; Conserv
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
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A;Residues: 1-484 <WIL>
A;Cross-references: UNIPROT:Q19704; EMBL:Z68336; PIDN:CAA92740.1; GSPDB:GN00022; CESP:F2
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betaine aldehyde dehydrogenase (EC 1.2.1.8) [imported] - Brucella melitensis (strain 16M C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH3424
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97213
R;Nolling, J.; Branct, G.; Jonelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97213
A;Accession: B97213
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97213
A;Residues: preliminary
A;Residues: 1-467 < KUR>
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A;Experimental source: strain 16M
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21235
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Pred. No. 3.3e+02;
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Pred. No. 3.4e+02;
2; Mismatches 1;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 71/1; 135/3; 223/3; 247/1; 309/3; 396/3
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submitted to the EMBL Data Library, January 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
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C,Superfamily: glycolate oxidase chain glcD
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                                                                                                                                                                                                                                                                                                                                                                                                                            79.3%;
57.1%;
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ilarity 57.1%;
Conservative
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hypothetical protein F22B3.8
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238 IMLVSEF 244
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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A; Molecule type: DNA
A; Residues: 1-500 <KUR>
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A;Gene: CESP:F22B3.8
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probable hydrolase STY1503 [imported] - Salmonella enterica subsp. enterica serovar Typh C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cjaccession: A10673
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, M. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
Ajatuhora: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Ajatuhora: Darry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Ajatie: Complete genome sequence of a multiple drug resistant Salmonella enterica servor. Ajreference number: AB0502; MUID:21534947; PMID:11677608
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A,Introns: 49/1; 91/3; 139/2; 179/2; 221/2; 270/1; 311/3; 342/2; 399/1; 481/1; 510/2; 55
C,Superfamily: ATP-binding cassette homology
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A;Cross-references: UNIPROT:076414; EMBL:AF067949; PIDN:AAC19238.1; GSPDB:GN00023; CESP:
A;Experimental source: strain Bristol N2; clone T10H9
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C; Genetics:
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C,Species: Caenorhabditis elegans
C,Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 16-Aug-2004
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Pred. No. 4.2e+02;
2; Mismatches 1; Indels
Length 500
                                                                      Indels
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R;Greco, T.; Bradshaw, H.; O'Brien, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid T10H9.
Score 23; DB 2; Le
Pred. No. 3.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.3%; Score 23; DB 2; I larity 71.4%; Pred. No. 4.2e+02; Conservative 1; Mismatches 1;
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submitted to the EMBL Data Library, December 1992
A;Description: Five additional avian Eph-related tyrosine kinases are differentially exp.
A;Reference number: S33502
                                                                                             A;Accession: S33506
A;Status: preliminary
A;Modecule type: DNA
A;Molecule type: DNA
A;Residus: 1-612 <8AJ>
A;Cross-references: EMBL: Z19060
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat hc
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat hc
C;Superfamily: protein-tyrosine kinase homology <3FR>
F;63-147/Domain: fibronectin type III repeat homology <3FR>
F;53-513/Domain: protein kinase homology <KIN>
F;53-51/Region: protein kinase AIP-binding motif
F;53-602/Domain: SAM homology <SAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cjaccession: C87377
Rivierman, W.C.; Feldblyuw, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.
R; Nierman, W.C.; Feldblyuw, T.V.; Paulsen, I.T.; Nelson, K.E.; Gwinn, M.L.; Haft, D.H.; Kolon,
B.; Lauch, M.T.; DeBoy, R.T.; Dodson, R.J.; Dirkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon,
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Title: Complete Genome Sequence of Caulobert crescentus.
A; Fitle: Complete Genome Sequence of Caulobert rescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT: Q9A9F7; GB: AE005673; NID: g13422325; PIDN: AAK23015.1; GSPDB: GP| C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tibroblast growth factor receptor 4 - rat
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1450; PT0191
R;Horlick, R.A.; Stack, S.L.; Cooke, G.M.
A;Horlick, R.A.; Stack, S.L.; Cooke, G.M.
A,Title: Cloning, expression and tissue distribution of the gene encoding rat fibroblast
A;Reference number: JC1450; MUID:93013049; PMID:1398143
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A, Molecule type: mRNA
A, Residues: 1-650 «HOR»
A, Cross-references: UNIPROT: Q63709, GB: M91599, NID: g204137; PIDN: AAA41157.1; PID: g204138
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Neuron 6, 691-704, 1991
A;Title: An extended family of protein-tyrosine kinase genes differentially expressed in
A;Reference number: PT0183; MUID:91222560; PMID:2025425
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C, Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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Pred. No. 4.3e+02;
0; Mismatches 2; Indels
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Pred. No. 4.4e+02;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative (
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C,Species: Deinococcus radiodurans
C,Species: Dainococcus radiodurans
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C,Accession: B7527

R,Mhite, O., Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S, Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A,Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A,Reference number: A75250; MUID:20036896; PMID:10567266
A,Accession: B7527
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                   hypothetical protein B208.250 [imported] - Neurospora crassa C;Species: Oc-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004 C;Accession: T49577 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, A;Reference number: Z25022 A;Reference number: Z25022 A;Reference number: Z25022 A;Status: preliminary A;Status: preliminary A;Noleoule type: DNA A;Residues: J-604 <SCH>A;Residues: J-604 <SCH>A;Residues: J-604 <SCH>A;Residues: UNIPROT: Q9P604; EMBL: AL355930; GSPDB: GN00116; NCSP: B208: 250
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A;Cross-references: UNIPROT:Q9RRC4; GB:AE002086; GB:AE000513; NID:g6460395; PIDN:AAF1210
A;Experimental source: strain R1
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C;Species: Gallus gallus (chicken)
C;Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 04-Feb-2000
C;Accession: S33506
R;Sajjadi, F.G.; Pasquale, E.B.
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C;Superfamily: Neurospora crassa hypothetical protein B2O8.250
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Pred. No. 4.3e+02;
1; Mismatches 1;
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A,Gene: DR2568
A,Map position: 1
C,Superfamily: Bacillus arginine-tRNA ligase
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ilarity 71.4%;
Conservative
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340 IMRVSEF 346
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277 IMDVSEF 283
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A;Map position: 6
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Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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516 VLNIAEF 522
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549 VMKIADF 555
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397 VIAIAEF 403
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A;Molecule type: mRNA
A;Residues: 1-682 <HAT>
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A; Residues: 465-588 <LAI>
A; Residues: 465-588 <LAI>
A; Residues: 465-588 <LAI>
C; Genetics:
A; Gene: PGFR4; tyro-9
C; Function:
A; Gene: PGFR4; tyro-9
C; Function:
A; Dene: PGFR4; tyro-9
C; Function:
A; Dene: PGFR4; tyro-9
C; Function:
A; Dene: PGFR4; tyro-9
C; Function:
A; Dete: expressed in normal lung; expressed in some carcinomas
C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology, rMD-
C; Reywords: AFP; autophosphorylation; duplication; glycoprotein; growth factor receptor;
F; 110-181/Domain: immunoglobulin homology <MIN>
F; 110-181/Domain: immunoglobulin homology <MIN>
F; 110-181/Domain: intracellular #status predicted <TWM>
F; 218-238/Domain: intracellular #status predicted <INT>
F; 113-538/Domain: protein kinase homology <KIN>
F; 121-329/Region: protein kinase AFP-binding motif
F; 121-329/Region: protein kinase AFP-binding motif
F; 131-1358/AGO/Active site: Lys, Glu, Asp #status predicted
F; 35, 1368, 460/Active site: Lys, Glu, Asp #status predicted
F; 455, 478/Binding site: magnesium (Asn, Asp) #status predicted
F; 491/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
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B97738
DNA topoisomerase (ATP-hydrolysing) (EC 5.99.1.3) - Rickettsia conorii (strain Malish 7)
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97738
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
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57.1%; Pred. No. 4.6e+02;
ive 2; Mismatches 1; Indels
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C,Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
C,Keywords: isomerase
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473 VMKIADF 479
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397 VISIAEF 403
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A,Cross-references: UNIPROT:Q92DU7; GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14690
A;Experimental source: strain Madrid B
G,Genetics, G,Genetics
A;Gene: gyrB1; RP227
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
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A;Note: Nostoc sp. etrain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB2017
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Accession: AB2017
A;Status: preliminary
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C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote.
C; Keywords: ATP; autophosphorylation; growth factor receptor; heparin binding; phosphopre.
R; 83-144/Domain: immunoglobulin homology <IMD.
F; 389-674/Domain: protein kinase homology <IMD.
F; 389-674/Domain: protein kinase ATP-binding motif
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C;Species: Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
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Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 1;
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Pred. No. 4.8e+02;
2; Mismatches 1;
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Pred. No. 4.7e+02;
2; Mismatches 1;
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Cincession: A54846
R:Takagi, Y.; Shrivastav, S.; Miki, T.; Sakaguchi, K.
Biol. Chem. 269, 23743-23749, 1994
J. Richer, Molecular cloning and expression of the acidic fibroblast growth factor recepton ility and covalent attachment of haparan sulfate glycosaminoglycan to the receptors.
A;Reference number: A54846
A;Accession: A54846
A;Accession: A54846
A;Accession: A54846
A;Residues: 1-707 craft
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protesion: Affactor receptor 1; immunoglobulin homology; protesion: P;57-118/Domain: immunoglobulin homology < IMPS
F;57-118/Domain: immunoglobulin homology < IMPS
F;57-118/Domain: immunoglobulin homology < IMPS
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C;Genetics:
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
Gaps
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Pred. No. 5e+02;
2; Mismatches 1; Indels
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fibroblast growth factor receptor 1 beta-isoform - rat
C;Species: Rattus norvegicus (Norway rat)
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A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                   fibroblast growth factor receptor a precursor - rat
C;Species: Rattus norvegicus (Norway rat)
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ilarity 57.1%;
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      4; Conservative
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525 VMKIADF 531
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                                                          1 VMXVAEF 7
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A; Residues: 1-713 <MAR>
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Best Local S:
Matches 4
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                                                                                                            셤
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                                                                                                                                                                                                                                              Accession: S51634
A,Reference number: S51634
A,Accession: S51635
A,Status: pre-liminary
A,Molecule type: mRNA
A,Residues: 1-705 <8AV>
A,Cross references: EMBL:235138; NID:9551271; PIDN:CAA84510.1; PID:9551272
A,Cross references: EMBL:235138; NID:9551271; PIDN:CAA84510.1; PID:9551272
A,Status: pre-liminary
A,Molecule type: mRNA
A,Residues: 37-12, "T,174-314, "TV,315-340,"T,342-705 <8A3>
A,Status: pre-liminary
A,Molecule type: mRNA
A,References: EMBL:235139; NID:9551273; PIDN:CAA84511.1; PID:9551274
B,Savagner, P.; Valles, A.M.; Jouanneau, J.; Yamada, K.M.; Thiery, J.P.
R,Savagner, P.; Valles, A.M.; Jouanneau, J.; Yamada, K.M.; Thiery, J.P.
A,Cross reference number: S48046; MUID:95102150; PMID:7803853
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C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 16-Jul-1999
C;Accession: A38429
R;Miki, T.; Fleming, T.P.; Bottaro, D.P.; Rubin, J.S.; Ron, D.; Aaronson, S.A.
Science 251, 72-75, 1991
A;Title: Expression cDNA cloning of the KGF receptor by creation of a transforming autoc A;Reference number: A38429; MUID:91095977; PMID:1846048
A;Accession: A38429
A;Accession: A38429
A;Accession: A38429
A;Residues: 1-707 <MIK>
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C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote C;Reywords: ATP; autophosphorylation; growth factor receptor; phosphoprotein; transmembr F;57-118/Domain: immunoglobulin homology <IMM>F;367-8650/Domain: protein kinase homology <IMN>F;365-650/Domain: protein kinase ATP-binding motif
                                                                                                   fibroblast growth factor receptor 2b, keratinocyte growth factor receptor - rat C; Species: Rattus norvegicus (Norway rat) C; Date: 15-Jul-1995 #sequence revision 21-Jul-1995 #text_change 16-Jul-1999 C; Accession: S51635; S51636; S48048; S48047 R; Savagner, P.
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 37-135,'R',137-314,'TV',315-340,'T',342-390,'K',392-705 <SA2>
A;Cross-references: EMBL:235139
A;Accession: $48047
A;Status: preliminary; nucleic acid sequence not shown
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A;Cross-references: EMBL:Z35138
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keratinocyte growth factor receptor precursor - mouse
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57.1%; Pred. No. 5e+02;
tive 2; Mismatches
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Pred. No. 5e+02;
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Best Local Similarity 57.1
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Best Local Similarity
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C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protes
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C.Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote:
F;101-162/Domain: immunoglobulin homology <IMM>
F;408-693/Domain: protein kinase homology <KIN>
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F;400-769/Domain: intracellular #status predicted <INT>
F;480-765/Domain: protein kinase homology <KIN.
F;488-496/Region: protein kinase ATP-binding motif
F;62-107,179-231,278-340/Disulfide bonds: #status predicted
F;83,123,228,241,265,297,318,329,350/Binding site: carbohydrate (Asn) (covalent) #status
F;518,535,627/Active site: Lys, Glu, Asp #status predicted
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: S16236
R;Seno, M.; Sasada, R.; Watanabe, T.; Ishimaru, K.; Igarashi, K.
Biochim. Biophys. Acta 1089, 244-246, 1991
A;Title: Two cDNAs encoding novel human FGF receptor.
A;Reference number: S16236; MUID:91274356; PMID:1647213
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Pred. No. 5.3e+02;
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Pred. No. 5.3e+02;
2; Mismatches 1; Indels
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                                                             F;101-162/Domain: immunoglobulin homology <IMM>F;406-691/Domain: protein kinase homology <KIN>
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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566 VMKIADF 572
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568 VMKIADF 574
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-750 <POU>
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Residues: 1-769 <SEN>
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C.Accession: 149293
R.Jin, Y.; Pasuwarthi, K.B.; Bock, M.E.; Lytras, A.; Kardami, E.; Cattini, P.A.
J. Mol. Cell. Cardiol. 26, 149-1455, 1994
A.Title: Cloning and expression of fibroblast growth factor receptor-1 isoforms in the A.Reference number: 149289; MUID:95205422; PMID:7897669
A.Accession: 149293
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL:U23445; NID:9733537; PIDN:AAC52183.1; PID:97335
A.Cross-references: UNIPROT:Qc0830; EMBL:U23445; NID:9733537; PIDN:AAC52183.1; PID:97335
C.Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology in the F.181-254/Domain: immunoglobulin homology KIN>
F.181-254/Domain: protein kinase ATP-binding motif
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: A56795
R;Kim, E.G.; Kwon, H.M.; Burrow, C.R.; Ballermann, B.J.
Am. J. Physiol. 264, F66-F73, 1993
A,Title: Expression of rat fibroblast growth factor receptor 1 as three splicing variant A,Feference number: A56795; MUID:93158788; PMID:8381605
A;Accession: A56795
A;Accession: A
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C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 841050
R;Poulin, M.L.; Chiu, I.M.
Biochim. Biophys. Acta 1220, 209-211, 1994
A;Title: Nucleotide sequences of two newt (Notophthalmus viridescens) fibroblast growth A;Reference number: 841050, MUID:94146117; PMID:8312364
A;Accession: S41050
A;Accession: Speciminary
A;Molecus preliminary
A;Residues: 1-748 <POU>
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57.1%; Pred. No. 5.2e+02;
iive 2; Mismatches 1;
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Best Local Similarity 57.1
Matches 4; Conservative
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543 VMKIADF 549
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VMKIADF 553
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A;Cross-references: UNIPROT:074504; EMBL:AL023705; NID:g3169070; PIDN:CAA19280.1; PID:g33. A;Cross-references: UNIPROT:0724; EMBL:AL023705; NID:g316999r, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G. submitted to the EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 95-791 <RIE>
A,Cross-references: EMBL:AL031523; NID:93560217; PIDN:CAA20660.1; PID:93560218; GSPDB:GN(
A,Experimental source: strain 972h-; cosmid c594
                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog C;Keywords: ATP; growth factor receptor; phosphotransferase; tyrosine-specific protein ki F;449-741/Domain: protein kinase homology <KIN>F;457-465/Region: protein kinase ATP-binding motif
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 04-Feb-2000 C;Accession: A39627; S16679 K;Glazer, L; Shilo, B.Z. Genes Dev. 5, 697-705, 1991 A;Title: The Drosophila FGP-R homolog is expressed in the embryonic tracheal system and A;Reference number: A39627; MUID:91184623; PMID:1849109 A;Accession: A39627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibroblast growth factor receptor 3 - Iberian ribbed newt (fragment) C;Species: Pleurodeles waltlii (Iberian ribbed newt) C;Date: 06-Jan.1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004 C;Accession: S38579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SPCC736.16 - fission yeast (Schizosaccharomyces pombe) N;Alternate names: hypothetical protein SPCC594.01 C;Species: Schizosaccharomyces pombe C;Species: 03-Dec-1999 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
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C,Genetics:
A,Gene: FlyBase:btl
A,Cross-references: FlyBase:FBgn0005592
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R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, May 1998
A;Reference number: 221991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 790;
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Pred. No. 5.6e+02;
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Pred. No. 5.6e+02;
2; Mismatches 1;
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A,Molecule type: DNA
A,Residues: 1-231 <WOO>
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A;Accession: T41445
A;Status: translated from GB/EMBL/DDBJ
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Similarity 71.4%;
5; Conservative (
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-790 <GLA>
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Cispecies: Helicobacter pylori
Cidate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
Cidate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
Cidatesion: Edst82
RiTomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
Altile: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A64582
A; Reference number: A64582
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Mesidues: 1-773 <TOM>
A; Residues: 1-773 <TOM>
A; Cross-references: UNIPROT: P55992; GB:AE000564; GB:AE000511; NID:g2313602; PIDN:AAD0756
                                                                                                                                                                                                                                                                                                                                  C;Species: Helicobacter pylori

A;Variety: strain J99

A;Variety: strain J99

C;Date: 12-Peb-1999 #sequence_revision 12-Peb-1999 #text_change 09-Jul-2004

C;Date: 12-Peb-1999 #sequence_revision 12-Peb-1999 #text_change 09-Jul-2004

C;Date: 12-Peb-1999 #sequence_revision 12-Peb-1999 #text_change 09-Jul-2004

B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUD:99120557; PMID:9923682

A;Status: preliminary
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A;Experimental source: strain J99
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protein-tyrosine kinase (EC 2.7.1.112) homolog - fruit fly (Drosophila melanogaster)
N;Alternate names: fibroblast growth factor receptor
C;Species: Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.3%; Score 23; DB 2; Length 773; ilarity 71.4%; Pred. No. 5.5e+02; Conservative 0; Mismatches 2; Indels
                                     Indels
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A;Gene: gyrB
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
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DNA gyrase, sub B - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                             B71931
DNA gyrase chain B - Helicobacter pylori (strain J99)
         Pred. No. 5.4e+02;
2; Mismatches 1
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      Best Local Similarity 57.1 Matches 4; Conservative
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640 VMKIADF 646
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Matches 5; Conserv
                                                                                              1 VMXVAEF 7
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Matches 5, Conserv
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A;Residues: 1-773 <ARN>
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A,Gene: GDB:FGFR2; JWS; CFD1; KGF; FLG2
A,Gene: GDB:FGFR2; JWS; CFD1; KGF; FLG2
A,KGp position: 10q25.3-10q26
C,Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote C;Kcywords: ATP; autophosphorylation; duplication: glycoprotein; growth factor receptor; F:1-21/comain: signal sequence #status predicted &SIG>
F;22-860/Product: fibroblast growth factor receptor fig-2 #status predicted <WAT>
E;22-860/Pomain: extracellular #status predicted <EXT>
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C,Accession: A48991
R;Katch, O.; Hattori, Y.; Sasaki, H.; Sakamoto, H.; Fujimoto, K.; Fujii, T.; Sugimura, T
Cancer Res. 53, 1136-1141, 1993
A;Title: Isolation of the complementary DNA encoding a mouse heparin-binding growth fact
A;Reference number: A48991; MUID:93177694; PMID:8382556
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C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: ATP; growth factor receptor; heparin binding; phosphotransferase; tyrosine-s
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R;Avivi, A.; Zimmer, Y.; Yayon, A.; Yarden, Y.; Givol, D.
Orocgene 6, 1089-1092, 1991
A;Title: F192-2, a new member of the family of fibroblast growth factor receptors. A;Reference number: A60350; MUID:91296390; PMID:1648703
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                                                                                                                                                                                                                   fibroblast growth factor receptor flg-2 precursor - human N;Contains: protein-tyrosine kinase (EC 2.7.1.112) flg-2 (5.8pecies: Homo sapiens (man) (C.5pecies: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000
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C, Comment: This may be a receptor for keratinocyte growth factor
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F;391-800/Domain: intracellular #status predicted <INT>
F;464-749/Domain: intracellular #status predicted <INT>
F;467-749/Domain: protein kinase homology <KIN>
F;472-480/Region: protein kinase ArP-binding motif
F;59-107,170-222,269-333/Disulfide bonds: #status predicted
F;56,219,256,288,309,322/Binding site: crabbydrate (Asn) (of F;502,519,611/Active site: Lys, Glu, Asp #status predicted
F;502,519,611/Active site: magnesium (Asn, Asp) #status predicted
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N,Contains: protein-tyrosine kinase (BC 2.7.1.112)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 57.1
Matches 4; Conservative
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A,Molecule type: nucleic acid
A,Residues: 1-800 <KAT>
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                                                                    622 VMKIADF 628
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624 VMKIADF 630
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         1 VMXVAEF
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submitteed to the EMBL Data Library, November 1993
A;Bescription: Expression of FGFR-3 in amphibian embryos.
A;Accession: S38579
A;Accession: S38579
A;Accession: S38579
A;Status: preliminary
A;Residues: 1-777 < SHI>
A;Residues: 1-777 < SHI>
A;Residues: 1-777 < SHI>
A;Residues: 1-777 < SHI
A;Residues: 1-771 / SHI
A;Residues: 1-771 / SHI
A;Residues: AFP; growth factor receptor
F;258-311/Domain: immunoglobulin homology < MMM>
F;456-741/Domain: protein kinase homology < MMM>
F;464-472/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NyAlternate names: tyrosine kinase Mpk-11
N;Contains: protein-tyrosine kinase Mpk-11
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Mus muculus (house mouse)
C;Decies: Mus muculus (house mouse)
C;Accession: 518209, 526751; 530497
C;Accession: 518209, 526751; 530497
B;Stark, K.L.; McMahon, J.A.; McMahon, A.P.
Development 113, 641-651, 1991
A;Title: FGPR-4, a new member of the fibroblast growth factor receptor family, expressed A;Reference number: $18209; MUID:92146274; PMID:1723680
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Pred. No. 5.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 797;
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K470-478/Region: protein Kinase APP-binding motif
F;54-98,169-221,268-330/Disulfide bonds: #status predicted
F;500,517,609/Active site: Lys, Glu, Asp #status predicted
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F;367-387/Domain: transmembrane #status predicted <TMM>
F;388-799/Domain: intracellular #status predicted <INT>
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Pred. No. 5.6e+02;
2; Mismatches 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.3%;
57.1%;
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57.1%;
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Best Local Similarity 57.10,
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616 VMKIADF 622
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fibroblast growth factor
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A; Residues: 1-799 <STAl>
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Best Local Similarity
Matches 4; Conserv
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A,Status: nucleic acid sequence not shown; not compared with conceptual translation A,Status: nucleic acid sequence not shown; not compared with conceptual translation A,Molecule type: mRNA A,Residues: 1-296, 'D'. 298-802 - RON>
A,Fexperimental source: mammary epithelial cell line B5/589
A,Note: sequence extracted from NCBI backbone (NCBIP:127650)
A,Note: binds acidic and basic fibroblast growth factors with high affinity R,Holtrich, U, Braeniniager, A.; Strebhardt, K.; Ruebsamen-Waigmann, H. Proc. Natl. Acad. Sci. U.S.A. 88, 10411-10415, 1991
A,Title: Two additional protein-tyrosine kinases expressed in human lung: fourth member of A,Reference number: S19025; MUID:92073297; PMID:1720539
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A, Description: receptor mediating effects of fibroblast growth factor

A, Note: expressed in normal lung; expressed in some carcinomas

C, Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protes)

C, Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protes)

C, Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;

F, 12-40 Domain: signal sequence #status predicted <SIG.

F, 25-369 Domain: stracellular #status predicted <EXT.

F, 50-103 Domain: immunoglobulin homology <IM3.

F, 165-226 Domain: immunoglobulin homology <IM3.

F, 165-226 Domain: immunoglobulin homology <IM3.

F, 167-390 Domain: intracellular #status predicted <INT.

F, 191-802 Domain: intracellular #status predicted <INT.

F, 465-750 Domain: protein kinase homology <XIN.

F, 465-750 Domain: protein kinase ATP-binding motif
F, 57-101, 172-224, 271-333 Disulfide bonds: #status predicted
F, 503, 520, 612 Active site: Lys, Glu, Asp #status predicted
F, 630, 520, 612 Active site: Lys, Glu, Asp #status predicted
F, 630, 101 ding site: magnesium (Asn, Asp) #status predicted
F, 6417 Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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C;Species: Homo sapiens (man)
C;Species: A1-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A38576; A55273; E38269; I51880
R;Keegan, K.; Johnson, D.E.; Williams, L.T.; Hayman, M.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 1095-1099, 1991
A;Title: Isolation of an additional member of the fibroblast growth factor receptor famil A;Reference number: A38576; MUID:91142118; PMID:1847508
                                     A,Title: Fibroblast growth factor receptor 4 is a high affinity receptor for both acidic A,Reference number: A46615, MUID:93194827; PMID:7680645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Nolecula type: mRNA
A;Residues: 399-534, M' 536-799, 'SG', 800-802 <HOL>
A;Residues: 399-534, M' 536-799, 'SG', 800-802 <HOL>
A;Experimental source: lung makelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
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Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels
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A;Residues: 614-670 <PA2>
A;Cross-references: GB:M37781
A;Experimental source: K-562 leukemia cell line
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A,Cross-references: GDB:127929; OMIM:134935
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625 VMKIADF 631
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B;Chellaiah A.T.; McEwen, D.G.; Werner, S.; Xu, J.; Ornitz, D.M.
J. Biol. Chem. 269, 11620-11627, 1994
A;Title: Fibroblast growth factor receptor (FGFR) 3. Alternative splicing in immunoglobu A;Reference number: A53627; MUID:94209351; PMID:7512569
A;Accession: B53627
A;Accession: B53627
A;Residues: 242-364 <CHE>
A;Residues: 242-364 <CHE>
A;Cross-references: GB:L26492
C;Genetics:
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A;Residues: 1-802 <PAR>
A;Cross-references: UNIPROT:P22455; EMBL:X57205; NID:g31371; PIDN:CAA40490.1; PID:g31372
A;Notes: binds acidic but not basic fibroblast growth factor with high affinity
R;Ron, D.; Reich, R.; Chedid, M.; Lengel, C.; Cohen, O.E.; Chan, A.M.; Neufeld, G.; Miki
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A;Introns: 304/3; 353/1
A;Introns: 304/3; 353/1
A;Introns: 304/3; 353/1
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote C;Keywords: ATP; growth factor receptor
F;262-335/Domain: immunoglobulin homology <IMM>
F;464-750/Domain: protein kinase homology <INM>
F;472-480/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibroblast growth factor receptor 3 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 155363; B53627
R;Ornitz, D.M.; Leder, P.
A;Ornitz, D.M.; Leder, P.
A;Title: Ligand specificity and heparin dependence of fibroblast growth factor receptors
A;Reference number: 155363; MUID:92355591; PMID:1379594
A;Accession: 155363
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NyAlternate names: protein-tyrosine kinase tkf
NyContains: protein-tyrosine kinase (EC 2.7.1.112)
NyContains: protein-tyrosine kinase (EC 2.7.1.112)
CySpecies Humo sapiens (man)
CySpecies Humo sapiens (man)
CySpecies 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
CyAccession: S15345; A46615; Ā41598; D38269
CyAccession: S15345; A46615; Ā41598; D38269
EMBO J. 10, 1347-1354, 1991
AyTitle: FGFR-4, a novel acidic fibroblast growth factor receptor with a distinct express AyReference number: S15345; MUID: 91224085; PMID:1709094
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                                                                                                                                                                       Length 800;
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                                                                                                                                                              79.3%; Score 23; DB 2; I ilarity 57.1%; Pred. No. 5.7e+02; Conservative 2; Mismatches 1;
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A;Molecule type: mRNA
A;Residues: 1-801 <RES>
F;262-335/Domain: immunoglobulin homology <IMM>F;464-749/Domain: protein kinase homology <KIN>F;472-480/Region: protein kinase ATP-binding motif
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624 VMKIADF 630
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Matches 4
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C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote: C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor; F;1-23/Domain: slignal sequence #status predicted <SIG> F;24-806/Product: protein-tyrosine kinase cak2 #status predicted <MAT> F;24-368/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;369-389/Domain: transmembrane #status predicted <TMM>
F;30-806/Domain: intracellular #status predicted <INT>
F;30-806/Domain: protein kinase homology <KIN>
F;472-480/Pomain: protein kinase homology <KIN>
F;472-480/Region: protein kinase APP-binding motif
F;61-107,170-222,269-333/Disulfide bonds: #status predicted
F;62,19,256,288,309,322/Binding site: carbohydrate (ABn) (covalent) #status predicted
F;502,519,611/Active site: Lys, Glu, Asp #status predicted
F;616,629/Binding site: magnesium (Asn, Asp) #status predicted
F;616,629/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predictec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibroblast growth factor receptor Al precursor - African clawed frog N. Containns fibroblast growth factor receptor Al, short splice form; protein-tyrosine kir C;Species: Xenopus laevis (African clawed frog) C;Species: Xenopus laevis (African clawed frog) C;Date: 07-Feb-1992 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/Molecule type: mRNA
A/Residues: 1-814 <FRI>
A/Cressidues: 1-814 <FRI>
A/Cressidues: 193752
A/Accession: B39752
A/Molecule type: mRNA
A/Residues: 1-30,119-814 <FR2>
A/Cross-references: GB:M55163
A/Cross-references: GB:M55163
C/Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protestication: glycoprotein; growths: alternative splicing; AFP; autophosphorylation; duplication; glycoprotein; growths: alternative splicing; AFP; autophosphorylation; duplication; glycoprotein; growths:
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;22-814/Product: fibroblast growth factor receptor Al, long splice form #status experime;22-372/Domain: extracellular #status predicted <EXT>
;22-372/Domain: extracellular #status predicted <EXT>
;22-30.119-814/Product: fibroblast growth factor receptor Al, short splice form #status ;47-102/Domain: immunoglobulin homology <IM>
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F/480-488/Region: protein kinase homology <KIN>
F/480-488/Region: protein kinase ATP-binding motif
F/54-100,114-226,273-337/Disulfide bonds: #status predicted
F/56-116,133,177,223,236,260,292,313,326/Binding site: carbohydrate (Asn) (covalent) #steres: 5/510,527,619/Active site: Lys, Glu, Asp #status predicted
F/56-16,137/Binding site: magnesium (Asn, Asp) #status predicted
F/550/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicter
                                                                                                                                                                                                                A;Cross-references: UNIPROT:P18460; GB:M35195; NID:g211442; PIDN:AAA48664.1; PID:g211443
C;Genetics:
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Mol. Cell. Biol. 11, 2481-2488, 1991
A,Title: cDNA cloning and developmental expression of fibroblast growth factor receptors
A,Reference number: A39752; MUID:91203867; PMID:1850097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.3%; Score 23; DB 2; Length 806; 57.1%; Pred. No. 5.7e+02; ive 2; Mismatches 1; Indels
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                                      A;Reference number: A35963; MUID:90332672; PMID:2165604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;131-138/Region: acidic
F;262-335/Domain: immunoglobulin homology
F;369-389/Domain: transmembrane #status pr
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R;Friesel, R.; Dawid, I.B.
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624 VMKIADF 630
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                                                                                                                  A; Status: preliminary A; Molecule type: mRNA
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A/Accession: A36578

A/Accession: A36578

A/Accession: WIPPOT: P22607; GB:WS6051; NID:g182568; PIDN:AAA52450.1; PID:g182568

A/COGGG-TECETORGGGG WIPPOT: P22607; GB:WS6051; NID:g182568; PIDN:AAA52450.1; PID:g182568

A/TILLE: A gene enrolling at fibroblast growth factor receptor isolated from the Huntingtc

A/Accession: A5273

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A35963
protein-tyrosine kinase (EC 2.7.1.112) cek2 precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C;Accession: A35963
R;Pasquale, E.B.
Proc. Natl. Acad. Sci. U.S.A. 87, 5812-5816, 1990
A;Title: A distinctive family of embryonic protein-tyrosine kinase receptors.
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Cipacesion: A41445, Assignation of the control of the sequence of shown; not compared with conceptual translation A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Molecule type: mRNA A; Residues: 1-819 <LES A; Anotes: UNIPROT: P21804 A; Note: part of the sequence was confirmed by protein sequencing R; Pasquale, E.B.; Singer, S.J. Proc. Natl. Acad. Sci. U.S.A. 86, 5449-5453, 1989 A; Note: mumber: A33908; MulD: 89315814; PMID: 2473471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein C; Superfamily: basic fibroblast growth factor receptor 1; Fi-21/Domain: signal sequence #status predicted <SIG> Fi-22-81s/Product: fibroblast growth factor receptor 1 #status predicted <MAT> Fi-22-74/Domain: extracellular #status predicted <EXT> Fi-22-74/Domain: extracellular #status predicted <EXT> Fi-22-75/Domain: immunoglobulin homology <IMM> Fi-35-135/Domain: immunoglobulin homology <IMM> Fi-35-135/Domain: intracellular #status predicted <INT> Fi-35-135/Domain: protein kinase homology <IMN> Fi-35-100,176-228,275-339/Disulfide bonds: #status predicted Fi-56-100,176-228,275-339/Disulfide bonds: #status predicted Fi-56-100,176-228,275-339/Disulfide bonds: #status predicted Fi-56-100,176-228,275-339/Disulfide bonds: #status predicted Fi-56-539/Binding site: magnesium (Asn, Asp) #status predicted Fi-56-539/Binding site: magnesium (Asn, Asp) #status predicted Fi-56-5539/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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C;Species: Mus musculus (house mouse)
C;Aar: 1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S17295
R;Raz, V.; Kelman, Z.; Avivi, A.; Neufeld, G.; Givol, D.; Yarden, Y.
Oncogene 6, 753-760, 1991
A;Title: PCR-based identification of new receptors: molecular cloning of a receptor for 1
A;Reference number: S17295; MUID:91270892; PMID:1711190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: this protein is expressed in embryonic tissues and, at low levels, in adult brair
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                                                                                                                                                                                                                                                                         fibroblast growth factor receptor 1 precursor - chicken
NyAlternate names: basic fibroblast growth factor receptor
NyContains: protein-tyrosine kinase (BC 2.7.1.112) cek1
C,Species: Gallus gallus (chicken)
C,Species: 31-Dec.1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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Pred. No. 5.8e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-89,'A',91-685,'M',687-819 <PAS>
A;Cross-references: GB:M24637
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Similarity 57.1%;
4; Conservative
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634 VMKIADF 640
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637 VMKIADF 643
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Best Local Similarity
Matches 4; Conserv
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1 VMXVAEF
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A; Status: preliminary
A; Molecule type: mRNA
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S17295
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fibroblast growth factor receptor-4 precursor - African clawed frog
C; pace: 29-Unn-1995 #sequence_revision 14-U1-1995 #text_change 09-Unl-2004
C; Accession: JG4058
R; Shiozaki, C: Tashiro, K:; Asano-Miyoshi, M.; Saigo, K.; Emori, Y.; Shiokawa, K.
Gene 152, 215-219, 1995
A; Title: Cloning of cDNA and genomic DNA encoding fibroblast growth factor rece ptor-4
A; Recession: JG4058
A; MUID: 95137391; PMID: 7835703
A; Residues: 1-818 cSHI
A; Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibroblast growth factor receptor 1 - Iberian ribbed newt
C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49151
R;Shi, D.L.; Feige, J.J.; Riou, J.F.; DeSimone, D.W.; Boucaut, J.C.
Development 116, 261-273, 1992
A;Title: Differential expression and regulation of two distinct fibroblast growth factor
A;Reference number: A49151; MUID: 93130775; PMID: 1483392
A;Rossion: A49151
A;Rossion: A49151
A;Rossion: A49151
A;Rossion: A9151
A;Rossion: A9151
A;Rossion: A9151
A;Rossion: A9151
A;Rossion: Les Carrences: UNIPROT: 091285
A;Rossion: Esquence extracted from NCBI backbone (NCBIN:122562, NCBIP:122597)
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Reywords: AFP; growth factor receptor
F;469-230/Domain: immunoglobulin homology <IMM>
F;472-757/Domain: protein kinase homology <IMM>
F;480-488/Region: protein kinase ATP-binding motif
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                                     Length 814;
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                                                                                                                      2; Mismatches
                             79.3%;
57.1%;
Query Match
Best Local Similarity 57.1.
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                    || :|:|
632 VMKIADF 638
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632 VMKIADF 638
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Matches
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Query Match

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Fil2-138/Region: acidic
Fil2-233/Domain: immunoglobulin homology <IMM>
Fil72-233/Domain: immunoglobulin homology <IMM>
Fil72-233/Domain: transmembrane #status predicted <IMM>
Fil2-234/Domain: transmembrane #status predicted <IMT>
Fil2-38/Domain: protein kinase homology <KIN>
Fil2-479-764/Domain: protein kinase homology <KIN>
Fil2-37-274/Edjon: protein kinase homology <IMIN
Fil2-107/179-231,278-342/Disulfide bonds: #status predicted
Fil2-107/179-231,278-342/Disulfide bonds: #status predicted
Fil2-107/179-231,278-342/Disulfide bonds: #status predicted
Fil2-107/179-231,644/Binding site: magnesium (Asn, Asp) #status predicted
Fil2-107/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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NyAlternate names: bek transforming protein; fibroblast growth factor receptor 2; keratir
NyContains: protein-tyrosine kinase (EC 2.7.1.112) bek
C;Species: Mus musculus (house mouse)
C;Date: 30-un-1991 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: A44142; A31378
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CiSuperfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protesi

CiSuperfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protesi

CiSuperfamily: algonal sequence #status predicted <51G.
Fi.1-21/Domain: signal sequence #status predicted <51G.
Fi.2-831/Product: fibroblast growth factor receptor bek #status predicted <MAT.>
Fi.17-2.33/Domain: immunoglobulin homology <IMM.>
Fi.17-2.33/Domain: protein kinase homology <KIN.>
Fi.37-398/Domain: protein kinase homology <KIN.>
Fi.479-764/Domain: protein kinase homology <KIN.>
Fi.479-764/Domain: protein kinase homology <IMN.>
Fi.479-764/Domain: grotein kinase homology immorified for firmin firmin
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R;Kornbluth, S.; Paulson, K.E.; Hanafusa, H.
Rnol. Cell. Biol. 8, 5541-5544, 1988
A;Title: Novel tyrosine kinase identified by phosphotyrosine antibody screening of cDNA A;Reference number: A31378; MUID:89219016; PMID:2468999
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Afritle: Characterization of the murine BEK fibroblast growth factor (FGF) receptor: ac
A;Reference number: A44142; MUID:92228773; PMID:1373495
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A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A;Molecule type: mRNA
A;Mesidues: 1-821 «MAN»
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A;Residues: 477-821 <KOR>
A;Cross-references: GB:M23362; NID:g533219; PIDN:AAA37285.1; PID:g533220
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        extracellular #status predicted <EXT>
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Pred. No. 5.8e+02;
2; Mismatches 1;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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639 VMKIADF 645
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639 VMKIADF 645
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                                                                          A;Cross-references: UNIPROT:P21803; EMBL:X55441; NID:g50141; PIDN:CAA39083.1; PID:g50142 (S.Quperfemanly: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote F;270-343/Domain: immunoglobulin homology <IMA-F;270-343/Domain: immunoglobulin homology <IMN-F;478-763/Domain: protein kinase homology <IMN-F;478-763/Domain <IMN-F;478-763/Domain <IMN-F;478-763/Domain <IMN-F;478-763/Doma
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A; Regidues: 1-821 <DIO>
A; Cross-references: EMBL:X52832; NID:g31373; PIDN:CAA37014.1; PID:g31374
A; Cross-references: EMBL:X52832; NID:g31373; PIDN:CAA37014.1; PID:g31374
B; Houssaint, E.; Blanquet, P.R.; Champion-Arnaud, P.; Gesnel, M.C.; Torriglia, A.; Court
Proc. Natl. Acad. Sci. U.S.A. 87, 8180-8184, 1990
A; Title: Related fibroblast growth factor receptor genes exist in the human genome.
A; Reference number: A36210; MUID:91045961; PMID:2172978
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A, Molecule type: mRNA
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A, Molecule type: mRNA
A, Cross-references: GB: MS5614, GB: M37715, NID: g339710, PIDN: AAA61188.1; PID: g339711
A, Cross-references: GB: MS5614, GB: M37715, NID: g339710, PIDN: AAA61188.1; PID: g339711
A, Title: Multiple mRNAs code for proteins related to the BEK fibroblast growth factor re
A, Reference number: A44775, MUD: 91296403; PMID: 1648704
A, Residues: 263-361 < CH2>
A, Molecule type: DNA
A, Residues: BNA
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C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; g
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A; Molecule type: mRNA
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A;Cross-references: GB:S41873
C;Comment: This receptor binds basic fibroblast growth factor and, with lower affinity,
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Pred. No. 5.8e+02;
2; Mismatches 1;
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Matches 4, Conservative
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VMKIADF 644
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A;Residues: 1-820 <RAZ>
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Molecule type: protein; Residues: 81-100 <RUS>
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A, Accession: 13169.

A, Thur. J, Kan, M.; McKeehan, K.; McBride, G.; Adams, P.; McKeehan, W.L.

S, Hou, J.; Kan, M.; McKeehan, K.; McBride, G.; Adams, P.; McKeehan, W.L.

S, Hou, J.; Kan, M.; McKeehan, K.; McBride, G.; Adams, P.; McKeehan, W.L.

A, Thirle: Fibroblast growth factor receptors from liver vary in three structural domains.

A, Reference number: 140062.

A, McCession: 18062.

A, McCession: 18063.

A, Mc
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N;Alternate names: basic fibroblast growth factor receptor; heparin-binding growth factor
N;Contains: HBGFR 3; HBGFR alpha bl; HBGFR beta al; HBGFR beta bl; HBGFR gamma al; HBGFR
C;Species: Hmom sapiens (man)
C;Date: 31-Mar-1989 #sequence revision 31-Dec-1993 #text change 09-Jul-2004
C;Accession: S11692; B40862; S09226; A61533; A61536; S26739; S26738; S17374; S17375; S17
R;Dionne, C.A.; Crumley, G; Bellot, F.; Kaplow, J.M.; Searfoss, G.; Ruta, M.; Burgess,
BMBO J. 9, S685-2692, 1990
A;Title: Cloning and expression of two distinct high-affinity receptors cross-reacting w
A;Reference number: S11691; MUID: 90360977; PMID: 1697263
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Accosation teferances | EMGL.X27119 | ND1911389; PIDN.CDAGAGGGL.1; PD1931389

All Process: this forms designated lasform II statent with that from Fig. 1 in lacking 25-Pro; Accosation 51377

Accosation 5137

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1-30,120-228,'S',230-255,'ILQ',259-269,'A',271-543,'M',545-755,'R',757-764,'I
                                                        Ajcross-references: GB:N33766; NID:913298; PIDN:AAA37622.1; PID:9309240
R;Harada, T.; Saito, H.; Kouhara, H.; Kurebayashi, S.; Kasayama, S.; Terakawa, N.; Kishin Biophys. Res. Commun. 205, 1057-1063, 1994
A;Title: Murine fibroblast growth factor receptor 1 gene generates multiple messenger RNJ A;Reference number: PC2277; MUID:95100926; PMID:7802632
A,Accession: PC2277
A,Molecule type: DNA A;Residues: 1-15 cHAR>
A;Cross-references: GB:S74765; NID:9833887; PIDN:AAB32845.1; PID:9833889
C;Comment: This protein mediates the biological actions of heparin-binding growth factor c;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protes: C;Reywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; gs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;22-822/Product: fibroblast growth factor receptor 1 #status predicted <MAT>
F;22-37(Domain: extracellular #status predicted <EXT>
F;22-30,120-822/Product: fibroblast growth factor receptor 1, short form #status predicte
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7,171-232/Domain: immunoglobulin homology <IMM>
7,377-397/Domain: transmembrane #status predicted <IVM>
7,378-822/Domain: intracellular #status predicted <IVM>
7,484-92/Domain: intracellular #status predicted <IVM>
7,484-92/Region: protein kinase ATP-binding motif
7,55-101,178-230,277-341/Disulfide bonds: #status predicted
7,55-101,178-230,277-341/Disulfide bonds: #status predicted
7,514,531,623/Active site: Lys, Glu, Asp #status predicted
7,514,531,623/Active site: magnesium (Asn, Asp) #status predicted
7,5628,641/Binding site: magnesium (Asn, Asp) #status predicted
7,554/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predictec
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J. Biol. Chem. 269, 23743-23749, 1994
A.Title: Molecular cloning and expression of the acidic fibroblast growth factor recepton alone on the condition of the acidic fibroblast growth factor recepton ility and covalent attachment of heparan sulfate glycosaminoglycan to the receptors. A.Reference number: A54846; MUID:94375484; PMID:8089146
A.Accession: B54846
A.Accession: B54846
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-822 <TAK>
C.Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protes
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 16-Jul-1999
C;Accession: B54846
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Pred. No. 5.8e+02;
2; Mismatches 1; Indels
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$1.72-233/Domain: immunoglobulin homology <IMM>
F;480-765/Domain: protein kinase homology <KIN>
F;488-496/Region: protein kinase ATP-binding motif
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Similarity 57.1%;
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F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-822/Product: fibroblast growth factor receptor 1, form alpha al #status predicted < F;22-822/Product: fibroblast growth factor receptor 1, form alpha bl #status prefit 25.22-376/Domain: extracellular #status predicted <EXT>
F;22-147,150-822/Product: fibroblast growth factor receptor 1, form 3 #status predicted F;22-147,150-822/Product: fibroblast growth factor receptor 1, form beta al #status predicted F;22-30,120-427,430-822/Product: fibroblast growth factor receptor 1, form beta al #status predicter F;126-133/Region: acidic
F;161-822/Product: fibroblast growth factor receptor 1, form gamma al #status predicted F;161-822/Product: fibroblast growth factor receptor 1, form gamma bl #status prefit F;161-427,430-822/Product: fibroblast growth factor receptor 1, form gamma bl #status prefit F;171-232/Domain: immunoglobulin homology <IMM>F;377-397/Domain: immunoglobulin homology <IMN>F;377-397/Domain: intracellular #status predicted <INT>F;444-492/Region: protein kinase ATP-binding motif F;644-492/Region: protein kinase ATP-binding motif F;77:117,227,240,264,2596;317,330/Binding stee: carbobydrate (Asn) (covalent) #status predicted F;614,511,623/Active site: Lys, Glu, Asp #status predicted F;628,641/Binding site: magnesium (Asn, Asp) #status predicted F;628,641/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted F;654/Binding site: phosphate (Tyr)
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Nighternate names: basic fibroblast growth factor receptor

Nicontains: protein-tyrosine kinase (EC 2.7.1.112) flg

Cipacies: Mus musculus (house mouse)

Cipace: 31-Dec-1993 #text change 09-Jul-2004

Cipace: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 09-Jul-2004

Riseid. H.H.; Wilks, AF.; Bernard, O.

Proc. Natl. Acad. Sci. U.S.A. 87, 1596-1600, 1990

A;Reference number: A34849; MUD:90160373; PMID:1689490

A;Reference number: A34849; MUD:90160373; PMID:1689490

A;Residues: 1-822 are references: UNIPROT:P16092; GB:M28998; NID:g192164; PIDN:AAA37290.1; PID:g309116

A;Residues: 1-30,120-822 are seperences: GB:M28998; NID:g192164; PIDN:AAA37290.1; PID:g309116

A;Residues: 1-30,120-822 are seperences: GB:M28998

A;Molecule type: mRNA

A;Residues: 1-30,120-82

A;Residues: 1-30,120-8398

A;Note: the shorter form is expressed at higher levels in neuronal cells at early stages

A;Note: the shorter form is expressed at receptor for fibroblast growth factor.

A;Reference number: S09953; MUID:90265603; PMID:2161096
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A;Cross-references: GB:M33760
R;Basilico, C.
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A;Molecule type: mRNA
A;Residues: 1-147,150-255,'ILQ',259-439,'A',441-755,'R',757-822 <SAF>
A;Ross-references: EMBL:X51893; NID:950959; PIDN:CAA36175.1; PID:950960
B;Mansukhani, A.; Moscatelli, D.; Talarico, D.; Levytska, V.; Basilico, C.
Proc. Natl. Acad. Sci. U.S.A. 87, 4378-4382, 1990
A;Title: A murine fibroblast growth factor (FGF) receptor expressed in CHO cells is A;Reference number: A35794; MUID:90272715; PMID:2161540
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A;Reference number: A43025
A;Accession: A43025
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C; Species: Homo sapiens (man)
C; Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C; Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C; Accession: A45081
R; Dell; KR.; Williams, L.T.
J. Biol. Chem. 267, 21225-21229, 1992
A; Title: A novel form of fibroblast growth factor receptor 2. Alternative splicing of th A; Reference number: A45081; MUD:93016048; PMID:1400433
A; Rocession: A45081
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Q74116 mycobacteri Q91687 salmonella Q88717 escherichia Q859e0 pseudomonas Q8ty74 methanopyru Q7wfx5 bordetella Q73k89 treponema d Q63000 rattus norv Q8wmp3 equus cabal Q61153 picrophilus	Copsilor acchaeced to the control of the copsilor acchaeced to Copsilor anopheles go Copsilor anopheles go Copsilor anopheles go Copsilor accordance to Copsilor	Q28111 bos taurus Q28332 callithiix Q200K5 sus scrofa Q69K45 oryza sativ Q9ceul lactococcus Q9ceul lactococcus Q964Q2 bacteroides	QUALES SUCOSCUELL QUALES SUPZIOSCUELL Q02529 oryzias lat Q01176 oryzias lat Q91177 oryzias lat Q91177 oryzias lat Q69117 oryza sativ Q67559 olkopleura Q6919 oryza sativ	Q81c12 escherichia Q9kkv1 vibrio chol Q81647 deschampsia Q898y8 clostridium Q7490 anopheles g Q8ty17 methanopyru Q6bmy0 debaryomyce Q6z056 oryza sativ	Q89129 bradyrhizob Q8dul8 streptococc Q8ns24 corynebacte Q7pwv1 anopheles g Q8fr32 corynebacte Q9piu8 campylobact Q9nhw7 aedes aegyp P07283 aeacharomyc Q70d77 saccharomyc		Q93aml drosophila Q93ag mus musculu Q7trr8 homo sapien Q645x0 homo sapien Q645x1 staphylococ Q7x1g1 leptospiril Q8hqj2 ornithodoro Q7xnl1 leptospiril Q9u8w3 branchiosto Q89ek5 bradyrhiosto Q9u8w4 eptatretus Q8tx93 methanopyru
	444444	00000000	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	00000000000	00000000000	0 H O O O H H O O O O	312 2 Q9GNN1 312 2 Q9GNN1 314 2 Q9EQB 314 2 Q6EQB3 321 2 QYSLG1 324 2 Q9HQJZ 325 2 QYXLN1 329 2 Q9UBW3 333 2 Q89EK5 333 2 Q8TX93

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This SWISS-PROT entry is copyright. It is produced through a collaboration
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01-FB2-1994 (Rel. 28, Last sequence update)
25-CCT2-2004 (Rel. 45, Last sequence update)
Genome polyprotein (Contains: Capsid protein C (Core protein); Matrix
protein (Envelope protein M); Major envelope protein E; Nonsetructural
proteins NS1, NS2A, NS2B, NS2A, NS2B, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92263794; PubMed=1316684; Iacono-Connors L.C., Schmaljohn C.S., "Cloning and sequence analysis of the genes encoding the nonstructural proteins of Langat virus and comparative analysis with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -Xbb bonds in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flaviviruses.";
Virology 188:875-880(1992).

-!- FUNCTION: The small proteins NS2A, NS4A and NS4B are hydrophobic, successful a possible membrane-related function. NS5 may play a role in the viral RNA replication. NS3 and NS2B form a protease which processes the viral polyprotein into separate proteins.

-!- CATALYTIC ACTIVITY: Selective hydrolysis of Xaa-Xaa-|-Xbb bonds is which each of the Xaa can be either Arg or Lys and Xbb can be either Ser or Ala.
                                                                                                                                                                                                                                                                                                                                                                Gaps
                         capable of controlling K homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence of the genes encoding the structural proteins of the low-
virulence tick-borne flaviviruses Langat TP21 and Yelantsev.";
Virology 185:891-895(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uangat virus (strain Tr21).
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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SUBUNIT: The virion of this virus is a nucleocapsid covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
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Heinz F.X.;
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                                                                                                                                                                                                                                                                                                                Length 776;
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Pred. No. 1e+02;
0; Mismatches
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MEDLINE=92074260; PubMed=1720591;
Regan S., Fromm J., Hedrich R.;
"Poplar potessium transporters of
and K -dependent xylogenesis.";
Plant J. 32:997-1009(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 777-3414 FROM N.A.
                                                                                                                                                                                                                                                                                                                   96.6%;
85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
eurosids I; Malpighiales, Salicaceae, Saliceae, Populus.
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MEDLINE=22381938; Pubmed=12492841;
Langer K., Ache P., Geiger D., Stinzing A., Arend M., Wind C.,
073rj6
Q63qb7
Q8yfy0
Q6tvz8
Q6tv86
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088dbn7
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
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0941L7
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InterPro; IPR0004847; Flavi NS2B.

InterPro; IPR001528; Flavi NS2B.

InterPro; IPR001528; Flavi NS5.

InterPro; IPR001528; Flavi NS5.

InterPro; IPR001528; Flavi PR05.

InterPro; IPR001650; Flavi PR05.

InterPro; IPR001650; Flavi PR01686 S7.

InterPro; IPR00169; Flavi PR01686 S7.

InterPro; IPR00169; Flavi PR05.

InterPro; IPR00169; Flavi PR06.

IPR061696; Flavi PR061696; Fl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nonstructural protein NS4A (Potential).
Nonstructural protein NS4B (Potential).
RNA-directed RNA polymerase (Potential)
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Nonstructural protein NS1 (Potential).
Nonstructural protein NS2A (Potential).
Flavivirin protease subunit NS2B
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Capsid protein C (Potential).
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(By similarity).
(By similarity).
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Potential.
Potential.
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Flavi_M.
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                                                                                                                               EMBL; M73835; AAA02740.1; ALT_TERM.
EMBL; S35365; AAB22165.1; -.
PIR; A42545; A42545.
HSSP; P14336; 1SVB.
                                                                                                                                                                                                                                                                     capsidC.
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Flavi NS2A.
Flavi NS2B.
Flavi NS4A.
Flavi NS4B.
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InterPro; IRR001410; DEAD.
InterPro; IRR001121; Flavi capai
InterPro; IRR001122; Flavi capai
InterPro; IRR000336; Flavi glycc
InterPro; IRR000157; Flavi glycc
InterPro; IRR001157; Flavi NS1.
InterPro; IRR001157; Flavi NS2A.
InterPro; IRR000445; Flavi NS2A.
InterPro; IRR000446; Flavi NS2A.
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1543
1567
1779
103
262
728
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206
281
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NP_BIND
ACT_SITE
ACT_SITE
ACT_SITE
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TRANSMEM
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CHAIN
CHAIN
CHAIN
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MEDLINE-20192178; PubMed=10725214; DOI=10.1006/viro.2000.0220;
Campbell M.S., Pletnev A.G.;
"Infectious cDNA clones of Langat tick-borne flavivirus that differ from their parent in peripheral neurovirulence.";
Virology 269:223-237(2000).
BMBL, AF23420; A8475260.1; -.
HSSP; P14316; 1SVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
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GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:00008026; F:ATP dependent helicase activity; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003724; F:RNA helicase activity; IEA.

GO; GO:0003729; Flavi NS2.

InterPro; IPR000487; Flavi NS2.

InterPro; IPR001529; Flavi NS4.

InterPro; IPR001529; Flavi NS4.
                                                                                                                                                                                                            ;
0
                                                                                                                                                                          Score 28; DB 1; Length 3414;
Pred. No. 4.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        PRT; 3414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA pol DS PS.
RNA pol PSvir.
RrmJFtsJ mtfrase.
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PF00869; Flavi_glycoprot; 1.
PF02832; Flavi_glycop_C; 1.
                                                                                                                                                                            96.68;
                                                                                                                                           378017
                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
   310
336
3385
401
570
618
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polyprotein precursor.
Langat virus.
                                                                                                                                                                                                                                                                                 929 VMTVAEF 935
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                                                                                                                                           3414 AA;
                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                 1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=11085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flavivirus.
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
                                                                                                                           CARBOHYD
                                                                                                                                             SEQUENCE
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                        091639
                                                                                                                                                                                                                                                                                                                                      RESULT 3
Q9IG39
   SOLUTION
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Solanum bulbocastanum (Wild potato).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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nonstructural protein NS4a.
nonstructural protein NS4b.
membrane-associated glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 2; Length 3414;
Pred. No. 4.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD001556; Flavi_glycoprotE; 1.
ProDom; PD001496; Flavi_glycoprotE; 1.
SWART; SM00487; DEXDC; 1.
SMART; SM00480; HELICC; 1.
ATP-binding; Helicase; Hydrolase; Polyprotein; Signal.
SIGNAL
780 1128 nonstructural protein NS1.
CHAIN 1129 1358 nonstructural protein NS2.
CHAIN 1359 1489 nonstructural protein NS2.
CHAIN 2100 2110 nonstructural protein NS2.
CHAIN 2260 2511 nonstructural protein NS3.
CHAIN 2260 2511 membrane-associated glycopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      envelope membrane-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycoprotein.
1 96 capsid protein.
3414 AA; 378138 MW; 8DE86A46A0E8F7E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nonstructural protein NS5
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative transposase-related protein.
ORFNames=CB3A14.3;
DEAD/DEAH N.
Flavi capsidC.
Flavi DEAD.
Flavi glycoprotE.
Flavi M.
Flavi M.
Flavi NS1.
Flavi NS2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor.
                                                                                                                                                                                                                                                                                                                    Flavi_propep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycoprot; 1
                                                                                                                                                                                                                                                                                                                                           PR001650; Helicase (PR001850; Peptidase
                                                                                                                                                                                                                                                                           Flavi_NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   propep; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEAD; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF01570, Flavi_proper
Pfam, PF01728, FtsJ; 1.
Pfam, PF00271, Helicase_C;
Pfam, PF00949; Peptidase_S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                              PR000069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane-associated glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G0:0019028; C:viral capsid; IEA.
G0:0019031; C:viral envelope; IEA.
G0:0019031; C:viral envelope; IEA.
G0:0008524; F:ATP binding; IEA.
G0:0008026; F:ATP-dependent helicase activity; IEA.
G0:0010723; F:RNA binding; IEA.
G0:0003723; F:RNA helicase activity; IEA.
G0:0003968; F:RNA-directed RNA polymerase activity; IEA.
G0:0003198; F:Structural molecule activity; IEA.
G0:00019079; P:viral genome replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    nonstructural protein NS1.
nonstructural protein NS2a.
nonstructural protein NS2b.
nonstructural protein NS3.
nonstructural protein NS4a.
nonstructural protein NS4a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 envelope membrane-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycoprotein.
96 capsid protein.
378018 MW; BF8F8ACEAB96D534 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nonstructural protein NS5
                                                                                                                                                                                                                                                                        ProDom; PD001556; Flavi_GlycoprotE; 1.
ProDom; PD001496; Flavi_NS1; 1.
SMART; SM00487; DEXDc; 1.
SMART; SM00490; HELICC; 1.
SIGNAL
97 116 nonstructural protein NS1
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 2; L
Pred. No. 4.2e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor.
                                              Pfam; PF01002; Flavi NS2B; 1.
Pfam; PF01349; Flavi NS4A; 1.
Pfam; PF001349; Flavi NS4B; 1.
Pfam; PF00972; Flavi NS5; 1.
Pfam; PF01570; Flavi Dropep; 1.
Pfam; PF001728; FfeJ; 1.
Pfam; PF00271; Helicase C; 1.
Pfam; PF00271; Helicase C; 1.
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Best Local Similarity 85...
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polyprotein precursor.
Langat virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       929 VMTVAEF 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3414 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=11085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plavivirus
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091640
110 091640
DT 01-00
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SEQUENCE FROM N.A.

STRAIN-CV. Columbia;

MEDLINE-20081488; PubMed=10617198; DOI=10.1038/47134;

MEDLINE-20081488; PubMed=10617198; DOI=10.1038/47134;

MAPER E., A. Schueller C., Wambutt R., Murphy G., Volckaert G.,

Mayer K.F.X., Schueller C., Mambutt R.-D., Terryn N.,

A Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,

Meichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

Kreis M., Delseny M., Puigdomench P., Watson M., Schmidthehin T.,

Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

Nos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,

Langham S.-A., McCullagh B., Bilham L., Robben J.,

Nan der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,

Racken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,

Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,

Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Defoor E.,

Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Defoor E.,

Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

Meitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

Merkeyser A., Buysshaert C., Galelen J., Villarroel R., Monday R.,

Nan Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,

Nan Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,

Rockova D., Bloecker H., Scharfe M., Grimm M., Lohnert T.-H.,
                                                                                                                                                                                                                                                                                   ö
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
                                               N [1]

P. SEQUENCE FROM N.A.

X. PubMed=12872003; DOI=10.1073/pnas.1533501100;

RA Song J., Bradeen J.M., Naess S.K., Raasch J.A., Wielgus S.M.,

RA Haberlach G.T., Liu J., Kuang H., Austin-Phillips S., Buell C.R.,

RA Helgeson J.P., Jiang J.;

RT Tesistance to potato late blight.";

RT resistance to potato late blight.";

RT resistance to potato late blight.";

RT Proc. Natl. Acad. Sci. U.S.A. 100:9128-9133(2003).

REPRI, AY303170; AP84516.1.;

REPRI, AY303170; AP84516.1.;

REPRI, AY303170; PRION PRION CRC64;
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9FE39; O22399; Q9SUR2; 29-MAR-2004 (Rel. 43, Created) 29-MAR-2004 (Rel. 43, Last sequence update) 29-MAR-2004 (Rel. 44, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) Potassium transporter 3 (AtPOT3) (AtKUP4) (AtKT3) (Tiny root hair 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=POT3; Synonyms=KT3, KUP4, TRH1; OrderedLocusNames=At4g23640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Columbia;
BEDLINE-21095911; PubMed=11158535;
Rigas S., Debrosses G., Haralampidis K., Vicente-Agullo F.,
Feldmann K.A., Grabov A., Dolan L., Hatzopoulos P.;
"TRH1 encodes a potassium transporter required for tip growth in
Arabidopsis root hairs";
Plant Cell 13:139-151(2001).
                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                     Score 27; DB 2; Length 433;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., FUNCTION, AND NULL MUTANT
                                                                                                                                                                                                                                                                                                                                                                                                                          775 AA.
                                                                                                                                                                                                                                                                                   1; Mismatches
              lāmiids; Solanales; Solanaceae; Solanum.
NCBI_TaxID=147425;
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71.4%;
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Best Local Similarity 71...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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29 IMTVAEF 35
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is no no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib.eib.ch). A Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,

A Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,

Neumann S., Argirtou A., Vitale D., Liguori R., Piravandi E.,

A Schnabl S., Hiller R., Schmidt W., Lecharny A., Rabber R.,

A Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,

Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta B.,

Chefdor F., Weber N., Vandenboll M., Bargues M., Terol J., Torres A.,

Berze-Perez A., Purnell B., Bent E., Johnson S., Tacon D., Jesse T.,

A Perze-Perez S., Scholler P., Heber S., Francs P., Bielke C.,

RA Zaccaria P., Bevan M., Wilson R.K., de la Baetide M., Habermann K.,

Parnell L., Dedhia N., Groff R.K., de la Baetide M., Habermann K.,

RA Schon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,

RA Sconeking T., Kalicki J., Graves T., Harmon G., Edwards J.,

A Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,

A Bentley D., Pulton B., Miller N., Scott K., Johnson D.,

A Minr P., Bentley D., Pulton B., Miller N., Greco T., Kemp K.,

Nalson J., Spieth J., Rardis E., Dante M., Pepin K., Hillier L.W.,

Nelson J., Spieth J., Rargines E., Dante M., Pepin K., Hillier L.W.,

Nalson J., Stodinic M., Strong C., Sun H., Lamar B., Yordan C.,

A Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,

Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,

Chan E., Marra M.A., Martiensen R., McCombie W.R.;

Squence and analysis of chromosome 4 of the plant Arabidopsis root hair growth. -!- SIMILARITY: Belongs to the HAK/KUP transporter (TC 2.A.72) family. -!- CAUTION: Ref. 2 sequences differ from that shown due to erroneous leaves and flowers of mature plants.
-!- DEVELOPMENTAL STAGE: Highly expressed in roots in the early stage of seedlings growth. Sze H., -i-FUNCTION: High-affinity potassium transporter required for tip growth of root hairs.
-i-SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane Quintero F.J., Blatt M.R.; $^{\prime}$ "A new family of K+ transporters from Arabidopsis that are conserved STRAIN-cv. Columbia; MEDLINE=98010480; PubMed=9350997; DOI=10.1016/S0014-5793(97)01125-3; -!- TISSUE SPECIFICITY: Detected at very low levels in roots, stems, Maeser P., Thomine S., Schroeder J.I., Ward J.M., Hirschi K., Sze Talke I.N., Amtmann A., Maathuis F.J.M., Sanders D., Harper J.F., Tchieu J., Gribskov M., Persans M.W., Salt D.E., Kim S.A., "Phylogenetic relationships within cation transporter families of Kim E.J., Kwak J.M., Uozumi N., Schroeder J.I.; "AtKUP1: an Arabidopsis gene encoding high-affinity potassium GENE FAMILY, AND NOMENCLATURE. MEDLINE=21392307; PubMed=11500563; DOI=10.1104/pp.126.4.1646; Arabidopsis."; Plant Physiol. 126:1646-1667(2001) TISSUE SPECIFICITY. MEDLINE=98138058; PubMed=9477571; FBBS Lett. 415:206-211(1997) SEQUENCE OF 1-344 FROM N.A. gene model prediction. Plant Cell 10:51-62(1998). Nature 402:769-777(1999). transport activity across phyla."; (Potential) Guerinot M.L.; thaliana

Length 814;

6350453B857BEBCB CRC64;

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GO; GO:0006813; P:potassium ion transport; IEA
               Pfam; PF02705; K trans; 1.
TIGRFAMS; TIGR00794; kup; 1.
SEQUENCE 814 AA; 91608 MW;
                                                                                   Query Match
Best Local Similarity
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P47296;
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SEQUENCE
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Spermatophyta, Magnoliophyta, Liliopsida, Cymodoceaceae, Cymodocea.
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MEDLINE=22261168; PubMed=12374296; DOI=10.1023/A:1019951023362;
MEDLINE=22261168; Benito B., Rodriguez-Navarro A.;
"Molecular Broining and functional expression in bacteria of the potassium transporters ChHAK1 and ChHAK2 of the seagrass Cymodocea
                                                                                        PIER, T05596, T05596. K+ transporter.
InterPro; IPR003855, K+ transporter.
Pfam; PF02705; K trans; 1.
TIGRPAMS; TIGR00794; kup; 1.
Multigene family; Potassium transport; Transmembrane; Transport.
DOMAIN 1 31 Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.1%; Score 27; DB 1; Length 775; 71.4%; Pred. No. 2e+02; ive 1; Mismatches 1; Indels
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EMBL; AJ427293; CAD20319.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015079; F:potassium ion transporter activity; IEA.
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B0C55068B48E8180 CRC64;
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01-JUN-2003 (TrEMBLrel. 20, Last sequence update)
Putative potassium transporter.
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                                              AL035394; CAA23030.1; ALT_SEQ.
AL161559; CAB79319.1; ALT_SEQ.
AF012658; AAC49846.1; -.
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                 CAC16137.1;
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286
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VMSIAEF 608
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TRANSMEM
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EMBL;
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084XQ3
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                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Deoxyribose-phosphate aldolase (EC 4.1.2.4) (Phosphodeoxyriboaldolase)
                                                          Gaps
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-1- PATHWAY: Nucleotide and deoxyribonucleotide catabolism.
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: Belongs to the deoC/fbaB aldolase family. DeoC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma genitalium.
Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma
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By similarity,
7 332430231CB99DB0 CRC64;
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Pred. No. 1.1e+02;
Score 27; DB 2; Length 814
Pred. No. 2.18+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                              223 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=deoC; OrderedLocusNames=MG050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
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InterPro; IPR0012915; DeoC.
InterPro; IPR003009; FMN_enzyme.
Pfam; PF01791; DeoC; 1.
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71.4%;
93.1%;
71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
                                                       5; Conservative
                                                                                                                                                                                                                                                                                                           STANDARD;
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HSSP; O66540; 1MZH.
TIGR; MG050; -.
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223 AA;
                                                                                                           1 VMXVAEF 7
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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicacese; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Barnstead M.B., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016832; F:aldehyde-lyase activity; IEA.
GO; GO:0009073; P:aromatic amino acid family biosynthesis; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
                                                                                                                                                                                                                                       STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422; Weiss R.B., Dunn D.M., Robb P.T., Brown J.R.; "The complete sequence of the Pyrococcus furiosus genome."; submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AE010267; ALB1814.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.7%; Score 26; DB 2; Length 324; 71.4%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 26; DB 2; Length 262;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                       01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Town C.D., Kaul S.,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006836; AAD20079.1; -.
PIR; B84452; B84452.
HSSP; P52839; 1044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 AA; 29225 MW; ED84D28FD5DEADC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 AA; 37717 MW; B488C799AB13E1D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0008146; F:sulfotransferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. Interpro; IPR000863; Sulfotransferase. Ffam; PF00685; Sulfotransferal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00793; DAHP_synth_1; 1.
TIGRFAMS; TIGR01361; DAHP_synth_Bsub; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD001218; SulfotransFerase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative steroid sulfotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.7%;
71.4%;
                   01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2004 (TrEMBLrel. 26,
                                                                                                       OrderedLocusNames=PF1690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                             Pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | | | | |
39 IMKVAEF 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 262 AA;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VMXVAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                         NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09ZPO5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9ZPQ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
  임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Deoxyribose-phosphate aldolase (EC 4.1.2.4) (Phosphodeoxyriboaldolase)
(Deoxyriboaldolase) (DERA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Loechel S., Inamine J.M., Hu P.-C.,
"Nucleotide sequence of the deoC gene of Mycoplasma pneumoniae.";
Nucleic Acids Res. 17:801-801(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acid, Nucleic Activity: 2-deoxy-D-ribose 5-phosphate = D-
-!- CATALYTIC ACTIVITY: 2-deoxy-D-ribose 5-phosphate = D-
glyceraldehyde 3-phosphate + acetaldehyde.
-!- PATHWAY: Nucleotide and deoxyribonucleotide catabolism.
-!- SUBCELDULAR DOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the deoC/fbaB aldolase family. DeoC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome; Lyase; Schiff base.

BINDING 152 152 Schiff-base with acetaldehyde similarity).

ACT SITE 181 181 By similarity.

SEQÜENCE 224 AA; 24878 MW; 73C3E4932E7881F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                          Name=deoC; OrderedLocusNames=MPN063; ORFNames=MP091; Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DB 1; I
Pred. No. 1.2e+02;
                                                                                                                             224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=89128453; PubMed=2492658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.7%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X13544; CAA31897.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000011; AAB95739.1;
PIR; S02216; S02216.
HSSP; Q9X1P5; 100Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAE; MF 00114; -; 1.
InterPro; IPR002915; DeoC.
Pfam; PF01791; DeoC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                           STANDARD;
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Best Local Similarity
5; Conserv
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93 VMNIAEF 99
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VMNIAEF 99
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                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae."
                                                                                                                             MYCPN
                      93
                                                                                                                                            P09924:
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DEOC_MYCPN
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RESULT 10 Q8U0A9 ID Q8

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Similarity 71.4%; Score 26; DB 2; Length 731; Similarity 71.4%; Pred. No. 3.5e+02; 5; Conservative 1; Mismatches 1; Indels
   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                               EMBL; AP005102; BAC83706.1; -.
InterPro; IPR007658; DUF594.
Pfam; PF04578; DUF594; 1.
Hypothetical protein:
SEQUENCE 731 AA; 82975 MW; 62C331F04D1716AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            821 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5601 (2003).
EMBL; AF153768; AAD38980.1;
EMBL; AEO17172; AAQ65462.1; -.
HSSP; Q90240; 10MU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008969; CarboxypepD re
InterPro; IPR000834; Peptidase_MI4:
InterPro; IPR000601; PKD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22829867; PubMed=12949112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porphyromonadaceae; Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00246; Peptidase_M14; 1.
Pfam; PF00801; PKD; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 89.7%;
Similarity 85.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391 IMGVAEF 397
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TIGR; PG0232; -.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 5; Conserv
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SEQUENCE 821 AA
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licheniformis and comparisons with closely related Bacillus species.";
Genome Biol. 5:R77-R77(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 14580;
Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J., Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B., Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., Berka R.M.;
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein OSDNBa0033014.4.
Name=OSJNBa0033014.4.
Name=OSJNBa0033014.4.
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G., "The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential.";
J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 479;
   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein tuaB. Name=tuaB; ORFNames=Bu03350, BLi03806; Bacillus licheniformis DSM 13. Bactlius Pirmicutes; Bacillase; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; CP000002; AAU2522.1; -.
EMBL; CP000002; AAU25249.1; -.
Hypothetical protein.
SEQUENCE 479 AA; 53318 MW; B25425B96AD39D62 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
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Last annotation update)
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Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                              479 AA.
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   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                          PRT;
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5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 57.1
les 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                   233 VMRIAEF 239
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                                                                           VMXVAEF 7
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AC 06559
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DT 0
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Nelson K.B., Fleischmann R.D., DeBoy, R.T., Paulsen I.T., Fouts D.E.,
Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
Dewhirst F.E., Freaser C.M.,
"Complete genome sequence of the oral pathogenic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ross B.C., Barr I., Patterson M., Agius C., Rothel L., Margetts M., Hocking D., Webb E.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                     OrderedlocusNames=PG0232;
Porphyromonas gingivalis (Bacteroides gingivalis)
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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Pred. No. 3.9e+02;
0; Mismatches 1; Indels
Q9XBW4; Q7BWB5;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Immunoreactive 92 kDa antigen PG21 (Zinc carboxypeptidase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       821 AA; 91517 MW; 250843B2C9C833E2 CRC64;
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SMART; SM00089; PKD; 3.
SMART; SM00631; Zn Dept; 1.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
PROSITE; PS50093; PKD; 3.
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Nature 390:249-256(1997).
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                                                                                             Best Local Similarity
Matches 5; Conserv
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PubMed=1537794;

A Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
A Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Bentley S.D., Sebainia M., Thomson N.R., Bason N., Beacham I.R.,
Bentley S.D., Schainia M., Tromen N.R., Bason N., Beacham I.R.,
Bentley S.D., Schainia M., Trosset B., Davis P., DeShazer D.,
Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
Reith K.E., Maddison M., Moule S., Price C., Quail M.A.,
A Reith K.E., Maddison M., Moule S., Price C., Quail M.A.,
Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
Nuhichend S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
Genomic plasticity of the causative agent of melioidosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                          Burkholderia mallei ATCC 23344.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.2%; Score 25; DB 2; Length 205; 71.4%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 205 AA; 21152 MW; 67216B40EBF4D59F CRC64;
                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative membrane protein.
ORFNames=BPSL1178;
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                                                                                                                                                                 PRELIMINARY;
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                                                        565 VMPVAEF 571
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                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=243160;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 23344;
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                 VMXVAEF
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MEDINE-1894044033; PubMace3384377; Doll-10.1088/36/16;

K Kunst F., Ogasawara N., Bessieres P., Bolotin A., Borchert S.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Barsiss R., Bourster L., Brans A., Braun M., Brighell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Ra Brouilst S., Bruschi C.V., Caldwell B., Capuano V., Daniel R.A.,

Broizof F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Ra Brian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,

Ra Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

Ra Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

A Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

A Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

A Guiseppi G., Guy B.J., Haga K., Lapidus A., Lardinois S., Lauber J.,

A Characrevic C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,

Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,

Ra Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,

Ra Hoose L.-M., Parro V., Pool T. M., Porteelle D., Porvallik S.,

Rask S.H., Parro V., Pool T. M., Porteelle D., Porvallik S.,

Rask S.H., Parro V., Pool T. M., Rivolta C., Rocha E., Roche B.,

Rochfone F., Sacol B., Schleich S., Schleich S., Schlock S., Schleich S., Schlock B.,

Rochfone F., Sacol B., Scrokin A., Tacconi E., Takagi T., Takahashi H.,

Rash B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,

Rash Rash M., Tosato V., Uchiyama S., Wanamoto H., Yamane K.,

Waltzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,

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Waltzenegger T., Willers P., Wipat A., Yamanetonin E., Takagi T., Terpstra P.,

Whillish W. Werner W. Poolika K., Yoshikawa H.F., Zumstein E.,

Rah Wasunotot K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein B.,

The Componia P. Poolika K., Yoshika K., Yoshika Waller B., Roche E.,

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                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                   Similarity 71.4%; Pred. No. 2e+02; Similarity 71.4%; Pred. No. 2e+02; 5; Conservative 1; Mismatches 1; Indels
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Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
EMBL; BX571965; CAH35173.1; -.
SEQUENCE 205 AA; 21152 MW; 67216B40EBF4D59F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YTBQ_BACSU STANDARD; PRT; 253 AA. P53560; 034914; 01-0CT-1996 (Rel. 34, Created) CCT-2096 (Rel. 34, Last sequence update) 25-0CT-2004 (Rel. 45, Last annotation update) Hypothetical protein ytb0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=ytbO, OrderedLocusNames=BSU30180,
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=96312354; PubMed=8763940;
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J. Bacteriol. 178:4122-4130(1996)
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Query Match
Best Local Similarity 71...
Si Conservative
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                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis.";
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Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Name-pepT-2; OrderedLocusNames-EF3080;
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the BNBL/GenBank/DDBJ databases.
EMBL; AE010154; AAL80426.1; -..
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0005806; F:iron ion binding; IEA.
Pfam; PP04055; Radical SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                           EMBL; U51868; AAB17463.1; -.
EMBL; AF008220; AAC00267.1; ALT_INIT.
EMBL; S99119; CAB14996.1; ALT_INIT.
Subtitist; B(31178); ytbQ.
Complete proteome; Hypothetical protein.
SEQUENCE 253 AA; 28233 MW; 572CC4681F04C650 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 AA; 32512 MW; B19557B14451FFCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.2%; Score 25; DB 1; I
57.1%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.2%; Score 25; DB 2; I
57.1%; Pred. No. 2.7e+02;
iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Co-factor modifying protein. OrderedLocusNames=PF0302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 57.1
nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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222 IMKIAEF 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|:|||
75 IMDIAEF 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Q82ZH7;
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0801327
AC 080132
AC 080132
DT 01-JU
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MEDLINE-2556, 3.7. VUCUCATION CONTROLLINE-2556, 3.7. VUCUCATION CONTROLLINE-2556, 3.7. VUCUCATION CONTROLLINE-2556, 3.7. VUCUCATION CONTROLLINE, Seshadri R., Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F., Tettellin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R., Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                  "Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.2%; Score 25; DB 2; Length 406; 71.4%; Pred. No. 3.8e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 AA; 44953 MW; 038ABFCD17BA85DE CRC64;
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SEQUENCE 617 AA; 66569 MW; 20512A41BAC1E599 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0008237; F:metallopeptidase activity; IEA. GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO: 0005524; F:ATP binding; IEA.
GO; GO:0016887; F:ATPase activity; IEA.
GO; GO:0051082; F:unfolded protein binding; IEA.
GO; GO:00526; P:iron-sulfur cluster assembly; IEA.
InterPro; IPR010236; HspA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGRO1882; peptidase-T; 1.
PROSITE; PS00758; ARGE DAPE_CPG2_1; 1.
PROSITE; PS00759; ARGE DAPE_CPG2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001261; ArgE dapE.
InterPro; IPR010161; Peptidase M20B.
TIGRFAMS; TIGR01882; peptidase T; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chaperone protein HscA.
Name=hscA; OrderedLocusNames=HD1087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                               Science 299:2071-2074(2003).
EMBL; AE016956; AA082761.1; -.
HSSP; P29745; 1VIX.
TIGR; EF3080; -.
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ProDom; PD000089; HSP70; 1.
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STRAIN=1;
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Q7UYJ7
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MEDLINE=21848401; PubMed=1185986. Bowman D., Hadland D., Hodgeon G., Antones S., McDonald S., McLean J., Mooney P., Monle S., Mungall K., Murphy L., Nibbett D., Odell C., RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Ratter S., Saunders D., Sanned D., Odell C., Sanned D., Odell C., Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Moother L., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Bepr P., Zinmernann W., Wandler H., Menhardt R., Purnelle B., Auglibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Albaga R.R., Cruzado L., Jimenez J., Sanchez M., Galzon A., Thode G., Cerutti L., Lowe T., Moreno S., Armstrong J., Forsburg S.L., Albaga R.R., Cruzado L., Jimenez J., Sanchez M., Medler H., Med
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                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: Reduced electron-transferring flavoprotein ubiquinone = electron-transferring flavoprotein + ubiquinol.
-!- COFACTOR: FAD and a 4Fe-4S cluster (By similarity).
-!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
                                                                                                                                                                                                                                                                                      ETED SCHPO STANDARD; PRT; 632 AA.
P87111.
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Probable electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial precursor (EC 1.5.5.1) (ETF-QO) (ETF-ubiquinone flavoprotein dehydrogenase)
flavoprotein dehydrogenase)
ORFNames=SPAC20G8.04c;
                                                             ..
0
86.2%; Score 25; DB 2; Length 617; 71.4%; Pred. No. 5.7e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SIMILARITY: Belongs to the ETF-QO / fixC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                  553 VLSVAEF 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces
                                                                                                             1 VMXVAEF 7
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GO; GO:0001844; F:1,4-alpha-glucan branching enzyme activity; IEA.

GO; GO:0004556; F:alpha-amylase activity; IEA.

GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl. ..; IEA.

GO; GO:0005975; P:cransferase activity, transferring glycosyl. ..; IEA.

GO; GO:0005975; P:carbohydrate metabolism; IEA.

InterPro; IPR00647; Alpha amyl cat.

InterPro; IPR004193; Glyco_hydro_13N.

InterPro; IPR001916; TOMB_BOX_N.

Pfam; PF00128; Alpha-amylase_N. 1.

Pfam; PF00122; Isoamylase_N. 1.
                                                                                                                                                                                   Mitochondrion (Potential).

Probable electron transfer flavoprotein-
ubiquinone oxidoreductase.

FAD (ADP part) (Potential).

Iron-sulfur (4Fe-45) (Potential).

Iron-sulfur (4Fe-45) (Potential).

Iron-sulfur (4Fe-45) (Potential).

Iron-sulfur (4Fe-45) (Potential).
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Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
                                                                                                                            4Fe-4S; Electron transport; FAD; Flavoprotein; Iron-sulfur; Mitochondrion; Oxidoreductase; Transit peptide; Ubiquinone. TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 2; Length 633; Pred. No. 5.8e+02; 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          86.2%; Score 25; DB 1; Length 632; 71.4%; Pred. No. 5.8e+02; ive 1; Mismatches 1; Indels
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Complete proteome; Glycosyltransferase; Transferase.
SEQUENCE 633 AA; 72019 MW; 708ECC306CC9D9E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         69472 MW; 1B0F22374E33771B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0cr-2003 (TrEMBLrel. 25, Created)
01-0cr-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
1,4-alpha-glucan branching enzyme (EC 2.4.1.18).
Name-glgB; OrderedLocusNames=RB548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Natl. Acad. Sci. U.S.A. 100:8298-8303(2003)
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EMBL, 295334; CAB08598.1; -. PIR, T38126; T38126. GeneDB Spende; SPAC20G8.04c; InterPro; IPR007859; ETFD.
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5; Conservative
                                                                                                 Pfam; PF05187; ETF QO; 1.
4Fe-4S; Electron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
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575
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193 VMSLAEF 199
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632 AA;
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SEQUENCE FROM N.A.
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RL13_HALMA
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
15-JUL-2004 (TrEMBLrel. 27, Last an
                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned P1 clones."; DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98069011; Pubmed-9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 400566; AABJ75911; -

EMBL; 40056700; BAB08968.1; -

EMBL; AB006700; BAB08968.1; -

HSSP; P12282; 1JW9.

GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0004839; F:ubiquitin activating enzyme activity; IEA.

GO; GO:0006512; P:ubiquitin activating enzyme activity; IEA.

R InterPro; IPR000205; NAD BS.

R InterPro; IPR000501; Upaci_repeat.

R InterPro; IPR00011; Uqtin-activ_enz.

R Fam; PF00184; UBACT; 2.

R PELNYS; PR01849; UBACT; 2.

R PELNYS; R GOST ACT; 2.

R TIGREAMS; TIGR01408; Ubel; 1.
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PROSITE; PS00120; LIPASE SER; UNKNOWN 1.
PROSITE; PS00536; UBIQUITIN_ACTIVAT 1; 1.
PROSITE; PS00865; UBIQUITIN ACTIVAT 2; 1.
SEQUENCE 1077 AA; 119622 WW; CE39A36AAA99A218 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRALM-secotype Columbia;
Hatfield P.M., Carpenter T.C., Vierstra R.D.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                 PRT; 1077 AA.
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                                                                                                                                                                                                                                                                                                                                              Ubiquitin activating enzyme 2
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                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03,
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                                                                                                 PRELIMINARY;
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VMSMAEF 60
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RESULT 23
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MEDLINE=20396344; PubMed=10937989; DOI=10.1126/science.289.5481.905;
Ban N., Nissen P., Hansen J., Moore P.B., Steitz T.A.;
"The complete atomic structure of the large ribosomal subunit at 2.4 A resolution.";
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"A pre-translocational intermediate in protein synthesis observed in crystals of enzymatically active 50S subunits.";

Nat. Struct. Biol. 9:225-230(2002).
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TISSUE-Spleen;
Chen S.L., Xu M.Y., Hu S.L., Li L.;
"Analysis of immune-relevant genes expressed in red sea bream
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Kroemer W.J., Arndt E.;
"Halobacterial S9 operon. Three ribosomal protein genes are "Halobacterial S9 operon."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cotranscribed with genes encoding a tRNA(Leu), the enolase, putative membrane protein in the archaebacterium Haloarcula
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ubbde=10931990; DOI=10.1126/science.289.5481.920;

Nissen P., Hansen J., Ban N., Moore P.B., Steitz T.A.;

"The structural basis of ribosome activity in peptide bond
                                                                                                                                                                                                                                                                 Length 140;
                                                                                                                                                                                                                                  Score 24; DB 2; Lengtn 14v., Pred. No. 2.7e+02;
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                                                                                                                                                                                                   SEQUENCE 140 AA; 15723 MW; 20EFF0F49C40EB09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haloarcula marismortui (Halobacterium marismortui).
Archaea, Euryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Haloarcula.
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PubMed=11483524; DOI=10.1093/emboj/20.15.4214;
Klein D.J., Schmeing T.M., Moore P.B., Steitz T.A.;
"The kink-turn: a new RNA secondary structure motif.";
EMBO J. 20:4214-4221(2001).
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01-DEC-1992 (Rel. 24, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
50S ribosomal protein L13P (Hmal13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 145 AA
                                                                                                                                                                                                                                                                                                                            1; Mismatches
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PubMed=11828326; DOI=10.1038/nsb758;
                                                                                                               Aquaculture 240:115-130(2004).
EMBL; AY190684; AAP20160.1; -.
                                                                                                                                                                                                                                                              h 82.8%;
Similarity 71.4%;
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            72 LMVVAEF 78
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                                                                                                                                                                                                                                                                                             Best Local Similarity
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P29198;
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Gaps

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MEDLINE=21929760; PubMed=11932289; DOI=10.1101/gr.223902; MEDLINE=21929760; PubMed=11932289; DOI=10.1101/gr.223902; Galagan J.E., Nusbaum C., Roy A., Endrizzi MG., Macdonald P., FitzHugh W., Calvos S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Leigh J.A., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T.,
Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
Jacobi C., Stratuviene V., Schlenczeck S., Dencker S., Huber R.,
Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
"The genome sequence of the extreme thermophile Thermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
3D-structure; Ribosomal protein; RNA-binding; rRNA-binding. SEQUENCE 145 AA; 16228 MW; 069CE666662AE3BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 71.4%; Pred. No. 2.8e+02; Similarity 71.4%; Pred. No. 2.8e+02; S; Conservative 1; Mismatches 1; Indels
                                                                    82.8%; Score 24; DB 1; Length 145;
83.3%; Pred. No. 2.7e+02;
Live 0; Mismatches 1; Indels
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InterPro; IPR009072; Histone-fold.
Complete proteome; Hypothetical protein.
SEQUENCE 148 AA; 16860 MW; 0AS40838B46F96AB CRC64;
                                                                                                                                                                                                                                                                                                                                                          072IL7;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=TTC1115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein MA2884.
OrderedLocusNames=MA2884;
                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thermophilus.";
Nat. Biotechnol. 22:547-553(2004).
                                                                                             Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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PubMed=15064768;
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                                                                                                                                                                                                                1 MSVAEF 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2214;
                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                         0721L7
                                                                                                                                                                                                                                                                                        RESULT 26
Q721L7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIFFERENT E SITE SUBSTRATES.
PubMed=14561884; DOI=10.1261/rna.5120503;
Schmeing T.M., MooI=10.85 Steitz T.A.;
Schmeing G. Geacylated tRNA mimics bound to the E site of the large "Structures of deacylated tRNA mimics bound to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA 9:1345-1352(2003).
-!- FUNCTION: Binds to the 238 rRNA.
-!- SUBUNIT: Part of the 508 ribosomal subunit. Interacts weakly with proteins L3 and L6.
-!- SIMILARITY: Belongs to the ribosomal protein L13P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF THE 50S SUBUNIT IN COMPLEX WITH FIVE ANTIBIOTICS AT THE PEPTIDYL TRANSFERASE CENTER. STRAIN=ATCC 43049;
                        X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF THE 50S SUBUNIT IN COMPLEX WITH FOUR MACROLIDE ANTIBIOTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hansen J.L., Moore P.B., Steitz T.A.; "Structures of five antibiotics bound at the peptidyl transferase center of the large ribosomal subunit."; J. Mol. Biol. 330:1061-1075(2003).
                                                                                                                                                                    "The structures of four macrolide antibiotics bound to the large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF THE 50S SUBUNIT WITH
                                                                                             PubMed=12150912; DOI=10.1016/S1097-2765(02)00570-1;
Hansen J.L., Ippolito J.A., Ban N., Nissen P., Moore P.B.
                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF THE 50S SUBUNIT.
                                                                                                                                                                                                                                                                                STRAIN=ATCC 43049;
PubMed=12185246; DOI=10.1073/pnas.172404099;
Hansen J.L., Schmeing T.M., Moore P.B., Steitz T.A.;
"Structural insights into peptide bond formation.";
Proc. Natl. Acad. Sci. U.S.A. 99:11670-11675(2002);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=12860128; DOI=10.1016/S0022-2836(03)00668-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 1NJI; X-ray; K=1-145.
PDB; 1Q7Y; X-ray; K=1-145.
PDB; 1Q8Y; X-ray; K=1-145.
PDB; 1Q8C; X-ray; K=1-145.
PDB; 1Q8C; X-ray; K=1-145.
PDB; 1QVC; X-ray; I=1-145.
PCODOM; PD001791; Ribosomal_L13; 1.
PROSITE; PS00783; RIBOSOMAL_L13; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M76567; AAA73097.1; -.
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1JJ2, X-ray, I=1-145.
1K73, X-ray, K=-.
1K8A, X-ray, K=1-145.
                                                                                                                                                                                          ribosomal subunit.";
Mol. Cell 10:117-128(2002)
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K=1-145.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B41715; B41715
                                                                         STRAIN=ATCC 43049;
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1KC8; X-ray;
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1KQS; X-ray;
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                                                                                                                                            Steitz T.A.;
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PDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyxhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002)
EMBL; AP005958; BACS1792.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 1; Length 157;
Pred. No. 3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.8%; Score 24; DB 2; Length 161; 71.4%; Pred. No. 3e+02; ive 1; Mismatches 1; Indels
                                                                                                         Xu X.-Y., Bewley J.D., Greenwood J.S.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the BetVI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000531; Bet v I; 1.
PROSITE; PS00451; PATHOGENESIS BETVI; 1.
Allergen; Pathogenesis-related protein; Plant defense.
SEQUENCE .157 AA; 17040 MW; 5892AB8593ABA7E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 AA; 17456 MW; 4B7895C4BF28D199 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000916; Bet v I. Pfam; PF00407; Bet v I; I. PRINTS; PR00634; BETALLERGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OrderedLocusNames=bl16527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 024248; 1E09
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SEQUENCE 161 AA;
          NCBI_TaxID=50225;
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30-MAY-2000 (Rel. 39, Last sequence update)
29-MAR-2004 (Rel. 43, Last annotation update)
29-MAR-2004 (Rel. 43, Last annotation update)
Root allergen protein (RAP).
Taraxacum officinale (Common dandelion).
Taraxacum officinale (Common dandelion).
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimura M., Tokai T., Matsumoto G., Fujimura M., Hamamoto H., Yoneyama K., Shibata T., Yamaguchi I.; Yoneyama K., Shibata T., Yamaguchi I.; "Trichothecene nonproducer Gibberella species have both functional nonfunctional 3-0-acetyltransferase genes."; Genetics 163:677-684(2003). EMBL; AB076255; BAC65219.1; -. HSSP; P07459; 2SCU.
Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander B., Metcalf W.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";

Genome Res. 12:532-542(2002).

GO, GO:0008168; F:methyltransferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
NCBI_TaxID=182099;
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                                                                                                                                                                                                                                                                                                                                     Score 24; DB 2; Length 149;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                   149 AA; 16402 MW; EF8576A410EC13F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 AA; 16632 MW; F46D6A325AD1EEC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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MEDLINE=22505401; PubMed=12618405;
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Pfam; PF02629; Coa binding; 1.
                                                                                                                                                                                                                                                                                                                                     82.8%;
                                                                                                                                                                                                                                                                                                                                                             71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 71.4
Matches 5; Conservative
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                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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049065;
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SEQUENCE
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RAP TAROF
RAP TAROF
AC 04906
DT 30-MA
DT 29-MA
DE ROOT
OC EUKAR
OC SPETM
OC SPETM
OC TARANA
OC TARANA
OC TARANA
OC TARANA
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10 68 203

10 0 006 6203

DT 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-10 01-
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Gaps

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Gaps

Q6AQ12;

Q6AQI2

RESULT 31

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
-!- FUNCTION: This protein is essential for replication of the chromosome. It is also involved in DNA recombination and repair (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                PS9922; QTUKV3;
9-9MR-2004 (Rel. 43, Created)
29-MR-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
sighte-strand binding protein (SSB) (Helix-destabilizing protein).
Name-ssb; OrderedLocusNames=RB9917;
Rhodopirellula baltica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=1;
MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.,
Schlesner H., Amann R., Reinhardt R.,
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                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, BX294150, CAD76529.1; -.
InterPro, IPR010913; SS binding.
InterPro, IPR000424; SSB protein.
Pfam, PF00416; SSB, 1.
PROSITE; PS50935; SSB; 1.
Complete proteome; DNA repair; DNA replication; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.8%; Score 24; DB 1; Length 169;
83.3%; Pred. No. 3.2e+02;
live 0; Mismatches 1; Indels
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 AA; 18108 MW; AA8F93E0FA51F287 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Multisubunit Na+/H+ antiporter, subunit E.
Name=mrpE, OrderedLocusNames=cg3027;
71.4%; Pred. No. 3.1e+02;
tive 1; Mismatches 1;
                                                                                                                                                                                                                169 AA.
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                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 83.3
Matches 5; Conservative
                      5; Conservative
                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                      107 VLLVAEF 113
                                                              -
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 MXVAEF 7
                                                              1 VMXVAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=117;
                                                                                                                                                                                                                   SSB RHOBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain 1.
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                                                                                                                                                                      RESULT 33
SSB_RHOBA
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                        Matches
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                                                                                                        셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                            Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M., Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K., Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R., Klenk H.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=GB-M1;
BDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.;
"Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
                                                                                                                                                                                            Desulfotalea psychrophila.
Bacteria, Proteobacteria, Deltaproteobacteria, Desulfobacterales,
Desulfobulbaceae, Desulfotalea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=ECU08_0680;
Encephalitozono cuniculi GB-MI.
Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI_TaxID=284813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 82.8%; Score 24; DB 2; Length 162; Best Local Similarity 57.1%; Pred. No. 3e+02; Matches 4; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.8%; Score 24; DB 2; Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AL590448; CAD26373.1; -. 60; 60:0006810; P:transport; ITA. InterPro; IPR011012; Longin like. SEQUENCE 165 AA; 18742 MW; 7CDAB6C35BC11A6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 AA; 19034 MW; 5E67041F45744728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
COATOMER ZETA SUBUNIT.
                                                                                                          Last sequence update)
Last annotation update)
                                            162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from permanently cold Arctic sediments.";
Environ. Microbiol. 6:897-902(2004).
Marbi. (R522870, CAG35391.1;
InterPro; IPR009921; DUF456.
                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                            PRT;
                                                                             25-OCT-2004 (TrEMBLrel. 28, Cl
25-OCT-2004 (TrEMBLrel. 28, Li
25-OCT-2004 (TrEMBLrel. 28, Li
Hypothetical protein.
OrderedlocusNames-DP0662;
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=LSv54 / DSM 12343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 414:450-453(2001).
                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|:|||
114 IMALAEF 120
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SEQUENCE 162 AA;
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                                                                                                                                                                                                                                                                                                                                           PubMed=15305914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=GB-M1;
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Q8SRD1;

RESULT 32
085RD1
005RD1
01-JU
07 01-JU

Q8SRD1

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Query Match

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Thymidine kinase.
OrderedLocusNames=CAC2887;
                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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                                                                                         WormBase Consortium
                                                                                                                                                                                                                                                                                                                                                                                                        37 VMTAAEF 43
                                                                                                                                                                                                                                                                                                                                                                              1 VMXVAEF 7
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
              STRAIN=Bristol N2;
SEQUENCE FROM N.A.
                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                           Wilson R
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                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
Burkovski A., Dusch N., Eggeling L., Eikmanns B.J., Gaigalat L.,
Goesmann A., Hartmann M., Huthmacher K., Kraemer R., Linke B.,
MCHardy A.C., Meyer F., Moeckel B., Pfefferle W., Puehler A.,
Eey D.A., Rueckert C., Rupp O., Sahm H., Wendisch V.F., Wiegraebe I.,
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                             "The complete Corynebacterium glutamicum ATCC 13032 genome sequence and its impact on the production of L-aspartate-derived amino acids and vitamins."; user acidin transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
WormBase Consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                        Score 24; DB 2; Length 169;
Pred. No. 3.2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Wilson R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
Bradabhaw-Cordum H., Scott K., Graves T.;
"The sequence of C. elegans cosmid Y71F9AL.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                              19166 MW; CB9AA69662E22A36 CRC64;
 Corynebacterium glutamicum (Brevibacterium flavum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seque
01-MAR-2004 (TrEMBLrel. 26, Last annoi
Hypothetical protein Y71F9AL.10.
Name=Y71F9AL.10, ORFNames=Y71F9AL.10;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                     InterPro, IPR002758, Cation_antiport.
ProDom; PD012569; DUF68; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                        82.8%;
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4%,
--koa 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2002)
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VMLMAEF 28
                                                                                                                                                                                                                                                                                                              169 AA;
                                                                                                                                                                                                                                                                                                                                                                                           VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                     NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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                                                                                                                                                                  rauch A.;
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                                                                                                                                                                                                                                                                                                             SEQUENCE
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Gaps
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MEDLINE=21359325, PubMed=11466286;

DOI=10.11284/JB.181-16.4828-11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Tatusov R.L., Sabathe F., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Genome sequence and comparative analysis of the solvent-producing bacterium Clostrialum acetobutylicum...;

J. Bacteriol 1. 183:4823-483812001.

-I. CATALYTIC ACTIVITY: ATP + thymidine = ADP + thymidine 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium acetobutylicum.
Bacteria, Firmicutes; Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                 Wormbase, Wales Wedenol022115; Y71P9AL.10.

Wormbase, Y71P9AL.10; CE31386.

GO; GO:000151; Crubiquitin ligase complex; IEA.

GO; GO:0008270; F:ubiquitin ligase activity; IEA.

GO; GO:0008270; F:ubiquitin-protein ligase activity; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

RO; GO:0008270; F:zinc ion binding; IEA.

RO; GO:0008270; F:zinc ion binding; IEA.

ROS:00097; Z:-C3HC4; I.

SWART; SM00184; RING; 1.

RPOSITE; PSS0089; ZF RING; 1.

PROSITE; PSS0089; ZF RING; 1.

PHYPOCHECICAL protein; Metal-binding; Zinc; Zinc-finger.

SEQUENCE 189 AA; 21048 MW; 7BDA2D05F0362CD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.8%; Score 24; DB 2; Length 189; 71.4%; Pred. No. 3.5e+02; rive 0; Mismatches 2; Indels
                                                                                                                                                                                 Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- SINILARITY: Concains 1 RING-type zinc finger.
EMBL; ACO24200; AAF35997.2; -.
HSSP; Q9LRB7; 11YM.
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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217 VLDVAEF 223
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Best Local Similarity
Matches 5; Conserv
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YP88 MYCBO
ID YP88 MYCBO
       SOW WHEN THE PROPERTY OF THE P
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X STAIN=GMI000;

X MEDLINE=ZNEAR1000;

X MEDLINE=ZNEAR1000;

X Ariat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Gangier P., Thebault P., Whalen M., Wincker P., Levy M.,

X Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,

Weissenbach J., Boucher C.A.;

X Genome sequence of the plant pathogen Ralstonia solanacearum.";

I Nature 415:497-502(2002).

R GG, GG:0016021; Cintegral L. omembrane; IEA.

Complete protecome; Transmembrane.

SEQUENCE 206 AA; 21783 MW; 8D49E45A150B8440 CRC64;
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PROSITE; PS00603; TK_CELJULAR_TYPE; UNKNOWN 1.
ATP-binding; Complete proteome; DNA synthesis; Kinase; Transferase.
SEQUENCE 195 AA; 22303 MW; 6EDB551986B203BA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Raistonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Raistonia.
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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                                                                                              Length 195;
                                                                                            Match 82.8%; Score 24; DB 2; Length 195
Local Similarity 57.1%; Pred. No. 3.6e+02;
es 4; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
PROBABLE TRANSMEMBRANE PROTEIN.
Name-RS011138; OrderedLocusNames-RSC2467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YPS8 MYCTU STANDARD; PRT; 236 AA. P65005; Q50740; 01-NOV-1997 (Rel. 35, Created) 25-0CT-2004 (Rel. 45, Last sequence update) 25-DAN-2005 (Rel. 46, Last annotation update) Hypothetical protein Rv2558/MT2635.
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Matches 4; Conservative
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                                                                                                                                                                                                                                       131 LMAIAEF 137
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                                                                                                                                                                                        1 VMXVAEF 7
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=2206494; PubMed=12218036;
MEDLINE=2206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey B.K., Kolonay J.F., Nalson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
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Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
|- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV2557.
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."; Maiture 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=AF2122/97; PubMed=12788972; DOI=10,1073/pnas,1130426100; MEDLINE=22709107; PubMed=12788972; DOI=10,1073/pnas,1130426100;
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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Interpro; IRR011008; Dimer A B barrel.
Complete protecome; Hypothetical protein.
SEQUENCE 236 AA; 25718 MW; 13E3B049DBF79C6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laboratory strains ";
J. Bacteriol. 1845479-5490(2002).
-!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV2557.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hypotherical protein Mb2588.
OrderedLocusNames=Mb2588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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Similarity 71.4%;
5; Conservative
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STRAIN=MoPn / Nigg;
MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
Bass S., Linher K.D., Weidman J.P., Khouri H.M., Craven B., Bowman C.,
Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
MCClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                    Name=L7610.05;
Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                   Ivens A.C., Murphy L., Quail M., Harris D., Oliver K., Lawson D., Stalandream M.A., Barrell B.G., Submitted (BPR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL139794; CAC22635.1; -. Hypothetical Tribals.
Hypothetical protein.
SEQUENCE 248 AA, 26365 MW, A80440E18B3F69B5 CRC64;
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NCBI_TaxID=83560;
                                                                                                                                                                                                                        Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M. Smith D.F.,
                                                                                                                                                                                                                                                                          "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h Similarity 71.4%; Score 24; DB 2; Length 248 Similarity 71.4%; Pred. No. 4.6e+02; 5; Conservative 1; Mismatches 1; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Serine/threonine protein phosphatase, putative.
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InterPro; IPR001932; PP2C-like.
Pfam; PF00481; PP2C; 1.
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EMBL; AE002321; AAF39372.1; -.
PIR; G81693; G81693.
                                                                                                                                                                                           STRAIN=Friedlin;
MEDLINE=98146435; PubMed=9477341;
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SMART; SM00331; PP2C_SIG; 1.
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Chlamydia muridarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE 249 AA;
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                                                                                                                        NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Bictype gravis / NCTC 13129;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
Cardeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
Whitehead S., Barrell B.G., Parkhill J.,
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=1717;
                                                                                                                                                                                                                                                                                                                 82.8%; Score 24; DB 1; Length 236; 71.4%; Pred. No. 4.3e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.8%; Score 24; DB 2; Length 238; 57.1%; Pred. No. 4.4e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                      EMBL, BX248343; CAD94773.1; -.
InterPro; IRR011008; Dimer A B barrel.
Complete proteome; Hypotherical protein.
SEQUENCE 236 AA; 25718 MW; 13E38049D8F79C6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome; Hypothetical protein.
SEQUENCE 238 AA; 24945 MW; 1560BB577A2194F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diphtheriae NCTC13129.";
Nucleic Acids Res. 31.6516.6523(2003).
BN248356; CAR54935.1;
GO, GO:0004222; F:metalloendopeptidase activity; IEA.
GO; GO:0005608; P:proteolysis and peptidolysis; IEA.
InterPro; IPR012886; Peptidase M238.
InterPro; IPR011054; Rudmnt hyb.motif.
PF01551; Peptidase M23; 1.
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Last sequence update)
Last annotation update)
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium diphtheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OrderedLocusNames=DIP0836;
                                                                                                                                                                                                                                                                                                                                        Local Similarity 71.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 VLDVAEF 223
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VLSIAEF 78
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RESULT 41 097008 ID 09700 AC 09700 DT 01-MA DT 01-MA

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Q9NE74 RESULT 43 Q9NE74

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Gaps
Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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STRAIN=ATCC BAA-334 / TIGR4;
MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 2928139; CABOTA17.2;
R WormBase; WBGene00011607; 108D2.2.
R WormPep; T08D2.2; CE25108.
R OG.0016020; Cimenbrane; IEA.
RO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0005829; P:lipid metabolism; IEA.
NR InterPro; IPR00118; F-box.
NR InterPro; IPR00118; Glyco_trans_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 317;
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28-FEB-2003 (Rel. 41, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
6-phosphofructokinase (BC 2.7.1.11) (Phosphofructokinase)
(Phosphohoxokinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 83.3%; Score 24; DB 2; Length 317 Similarity 83.3%; Pred. No. 5.7e+02; 5; Conservative 0; Mismatches 1; Indels
Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 317 AA; 36591 MW; 145E88B02B75AE42 CRC64;
                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein T08D2.2.
ORFNames=T08D2.2;
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                                                                                                                                                                                                                                                            317 AA.
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  Mismatches
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                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00646; F-box; 1. Pfam; PF00953; Glycos_transf_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       investigating biology.";
Science 282:2012-2018(1998)
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
                                                                                         || :||:
244 VMSIAEY 250
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
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01-MAY-2000 (
01-MAY-2000 (
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Q97RCG;
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                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 15, Last sequence update)
Hypotherical protein L5075.02.
Name=L5075.02;
Eleishmania major.
BUKaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
N.BL TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia garinii PBi.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
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Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
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A Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
A Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
A Schulte-Spechtel U., Wilske B., Suchnel J., Platzer M.;
"Comparative analysis of the Borrelia garinii genome.";
"Comparative analysis of the Borrelia garinii genome.";
"Comparative analysis of the EMBL/GenBank/DDBJ databases.
E Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
R GO; GO:0016140; Fracyltransferase activity; IEA.
R GO; GO:0016740; Frtransferase activity; IEA.
R GO; GO:0016740; Frtransferase activity; IEA.
R GO; GO:0016740; Frtransferase.
R GO; GO:0016740; Transferase.
R GO; GO:0016740; Transferase.
R GO; GO:0016740; Transferase.
R GO; GO:0016740; Frtransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith D.F.;
"A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.8%; Score 24; DB 2; Length 270; 71.4%; Pred. No. 4.9e+02;
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Beck A., Klages S., Reinhardt R., Ivens A.C., Quail M.,
Rajandream M.A., Barrell B.G.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, Ali63552, CAB86964.1; -.
Hypothetical protein.
SEQUENCE 270 AA; 29335 MW; 5B91DA37A16FC3CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Glycerol-3-phosphate O-acyltransferase, putative. ORFNames=BG0328;
                                                                                                                                                                                                         270 AA
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25-OCT-2004 (TrEMBLrel. 28,
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les 5; Conservative
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148 VMNLAEF 154
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1 MMIVAEF 7
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RESULT 44
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AC 0661U
AC 0661U
DT 25-0C
DT 25-0C
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DB GIYCE
GN BORTES
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RR SCHUI
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE008456; AAK99600.1; -.
HSSP; P09791; D97971.
HSSP; P00512; 3PFK.
HAMAP; MF 00339; -; 1.
InterPro; IPR000023; Ppfruckinase.
Pffam; PP00365; PFK; 1.
PRINTS; PR00476; PFFKTKINASE.
PRODOM; PD000707; Ppfruckinase; 1.
PROSITE; PS00473; PHOSPHOFRUCTOKINASE; 1.
Allosteric enzyme; AIP-binding; Complete proteome; Glycolysis; Kinase; Magnesium; Transferase.
                        Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz B.J., Lu J., Matuushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Rochetson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
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STRAIN=NCIMB 8826 / WCFS1;
MEDLINE=22480296; PubMed=1256656; DOI=10.1073/pnas.0337704100;
                                                                                                                                                                                                                       "Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
-!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
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Substrate (By similarity).
Substrate (By similarity).
                                                                                                                                                                                                                                                                                      fructose 1,6-bisphosphate.
-!- PATHWAY: Key control step of glycolysis.
-!- SUBGELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the phosphofructokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24; DB 1; Length 335; Pred. No. 6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35213 MW; 930324A2307FFC6F CRC64;
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01-0707-2003 (TrEMBLrel. 24, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last amnotation update)
Transcription regulator of beta-galactosidase gene.
Name=lacR; OrderedLocusNames=lp_3470;
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(By similarity).
(By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch)
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        DOI=10.1128/JB.183.19.5709-5717.2001;
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ATP
ATP
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71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactobacillus plantarum.
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253
253
335 AA;
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                                                                                                                                                                                                       Glass J.I
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ACT SITE
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PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
Allosteric enzyme; ATP-binding; Complete proteome; Glycolysis; Kinase;
Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E.K., Khouri H.M., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T., Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                  Science 293:498-506(2001).
-!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
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Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
                                                                                                                                                                                                                                                             fructose 1,6-bisphosphate.
--- PATHWAY: Key control erep of glycolysis.
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
--- SIMILARITY: Belongs to the phosphofructokinase family.
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05-JUL-2004 (Rel. 44, Last annotation update)
6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2DFFBAACC58CAF66 CRC64;
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ATP (By similarity)
ATP (By similarity)
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Substrate
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HSSP; P00512; 3PFK.
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250
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335 AA;
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STRR6 KGPF

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GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0004106; F:chorismate mutase activity; IEA.
GO; GO:0004764; F:shikimate 5-dehydrogenase activity; IEA.
GO; GO:0016089; P:aromatic amino acid family biosynthesis, sh. . .; IEA.
                                                                                                                                                                                                                                                                                                                                               DOI=10.1128/JB.183.16.4823-4838.2001;
Noelling J., Breton G., Omelbenko, Wakarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
Bacteriul 183:4823-4838 (2001).
BENBL, AR007605, AAK78873.1;
BIR: F97010; P97010.
                                                                                                                                                               OrderedLocusNames=CACO897;
Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                         01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Fusion: chorismate mutase and shikimate 5-dehydrogenase.
                        367 AA
                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
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InterPro; IPR01242; AroE.
InterPro; IPR01279; CM mono_grmpos.
InterPro; IPR016151; Shikimate_DH.
Pfam; PF01817; CM 2; 1.
Ffam; PF01848; Shikimate_DH; 1.
TIGREAMS; TIGR00507; aroE; 1.
TIGREAMS; TIGR01805; CM mono_grmpos; 1
                                                                      (TrEMBLrel. 18, Created)
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                        PRT;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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                        PRELIMINARY;
                                                                      01-OCT-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Q7Q854;
                        Q97KM0
Q97KM0;
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                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).

Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).

Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).

R MSSP, AL935-62; CAD65557.1; -.

R RSSP, PLS039; 1DBQ.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR01962; Lambda_like_DNA.

R InterPro; IPR01962; Lambda_like_DNA.

R InterPro; PF001356; Laci; 1.

Pfam; PF00356; Laci; 1.

R PR031TE; PS03021; HTH_LACI_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15377794;
Holden M.T. G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M., Akting T., Crospanan L.C., Pitt T., Churcher C., Mungall K., Bentley S.D., Sebaiha M., Thomson N.R., Bason N., Baccham I.R., Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I., Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D., Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K., Kabbinowitsch E., Rutherford K., Sanders M., Simmonds M., Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Whitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.; "Genomic plasticity of the causative agent of melioidosis,
Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiers M.W.B.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing
De Vos W.M., Siezen R.J.,
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Burkholderiaceae, Burkholderia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 82.8%; Score 24; DB 2; Length 336; Local Similarity 71.4%; Pred. No. 6.1e+02; les 5; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burkholderia pseudomallei.";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
EMBL: BX571965; CAH35831.1; -
SEQUENCE 337 AA; 34345 MW; 283FDD1DB18D947D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              336 AA; 37694 MW; 8DE5C36A11C2A419 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative ribose transport system, permease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 VMAVGEF 117
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                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Q63TY5 Q63TY5

ò g RESULT 49
Q63TYS
ID Q63TY
AC Q63TY
AC Q63TY
AC DT 25-0C
D

RESULT 50

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ö Gaps Anopheles gambiae str. PEST. Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles. Anopheles Genome Sequencing Consortium; Submitted (MAR-2002) to the BMBL/GenBank/DDBJ databases. -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is ; Score 24; DB 2; Length 367; Pred. No. 6.6e+02; 1; Mismatches 1; Indels 41989 MW; CEACFA0B77F14842 CRC64; 01-MAR-2004 (TrEMBLrel. 26, Created) 01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Name=agCG50918; ORFNames=ENSANGG00000009886; 375 AA. 5; CM_mono_grmpos; 1. Oxidoreductase. preliminary data. EMBL; AAAB01008944; EAA10268.1;

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48 VMNMAEF 54
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                                                                                                                RESULT 53
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Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Sarou M.,
Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,
Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
Theologis A., Davis R.W.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,

Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,

Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayabizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Sarou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Contains I RING-type zinc finger.
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                82.8%; Score 24; DB 2; Length 375;
83.3%; Pred. No. 6.7e+02;
ive 0; Mismatches 1; Indels
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GO; GO:0009966; P:regulation of signal transduction; IEA. GO; GO:0009607; P:response to bioric erimine. TEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L; BT000229; AAN15548.1; -. GO:000151; C:ubiquitin ligase complex; IEA. GO:0001576; F:ubiquitin ligase complex; IEA. GO:0004676; F:ubiquitin-protein ligase activity; IEA. GO:0004270; F:zinc ion binding; IEA. GO:0016567; P:protein ubiquitination; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00356; ZnF C3H1; 1.
PROSITE; PS00518; ZF RING 1; UNKNOWN 1.
PROSITE; PS50089; ZF RING 2; 1.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 378 Aa; 42518 MW; 142E4A6534BECA4D CRC64;
                                                                                                                                    375 AA; 43422 MW; B320E106818EC77A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                   GO; GO:0009607; P:response to biotic stimulus; IEA InterPro; IPR007304; TAP42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein At5g06420.
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InterPro; IPR001841; ZnE_ring.
Pfam; PF00097; Zf_C3HC4; 1.
Pfam; PF00642; Zf_CCCH; 1.
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Matches 5; Conservative
                                                                                                                                                                                                                                        Conservative
                                                                                    Pfam; PF04177; TAP42; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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SMART; SM00356; ZnF_C3
                                                                                                                                                                                                                                                                                                                                 291 MTVAEF 296
                                                                                                                                                                                                            Local Similarity
les 5; Conserv
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                                                                                                                               SEQUENCE
                                                                                                                                                                                     Query Match
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081789
AC 081789
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
DC Bukar
OC 
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               STREETS
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DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98069011; PubMed-9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Similarity to zinc finger protein (Hypothetical protein).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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BMBL; ABO06700; BAB08964.1; -. BMBL; ABO06700; BAB08964.1; -. GO; GO: 0000151; Cubiquitin ligase complex; IEA.

GO; GO: 00003676; F: nucleic acid binding; IEA.

GO; GO: 00003676; F: nucleic acid binding; IEA.

GO; GO: 00008770; F: zinc ion binding; IEA.

R GO; GO: 0016567; P: zinc ion binding; IEA.

R GO; GO: 0016567; P: zinc ion binding; IEA.

R D: Fight PRO0097; Zif CCCH.

R D: Fight PRO0097; Zif CCCH.

R PFam; PF00097; Zif CCH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00184; RING; 1.
SMART; SM00186; ZnF CH1; 1.
SMART; SM00356; ZnF CH1; 1.
PROSITE; PS00089; ZF RING 1; 1.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 378 AA; 42460 MW; 173D71BBB8BA3FE2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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71.4%; Pred. No. 6.8e+02;
iive 1; Mismatches 1;
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   378 AA
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Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          annotation.";
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Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6K7P6;
05-JUL-2004
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Gaps

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1; Indels

1; Mismatches

Gaps ö Length 419; 1; Indels 419 AA; 45695 MW; B125377DF01D82C3 CRC64; 82.8%; Score 24; DB 2; I 71.4%; Pred. No. 7.5e+02; iive 1; Mismatches 1; RESULT 56

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01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PREPROTEIN TRANSLOCASE SUBUNIT.
Wanne-SECY; OrderedLocusNames-WS1698;
Wolinella succinogenes.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Q7M8F1 Q7M8F1; OSSEPTIFIC

419 AA

PRT;

PRELIMINARY;

ö Gaps Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O., Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B., Meyer F., Lederer H., Schuster S.C.,

"Complete genome sequence and analysis of Wolinella succinogenes.";

Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695 (2003).

-!- FUNCTION: Involved in protein export (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-!- SIMILARITY: Belongs to the secx/SEC61-alpha family. Pfam; PF00344; SecY; 1.
PRINTS; PR00303; SECYTRNLCASE.
TIGRRAMs; TIGR00967; 3a05018007; 1.
PROSITE; PS00755; SECY_1; 1.
PROSITE; PS00756; SECY_2; 1.
Complete protecome; Protein transport; Translocation; Transmembrane; MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100; ö n 82.8%; Score 24; DB 2; Length 419; Similarity 57.1%; Pred. No. 7.5e+02; 4; Conservative 2; Mismatches 1; Indels 419 AA; 45248 MW; 7CAAFC2EA0FBCF5C CRC64; EMBL, SESTIGE1, CARIOTS-1, -. GO, GO: 0016021, C: Integral to membrane, IEA. GO, GO: 0016021, C: Integral to membrane, IEA. GO, GO: 00160316, P: protein translocase activity, IEA. GO, GO: 0006605, P: protein targeting, IEA. GO, GO: 0015031, P: protein transport, IEA. IEA. GO, GO: 0015031, P: protein transport, IEA. Helicobacteraceae; Wolinella || :|:| 285 VMAIADF 291 1 VMXVAEF 7 Best Local Similarity SEQUENCE FROM N.A NCBI_TaxID=844; Fransport. SEQUENCE Query Match Matches ð

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Gaps

0

1; Indels

Length 414;

Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas. 01-0CT-2002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Similar to UDP-glucose/GDP-mannose dehydrogenase. 422 AA. PRT; PRELIMINARY; Pseudomonas aeruginosa SEQUENCE FROM N.A. NCBI_TaxID=287; **08KI64** RESULT 57 Q8K164

MEDLINE=22053227; PubMed=12057956; DOI=10.1128/JB.184.13.3614.3622.2002; Raymond C.K., Sims E.H., Kas A., Spencer D.H., Kutyavin T.V., Ivey R.G., Zhou Y., Kaul R., Clendenning J.B., Olson M.V.; "Genetic variation at the O-antigen biosynthetic locus in Pseudomonas aeruginosa.";

Gaps . 0 Score 24; DB 2; Length 422; Pred. No. 7.5e+02; 0; Mismatches 1; Indels Similarity 83.3%; 5; Conservative Query Match Best Local Similarity Matches 5; Conserv

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Gaps

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RESULT 58 **07P4E5**

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de la Torre J.R., Christianson L.M., Beja O., Suzuki M.T., Karl D.M., Heidelberg J.F., DeLong B.F.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUDMEd=14566056; DOI=10.1073/pnas.2133554100;
PubMed=14566056; DOI=10.1073/pnas.2133554100;
De La Torre J.R., Christianson L.M., Beja O., Suzuki M.T., Karl D.M., Heidelberg J., DeLong E.F.;
"Proteorhodopsin genes are distributed among divergent marine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Christianson L.M., Beja O., Suzuki M.T., Karl D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amnotation update)
05-JUL-2004 (TrEMBLRel. 27, Last amnotation update)
Predicted metal-dependent amidase/aminoacylase/carboxypeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 426;
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71.4%; Pred. No. 7.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h S2.8%; Score 24; DB 2; Length 426 Similarity 71.4%; Pred. No. 7.6e+02; 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        de la Torre J.R., Christianson L.M., Beja O., Suzuki M.7
Heidelberg J.F., DeLong E.F.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
EMBL, AX372452, AAR05211.1;
                                                                                                                                                                                                                                                                                                                                                                                                    Carboxypeptidase.
SEQUENCE 426 AA; 46506 MW; 28B6CFFA7F07F438 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426 AA; 46479 MW; FC983028A03E345B CRC64;
                                                                                                                                            EMBL; A372453; AAR05239.11; ...
GO; GO:0004180; F:carboxypeptidase activity; IEA.
GO; GO:0006508; F:carboxypeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002933; Peptidase_M20.
InterPro; IPR010168; Peptidase_M20.
ITGRFAMS; TIGR01891; amidohydrolases; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0004180; F:carboxypeptidase activity; IEA.
GO; GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002933; Peptidase_M20.
InterPro; IPR010168; Pept M20D amidh.
Pf01546; Peptidase M20; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 100:12830-12835(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uncultured marine proteobacterium ANT8C10.
Bacteria; Proteobacteria; environmental samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01546; Peptidase M20; T.
TIGRFAMs; TIGR01891; amidohydrolases; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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139 LMGVAEF 145
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Best Local Similarity
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[2]
SEQUENCE FROM N.A.
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SEQUENCE 426 AJ
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Matches
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ID QE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyrpides N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN 2003)
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ detabases.
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL/ABPD100120; EAA23508.1; -. HSSP; P80319; 1GTM.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Predicted metal-dependent amidase/aminoacylase/carboxypeptidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO: GO:0004352; F:glutamate dehydrogenase activity; IEA. GO: GO:0016491; F:oxidoreductase activity; IEA. GO: GO:0006520; P:amino acid metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 AA; 46526 MW; 1269189AA6C03038 CRC64;
                                                                                                                                                                                                                                                                                                                                    01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
NAD-specific glutamate dehydrogenase (EC 1.4.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusobacterium nucleatum subsp. vincentii ATCC 49256
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Bacteria; Proteobacteria; environmental samples.
NCBI_TaxID=248048;
                                                                                                                                                                                                                                              425 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR066095; GLFV dehydrog.
InterPro; IPR066095; GLFV dehydrog_C.
InterPro; IPR006097; GLFV dehydrog_C.
Pfam; PF002008; GLFV dehydrog_N.
Pfam; PF0020812; GLFV dehydrog_N.
PRINTS; PR00082; GLFDHDRGNASE.
                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                     305 MAVAEF 310
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Les 5; Conserv
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                            7
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                            MXVAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                Name=FNV0417;
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Best Loc Matches

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Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., A Otsuki T., Saito H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., A Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kanda K., Wagatsuma M., A Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL, AKIST634; BASC87065.1; -
R EMBL, AKIST634; BASC87065.1; -
R GO; GO:0015622; F:ATPase activity, coupled to transmembrane m. ..; IEA.

GO; GO:0015622; F:ATPase activity, coupled to transmembrane m. ..; IEA.

R O; GO:0016912; P:CATATPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pleurotus ostreatus (Oyster mushroom) (White-rot fungus).
Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Homobasidiomycetes,
Agaricales, Pleurotaceae, Pleurotus.
NCBI_TaxID=5322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                              82.8%; Score 24; DB 2; Length 442;
83.3%; Pred. No. 7.8e+02;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.8%; Score 24; DB 2; Length 457; 71.4%; Pred. No. 8.1e+02; ive 1; Mismatches 1; Indels
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databages.
EMBL; AJ420741; CAD12640.1; -.
HSSP; P04191; ISU4.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
Pfam; PF03108; MuDR; 1.
SEQUENCE 442 AA; 50695 MW; 214F0711137BE6F1 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FL745732.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Putative ENA-ATPase (Fragment).
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Best Local Similarity 71.4.4
Fig. Conservative
                                                                                                                                                                            5; Conservative
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                                                                                                                                 Best_Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                              1 MTVAEF 6
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                                                                                                         Query Match
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Q6ZS89
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MEDLINELALBEDS'19; FURDERCELIBOSIOS;
MEDLINELALBEDS'19; FURDERCELIBOSIOS;
MEDLINELALBEDS'19; FURDERCENII, Ivanova N., Reznik G., Los T., Lykidis A.,
Medatral V., Anderson I., Ivanova N., Reznik G., Zohu L.,
Medlinelarya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Medlinelar D., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Medlinelar D., Coverbeek R.;
Medlinelar D., Medlinelar D., Overbeek R.;
Medlinelar D., Medlinelar D., Overbeek R.;
Medlinelar D., Barterion ATCC 25586.";
Medlinelar D., Barterion D., Medlinelar D., Medlinelar D.,
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Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
NCBI_TaxID=147425;
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Pubmed=12872003; DOI=10.1073/pnas.1533501100;
Song J., Bradeen J.M., Naess S.K., Raasch J.A., Wielgus S.M.,
Haberlach G.T., Liu J., Kuang H., Austin-Phillips S., Buell C.R.,
Helgeson J.P., Jiang J.;
Helgeson J.P., Jiang J.;
Helgeson J.P., Jiang J.;
Helgeson J.P., Jiang J.;
Facene Re Joned from Solanum bulbocastanum confers broad spectrum
resistance to potato late blight.";
Proc. Natl. Acad. Sci. U.S.A. 100:9128-9133(2003).
Embl., ANJ 303171, AAP451871;
InterPro; IPR004312; MuDR.
InterPro; IPR000817; Prion.
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                                                                                                                                                                                                                                              Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 AA, 48243 MW; AC999236B6713FD5 CRC64;
                            01-070-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
NAD-specific glutamate dehydrogenase (EC 1.4.1.2).
OrderedLocusNames=FN0488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                    Fusobacterium nucleatum (subsp. nucleatum)
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Solanum bulbocastanum (Wild potato)
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
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                                                                                                                                                                                                                                                                                                          NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                              Fusobacterium
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GENOME REANNOTATION.
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SEQUENCE
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KRAIN-Berkeley;

KRAIN-Berkeley;

KRAIN-Berkeley;

KRAIN-Berkeley;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Richards S., Ashburner M., Hederson S.N.,

RA Gorger R.A., Lewis S.E., Richards S., Ashburner M., Hederson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Prannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,

RA Beeson K.Y., Bulke C., Davemport L.B., Center A., Chandra I.,

RA Ballew R.M., Cawley S., Dahlke C., Davemport L.B., Daviss P.,

RA Ballew B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Glodek A., Goup L.E., Downes M., Digart Rocha S., Durkov B.C., Dunn P.,

RA Glodek A., Goup L.E., Downes M., Digar R., Hourk J.,

RA Hostin M., Harvey D.A., Heiman T.J., Hernardez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Jalali M., Kaluuk F., Karpen G.H., Ke Z., Kamison J.A., Ketchum K.A.,

Jalali M., Kaluuk P., Karpen G.H., Ke Z., Kamison J.A., Kedchum K.A.,

Jalali M., Kaluuk P., Murphy E., Murphy L., Murny D.M., Nelson D.L.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,

Rainer K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Spire R., Spradling A.C., Standers R.D.C., Scheeler F., Shen E.,

RA Williams S.Y., Wassarman D.A., Weinstenbach J.,

Walliams S.W., Woodey T., Wolly W., Whisesenbach J.,

Walliams S.W., Woodey T., Wolly W., Walliams S.,

Walliams S.W., Woodey T., Whole K.C., Whu P., Nelson D.K.,

Walliams S.W., Woodey T., Whan S., Zhan M., Zhuo S., Zhan K., Zhan W., Zhuo S., Zhan W., Zhuo S., Zhan S., Zhu X., Zhan S., Zhu X., Zhu S., Zhu X., Zhu S., Zhu S., Zhu S.
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   . .; IEA.
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GO; GO:0015662; F:ATPase activity, coupled to transmembrane m. GO; GO:0003824; F:Catalytic activity; IEA. GO; GO:0008812; P:Catalytic activity; IEA. GO; GO:0008812; P:Cation transport; IEA. GO; GO:000812; P:metabolism; IEA. From; PF007702; P:metabolism; IEA. PRINTS; PR00119; CATATPASE. TIGREMAS; TIGR01494; ATPase_P-type; 1.
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Name-Gr64f; ORFNames=CG32255;

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                             Score 24; DB 2; Length 463; Pred. No. 8.2e+02; 0; Mismatches 2; Indels
                                                                                                                                49188 MW; C38AE05528AAFB28 CRC64;
                                                                                                                                                                                                                                                                                                                        GG4F_DROME STANDARD; PRT; 469 AA. P83297; Q9VZJ5; 28-F82003 (Rel. 41, Created) 05-JUL-2004 (Rel. 44, Last sequence update) 25-JAN-2005 (Rel. 46, Last annotation update)
                                                                                                                                                          82.8%;
71.4%;
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tes 5; Conservative
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                                                                                                                  463 AA;
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NON TER
SEQUENCE
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                                                                                                                                  MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D. N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21407712; PubMed=11516643; DOI=10.1016/S0960-9822(01)00258-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunipace L., Meister S., McNealy C., Amrein H.;
"Spatially restricted expression of candidate taste receptors in the Drosophila gustatory system.";
curr. Biol. 11:822-835(2001).
-!- FUNCTION: Probable role in the gustatory response.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the G-protein coupled receptor Dr-tr
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GO; GO:0016021; C:integral to membrane; NAS.
GO; GO:0016021; E:taste receptor activity; NAS.
GO; GO:0050909; P:perception of taste; NAS.
Pfam, PF06151; Trehalose_recp; 1.
Pfam, PF06151; Trehalose_recp; 1.
Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                     Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome:
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4 (Potential).
Extracellular (Potential).
5 (Potential).
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Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                               systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family. Subfamily II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138
146
167
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5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus horikoshii
                                                                                                                                                                                                                                                          HSSP; 005207; 1MX0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; E71052; E71052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 MSVAEF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 MXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   guanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=OT3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        058843;
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058843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
-!-FUNCTION: Relaxes both positive and negative superturns and
-xhibits a strong decatenase activity. The B subunit binds ATP (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBUNIT: Heterotetramer of two subunits A and two subunits B (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ξ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Type II DNA topoisomerase VI subunit B (EC 5.99.1.3) (TopoVI-B)
Name=top6B; OrderedLocusNames=APE0706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Town C.D., Kaul S.;
Submitted (GAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC068667; AAG51739.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 484 AA; 52066 MW; F94D3EA5C96059B3 CRC64;
                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F15D2.29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         565 AA.
                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desulfurococcaceae; Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR008892; WCOR413.
Pfam; PF05562; WCOR413; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 82.8%;
Local Similarity 71.4%;
les 5; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E86416; E86416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aeropyrum pernix.
                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
                                                                                                                                          Name=F15D2.29;
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Q9YE64;
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Matches
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SOOR REAL SOOR R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGERAMS; TIGRO1052; top6b; 1.
ATP-binding; Complete proteome; DNA-binding; Isomerase; Topoisomerase.
SEQUENCE 565 AA; 64096 MW; E4A3DFCC5E53D508 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida M., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H., "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deazaguanine in tRNAs with GU(N) anticodons (tRNA-Asp, -Asn, -His and -Tyr). After this exchange, a cyclopentendiol moiety is attached to the 7-aminomethyl group of 7-deazaguanine, resulting in the hypermodified nucleoside queuosine (0) (7-((4,5-cis-dhydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SIMILARITY: Belongs to the queuine tRNA-ribosyltransferase family.
EMBL; AP000005; BAA30215.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 11Q8; X-ray; A/B=1-582.
PDB; 11T7; X-ray; A/B=1-582.
PDB; 11T8; X-ray; A/B=1-582.
PDB; 1J2B; X-ray; A/B=1-582.
GO; GO:0008479; P:queuine tRNA-ribosyltransferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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CATALYTIC ACTIVITY: tRNA guanine + queuine = tRNA queuine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.8%; Score 24; DB 1; Length 565;
83.3%; Pred. No. 9.9e+02;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            582 AA.
                                                                                                                                                                                                                                                                                                                                                                                  INCEPTO, IPRO0322; -; 1.
INTERPRO, IPRO03594; ATPbind ATPase.
INTERPRO; IPRO05734; DNA_top6B.
INTERPRO; IPRO10979; Ribosomal_H2TH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                             EMBL; AP000060; BAA79682.1; -. PIR; B72660; B72660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein PH1116.
OrderedLocusNames=PH1116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02518; HATPase c; 1
SMART; SM00387; HATPase c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25,
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InterPro; IPR004521; Unchar dom 2.
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Submitted
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 70
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      DR XX D DR B DR XX XX S OX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAINGES / Orsay;

MEDLINE-22511545; PubMed=12622808;

MEDLINE-22511545; PubMed=12622808;

Cohen G.N., Barbe V., Ralment D., Galperin M., Heilig R., Lecompte O.,

Doch G., Prieur D., Querellou J., Ripp R., Thierry J.-C.,

Nan der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;

Tachaeon Pyrococcus abyssis.";

Tachaeon Pyrococcus abyssis.";

Mol. Microbiol. 47:1495-1512(203).

-I- FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAs with GU(N) anticodons (tRNA-Asp. -Asn. -His and -Tyr). After this exchange, a cyclopentendiol moiety is attached to the 7-aminomethyl group of 7-deazaguanine, resulting in the hypermodified nucleoside queuosine (Q) (7-(((4,5-cis-dihydroxy.2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
GO; GO:0008616; P:queucosine biosynthesis; IEA.
GO; GO:0008033; P:tRNA processing; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0008479; F:queuine tRNA-ribosyltranbferase activity; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0016757; F:tranbferase activity, transferring glycosyl. .; IEA.
GO; GO:0008015; P:queuosine biosynthesis; IEA.
GO; GO:0008033; P:tRNA processing; IEA.
InterPro; IPR004804; AtRNA_ribo_trans.
InterPro; IPR002478; PUA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: Binds 1 zinc ion per subunit (By similarity).
SIMILARITY: Belongs to the queuine tRNA-ribosyltransferase family.
b; AJ248286; CAB50027.1; -.
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Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome, Glycosyltransferase, Hypothetical protein, Queuosine biosynthesis; Transferase; Zinc; tRNA processing. SEQUENCE 582 AA; 66595 MW; B96F1D5EC0D73AC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: tRNA guanine + queuine = tRNA queuine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.8%; Score 24; DB 2; Length 582; 57.1%; Pred. No. 1e+03; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Queuine-archaeosine tRNA ribosyltransferase.
                                                                                                                                                                                                                                                                                                              SMART; SM0359; PUA; 1.
TIGRFAMS; TIGR00432; arcsn tRNA tgt; 1.
TIGRFAMS; TIGR00449; tgt_general; 1.
TIGRFAMS; TIGR00451; unchar_dom_2; 1.
                                                                                                                          InterPro; IPR004804; AtRNA_ribo_trans.
InterPro; IPR002478; PUR.
InterPro; IPR002616; tRNA_ribo_trans.
InterPro; IPR004521; Unchār_dom_2.
Pfam; PF01472; PUR; 1.
Pfam; PF01702; TGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002478; PUA.
InterPro; IPR002616; tRNA_ribo_trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
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Best Local Similarity 5...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50890; PUA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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440 VMAIAEY 446
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PIR, F75090; F75090.
HSSP, O58843; 1108.
GO; GO:0008479; F:qu
GO; GO:0001723; F:RN
GO; GO:0008616; P:qu
GO; GO:0008616; P:qu
GO; GO:0008616; P:qu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames=PAB0740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity)
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0990ZNO
DD 0910ZNO
DD 01-MA
DT 01-MA
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GO, GO:0005534; C:nucleus; IEA.
GO; GO:0005534; F:ATP-binding; IEA.
GO; GO:000403; F:ATP-dependent DNA helicase activity; IEA.
GO; GO:0003577; F:DNA binding; IEA.
GO; GO:0003577; F:DNA binding; IEA.
GO; GO:00061819; F:Mydrolase activity, acting on acid anhydrid. ..; IGO; GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. ..; IGO; GO:0006289; P:nucleotide-excision repair; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE=21576510; PubMed=11719906; DOI=10.1038/35106579;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P. Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.; Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Encephalitōzoon cuniculi GB-Mi.
Eukaryota, Fungi, Microsporidia, Unikaryonidae, Encephalitozoon.
NCBI_TaxID=284813;
                                                                                                                                                                                                                       Complete proteome; Glycosyltransferase; Queuosine biosynthesis;
Transferase; Zinc; tRNA processing.
SEQUENCE 584 AA; 66667 MW; E31755EAE3681666 CRC64;
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                                                                                                                                                                                                                                                                                                                                                          Length 584;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ATP DEPENDENT DNA BINDING HELICASE (RAD3/XPD SUBFAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              619 AA; 69072 MW; 9574F09FD2B52A67 CRC64;
                                                                                                                                                                                                                                                                                                                                                       Query Match 82.8%; Score 24; DB 2; Best Local Similarity 57.1%; Pred. No. 1e+03; Matches 4; Conservative 2; ·Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGREAMS; TIGRO0604; rad3; 1.
PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
PROSITE; PS00962; RIBOSOWAL_S2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    619 AA.
Pfam; PF01472; PUA; 1.
Pfam; PF01102; TGT; 1.
SMART; SM00359; PUA; 1.
TIGRPAMs; TIGR00432; arcsn_tRNA_tGt; 1.
TIGRPAMs; TIGR00451; tGt_General; 1.
TIGRPAMs; TIGR00451; unchar_dom_2; 1.
PROSITE; PS50890; PUA; 1.
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InterPro; IPR002464; DEAH_box.
InterPro; IPR006554; DENDC2.
InterPro; IPR006555; Helic c2.
InterPro; IPR001965; Ribosomal_S2.
InterPro; IPR001945; Ribosomal_S2.
Pfam; Pf06733; DEAD_2; I.
SMART; SM00488; DEXDC2; I.
SMART; SM00491; HELICC2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || :||:
440 VMAIAEY 446
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09730329-60ed.rup

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SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson D.;
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                                                 P91063
P91063;
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Q846V6
  RESULT 72
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STRAIN=ATCC 33913 / NCPPB 528;

MEDLINE=2022145; PubMed=12024217; DOI=10.1038/4174599;

MEDLINE=2022145; PubMed=12024217; DOI=10.1038/4174599;

A silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A loaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alveb L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapha L.P.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapha L.P.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Locall E.C., Machado M.A., Madeira A.M.B.N., Martinez Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Taudfi D., Teai S.M., White F.F.,

Setubal J.C., Kitajima J.P.;

R. Comparison of the genomes of two Xanthomonas pathogens with differing the septimicities of two setupances.
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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Score 24; DB 2; Length 619;
Pred. No. 1.1e+03;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 417:459-463 (2002).

EMBL; AE012336; AAM41570.1; -.

EMBL; AE012336; AAM41570.1; -.

GO; GO:00044671; F:signal transducer activity; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR002086; Aldehyd_dehydrog.

InterPro; IPR011006; Chey_like.

InterPro; IPR001633; EAL.

InterPro; IPR0000160; GOBER.
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Pfam; PF00563; BAL; 1.
Pfam; PF00990; GGDEF; 1.
SMART; SM00052, DUF2; 1.
TIGRFAMS; TIGR00254; GGDEF; 1.
TIGRFAMS; TIGR00229; Sensory box; 1.
PROSITE; PS500687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
PROSITE; PS50883; EAL; 1.
                                                                                                                                                                                                                                                                  689 AA.
                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, C)
01-0CT-2002 (TrEMBLrel. 22, L,
01-0CT-2002 (TrEMBLrel. 26, L,
01-MAR-2004 (TrEMBLrel. 26, L,
Hypothetical protein XCC2291.
82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=XCC2291;
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Best Local Similarity 57.1-
--- 4; Conservative
Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                            284 VMGVSEF 290
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                                                                                                1 VMXVAEF 7
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SEQUENCE 689 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=340;
                                                                                                                                                                                                                                                                Q8P8F1
Q8P8F1;
                                                                                                                                                                                                              RESULT 71
108 PRF 11
108 PRF 12
10 PRF 13
10 PRF 13
10 PRF 13
10 PRF 13
10 PRF 14
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Yun H.J., Lee S.W., Yoon G.M., Kim S.Y., Choi S., Lee Y.S., Choi E.C.,
Kim S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                       Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                  investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                   WormBase Consortium;
"Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.8%; Score 24; DB 2; Length 738; Best Local Similarity 83.3%; Pred. No. 1.3e+03; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; U80847; AAB37983.2; -.
PIR; T25551; T25551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The sequence of C. elegans cosmid C17H11.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston R.; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WormPep; C17H11.2; Carrier Hypothetical protein.
Hypothetical protein.
From From T38 AA; 83764 MW; D41414064A4944F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis.
Bacteria, Firmicutes, Bacillales, Staphylococcus
738 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 871 AA
                                       01-MAY-1997 (TrEMBLrel. 03, Created) 01-OCT-2001 (TrEMBLrel. 18, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WormBase; WBGene00015922; C17H11.2. WormPep; C17H11.2; CE27703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                   01-OCT-2003 (TrEMBLrel. 25, Last e typothetical protein C17H11.2. Name=C17H11.2; ORFNames=C17H11.2; Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soleucyl-tRNA synthetase.
PRELIMINARY;
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원 ð

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Query Match
Best Local Similarity 83.35,
Then 5; Conservative
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STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 MSVAEF 120
                                                                                                                                                                                                                                                                                                                                                                                                  2 MXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleRS)
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          S F F F W KW D D R D S
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Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

Vana Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-W.;

"Genome-based analysis of virulence genes in a non-biofilm-forming
Staphylococcus epidermidis strain (ATCC 12228).";

Mol. Microbiol. 49:1577-1593 (2003).

-!-CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(Ile) = AMP +

diphosphate + L-isoleucyl--ENA(Ile).

-!-COFACTOR: Binds 1 zinc ion per subunit (By similarity).

-!-SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!-SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!-SUMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
25-GCT-2004 (Rel. 45, Last annotation update)
Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                         82.8%; Score 24; DB 2; Length 871; 83.3%; Pred. No. 1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                           100133 MW; 2E140C3F74318A15 CRC64;
                                   HSSE; F413/12; LT.1.
GO: GO: 000524; F: ATP binding; IEA.
GO: GO: 0004822; F: ATS binding; IEA.
GO: GO: 0006428; P: Isoleucine-tRNA ligase activity; IEA.
GO: GO: 0006428; P: Isoleucyl-tRNA aminoacylation; IEA.
INCERPRO; IPR003300; TRNA-synt_Ia.
INCERPRO; IPR00311; tRNA-synt_Ii.
INCERPRO; IPR009080; tRNA-synt_ila.
INCERPRO; IPR009080; TRNA-NA-Ia bind.
INCERPRO; IPR009080; VAIRS_INRS_GOIT.
PFR00133; TRNA-SYNT_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   916 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                           Pfam; PF00133; ERNA-synt 1; 1.
PRINTS; PR00984; TRNASYNTHILE.
TIGRFAMS; TIGR00392; iles; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
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InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR002301; tRNA-synt_ile.
InterPro; IPR009080; tRNASyn_la_bind.
InterPro; IPR009008; ValRS IIeRS edit
InterPro; IPR00663; ZF-FPG_IIeRS.
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EMBL; AF516209; AAO65848.1; -. HSSP; P41972; 1FFY.
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                                                                                                                                                                                                                                                                                                                                                 Aminoacyl-tRNA synthetase
SEQUENCE 871 AA; 10013:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 MSVAEF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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STRAIN=ATCC 12228;
PubMed=12950922;
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Q8CSX1;
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SYI_STAREP

DY SYAEP

DT 29-MAD

DT 29-MAD

DT 29-MAD

DE 110016

DE 110016
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RA XINDELNE-189044031; PubMed-2934377; DOI=10.1038/36786;

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Bareved V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Bruschi C., Brans A., Braun M., Briganell S.C., Bron S., Broulet E., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., RA Entia C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N., A Fritz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N., A Hibert H., Holsapel S., Hosono S., Hullo M.F., Itaya M., Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medina N., Mellado R.P., Mizuno M., Moski S., Marsevic C., Medina N., Mellado R.P., Mizuno M., Moski S., Raperca C., Sato T., Scanlan E., Schleich S., Schroeter R., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Rose M., Sadaie Y., Sato T., Schowska A., Sertor P., Sertor P., Schleich S., Marman K., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Minters P., Wipat A., Yamanoto H., Yamane K., Yasunoto K., Yata K., Yashida K., Yashame H.F., Zumstein E., Weller B., Weltzeneger T., Winters P., Wipat A., Yamanoto H., Yamane K., Yashikwa H., Danchin A., The Complete genome sequence of the Gram-positive bacterium Bacillus M., The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                               Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYI BACSU STANDARD; PRT; 921 AA.
045477; 031730; P71022;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
1soleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
Pfam; PF00133; tRNA-synt_1; 1.
Pfam; PF06827; zf-FPG IlaRS; 1.
PRINTS; PR00984; TRNASIVITHILE.
TIGRPAMs; TIGRO0392; ileS; 1.
PROSITE; PS00179; AA TRNA_LIGASE I; 1.
PROSITE; PS00179; AA TRNA_LIGASE I; 1.
Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Metal-binding; Protein biosynthesis; Zinc.
SITE 595 S99 "RMSKS" region.
SITE 595 S99 "RMSKS" region.
BINDING 598 S99 ATP (By similarity).
SEQUENCE 916 AA; 105185 MW; C5155509A91FCEEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%; Score 24; DB 1; Length 916
83.3%; Pred. No. 1.6e+03;
.ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
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Gaps

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SEQUENCE FROM N.A.

PubMed=14960714; DOI=10.1093/nar/gkh258;

Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,

Shores K.A., Foute D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,

Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;

Nelson W.C., Kolstoe A. Bacillus cereus ATCC 10987 reveals metabolic
adaptations and a large plasmid related to Bacillus anthracis pXOI.";

Nucleic Acids Res. 32:977-988(2004).

EMBL, ASD17276, A&A42843.1;

TIGR; BCE3940;
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin B., Tice H., "Complete genome sequence of Bacillus cereus ZK."; submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%; Score 24; DB 2; Length 921; 83.3%; Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                      Score 24; DB 2; Length 921;
Pred. No. 1.6e+03;
0; Mismatches 1; Indels
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                                                                                                                                                         EMBL; CP000001; AAU16613.1; -. Aminoacyl-tRNA synthetase; Ligase. SEQUENCE 921 AA; 104620 MW; FBF96E6AE4D5D3BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus cereus (strain ATCC 10987).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104589 MW; B531AF210A8036C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
15oleucyl-cRNA synthetase (EC 6.1.1.5).
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InterPro; IPR009000; tRNAsyn ia bind.
InterPro; IPR009000; valks IleRS edit.
InterPro; IPR010663; ZF-FPG ileRS.
Pfam; PF00133; tRNA-synt i. 1.
Pfam; PF00133; tRNA-synt i. 1.
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PROSITE; PS00178; AA TRNA LIGASE I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=ileS; OrderedLocusNames=BCE3940;
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                                                                                                                                                                                                                                                                                                              82.8%;
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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Matches 5; Conserv
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SEQUENCE 921 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Q819R4
ID Q819R-
AC Q819R-
DT 01-JUD
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           SOWRER
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InterPro; lrw...

R InterPro; lrw...

R Ffam; PF00133; tENA-synt 1; 1.

DR Pfam; PF00627; zf-PF0 IleRs; 1.

DR PRINTS; PR00984; TRNASYNTHILE.

DR TIGRFAMs; TIGR00392; lies; 1.

DR Aminoacyl-ENA synthetase; ATP-binding; Complete protecome; Ligase; KW Aminoacyl-ENA synthetase; ATP-binding; Complete protecome; Ligase; KW Metal-binding; Protein biosynthesis; zinc.

Synthematal Synthema
                                                                                                                                                                                                G., Bron S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
1soleucine--EXMA ligase (Isoleucyl-tRNA synthetase) (EC 6.1.1.5).
Name=ileS; ORFNames=BTZK3654;
                                                                                                                                                                                                                                                                                                      diphosphate + Lisoleucyl-tRNA(IIe).
--- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
--- SUBUNIT: Monomer (By similarity).
--- SUBCELLULAR LOCATION: Cycoplasmic.
--- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                     STRAIN=168;
Pragai Z., Tjalsma H., Bolhuis A., van Dijl J.M., Venema G., Br
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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83.3%; Pred. No. 1.6e+03;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
       Stewart G.C., Cha J.H.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                921 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; H69093; MOUS.
HSSP, P41972; 1003.
Subtilist; BG11792; ileS.
InterPro; IPR001300; ERNA-synt_I.
InterPro; IPR001412; ERNA-synt_I.
InterPro; IPR001301; ERNA-synt_I.
InterPro; IPR009008; ValRS_IleRS_edit.
InterPro; IPR010663; ZF-FPG_ILERS.
InterPro; IPR010663; ZF-FPG_ILERS.
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                                                                                                                 SEQUENCE OF 733-921 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, Z99112; CAB13417.1; -.
EMBL, U60901; AAB49280.1; -.
EMBL; U48870; AAB57764.1; -.
PIK, H69643; H69643.
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les 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 MSVAEF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus cereus ZK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 MXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q636D1;
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0636D1
10 0636D
AC 0636D
DT 25-0C
DT 2
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Gaps

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STRAIN=Ames / isolate 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L., Frager C.M.;
Frager C.M.;
"Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin E., Tice H.;
Richardson P., Rubin E., Tice H.;
Submitted (JAN-2004) to the EML/GenBank/DDBJ databases.
EMBL, AE017036; AAP27760.1; -.
EMBL, AE017225; AAT33151.1; -.
EMBL, AE017225; AAT56048.1; -.
genome sequence of Bacillus anthracis Ames and comparison to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00133; tRNA synt 1; 1.
Pfam; PF00131; tRNA synt 1; 1.
Pfam; PF06827; zf-FPG_IleRS; 1.
PRINTS; PR00984; TRNASYNTHILE.
TIGRAMA; TIGR00392; ileS; 1.
Aminoacyl-tRNA synthetase; Complete proteome.
SEQUENCE 921 AA; 104610 MW; 4B383BCCC606348B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus halodurans.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; GBAA4034; -.
60; GO:000522; F:ATP binding; IEA.
60; GO:0004222; F:isOleucine-tRNA ligase activity; IEA.
60; GO:0006428; P:isOleucyl-tRNA aminoacylation; IEA.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            921 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro, IPR002300, tRNA-synt_la.
Interpro, IPR001412; tRNA-synt_l.
Interpro, IPR002301, tRNA-synt_ile.
Interpro, IPR009080; tRNA-syn is bind.
Interpro, IPR009080; tRNA-syn is bind.
Interpro, IPR009081, Yalks_IleRS_dit.
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                                      closely related bacteria.";
Nature 423:81-86(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [soleucyl-tRNA synthetase.
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 MXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; BA4034; -.
TIGR; GBAA4034; -
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sterne;
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          à
                                                                                                                                                                                                                                                      MEDLINE=222608415; PubMed=12721630; DOI=10.1038/nature01582; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kaparral V., Bhattacharyya A., Reznik G., Mithailova N., Lapidus A., Grechkin Y., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Overbeek R., Kyrpides N.C.; Chonge G., Rostein M., Ehrlich S.D., Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-22608414; PubMed-12721629; DOI=10.1038/nature01586; Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T., Nelson K.E., Tettellin H., Pouts D.E., Bisen J.A., Gill S.R., Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L., Delsoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C., Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O., Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolstoe A.-B., Fraser C.M.;
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83.3%; Pred. No. 1.6e+03;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSRP; P417/2; Irri.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO:0004824; F:ligase activity; IEA.
GO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
CO; GO:0006428; P:isoleucyl-tRNA aminoacylation; IEA.
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_lie.
InterPro; IPR009008; tRNA-synt_lie.
InterPro; IPR019008; VAIRS lieRS edit.
R InterPro; IPR010663; ZF-FPG_IIERS.
Pfam: PF00133; tRNA-synt_lil.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00133; ERNA-synt 1; 1.
Pfam; PF00133; ERNA-synt 1; 1.
Pfam; PF06827; zf-FPG 11eRs; 1.
PRINTS; PR00984; TRNASYNTHILE.
TIGRFAMS; TIGRO929; iles; 1.
PROSITE; PS001078; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA syntherase; Complete proteome; Ligase.
SEQUENCE 921 AA; 104561 MW; 522D045A316EEIE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1392;
                                                                                                 Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q81WE4; Q6HUJ1; Q6KNS7;
01-JUN-2003 (TFEMBLrel. 24, Created)
10-JUN-2003 (TFEMBLrel. 24, Last sequence update)
25-CCT-2004 (TEMBLrel. 28, Last annotation update)
Isoleucyl-tRNA synthetase.
   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Isoleucyl-tRNA synthetase (BC 6.1.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 423:87-91(2003).
EMBL; AE017010; AAP10816.1; -.
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STRAIN=Ames / isolate Porton;
                                                                     OrderedLocusNames=BC3895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 83.3
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 MTVAEF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus anthracis.
                                                                                                                                                            NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P41972; 1FFY
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Matches
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081WE4
10 081WE4
AC 081WE
DT 01-JU
DT 01-JU
DT 25-OC
GN Name=
GN Name=
CN NCBI
CN NC
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"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000). MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317; Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;

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NCBI_TaxID=279010;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                            STRAIN=DSM 13;
PubMed=15383718;
                                                                       Q65JV7
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                                                      Q65JV7
                            RESULT 82
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                                          265JV7
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Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Wubin E., Tice H.;
Richardson P., Rubin E., Tice H.;
"Complete genome sequence of Bacillus thuringiensis 97-27.";
"Complete genome sequence of Bacillus thuringiensis 97-27.";
"Complete genome sequence of Bacillus thuringiensis 97-27.";
"Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases."

Red (JUN-2004) to the EMBL/GenBank/DDBJ databases.

Red (JOS) 00005524; F.ATE binding; IEA.

GO; GO:0006428; P.:isoleucine-tRNA ligase activity; IEA.

RO; GO:0006428; P.:isoleucine-tRNA minoacylation; IEA.

RICHEPPO; IPRO03300; tRNA-synt_I.

RICHEPPO; IPRO03301; tRNA-synt_I.

RICHEPPO; IPRO03008; VAIRS IIARS edit.

RICHEPPO; IPRO03008; VAIRS IIARS edit.

RICHEPPO; IPRO03008; VAIRS IIARS edit.

RED FEMI; PF00133; tRNA-synt_I.

RED FEMI; PF00133; tRNA-synt_I.

RED FEMI; PF00133; tRNA-synt_I.

RED FEMI; PF00133; tRNA-SynTHILE.
                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
150-Latone--tRNA ligase (Isolaucyl-tRNA synthetase) (EC 6.1.1.5).
Name=ileS; OrderedLocusNames=Baclels, OrderedLocusNames=Baclels, CorderedLocusNames=Baclels, Parinicutes; Bacillus thuringiensis (subsp. konkukian).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                   GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 0004822; F:isoleucine-tRNA ligase activity; IEA.
GO; GO: 0004824; F:isoleucine-tRNA ligase activity; IEA.
GO; GO: 0004826; F:isoleucine-tRNA ligase activity; IEA.
GO; GO: 000428; F:isoleucine-tRNA aminoacylation; IEA.
InterPro; IPR001300; tRNA-synt_1.
InterPro; IPR002300; tRNA-synt_1.
InterPro; IPR009080; tRNA-synt_1.
InterPro; IPR009080; ValRS ILERS edit.
InterPro; IPR009080; ValRS ILERS edit.
R Ffam; PF06827; Zf-FPG ILERS.
R PFam; PF06827; Zf-FPG ILERS.
R TIGRAMS; TIGR0032; ileS; 1.
R PROSITE; PS00178; AA TRNA_LIGASE I; 1.
Maninoacyl-tRNA synthetase; Complete proteome.
SEQUENCE 921 AA; 104562 MW; 5D9A17ED5A741B9A CRC64;
                                                                                                                                                                                                                                                                 Query Match 82.8%; Score 24; DB 2; Length 921; Best Local Similarity 83.3%; Pred. No. 1.6e+03; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%; Score 24; DB 2; Length 921;
83.3%; Pred. No. 1.6e+03;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      921 AA; 104633 MW; ABF082F44E94A891 CRC64;
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PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         115 MSVAEF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 MTVAEF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=180856;
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                                                                                                                                                                                                                                                                                                                             2 MXVAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 921 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6HER9;
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Pubmed=15220978; DOI=10.1073/pnas.0305659101;
Alsmark U.C.M., Frank A.C., Karlberg B.O., Legault B.-A., Ardell D.H.,
Canbacck B., Eriksson A.-S., Nasslund A.K., Handley S.A., Huvet M.,
La Scola B., Holmberg M., Andersson S.G.E.;
"The louse-borne human pathogen Bartonella quintana is a genomic
derivative of the zonoctic agent Bartonella henselae.";
Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         licheniformis and comparisons with closely related Bacillus species.";

Genome Biol. 5:R77-R77(2004).

EMBL; AE017333; AAU40657.1; -.

EMBL; CP000002, AAU23298.1; -.

Aminoacyl-tRNA synthetase.

SEQUENCE 922 AA, 104355 MW; DFCB33B0F71906B6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAINS-ATCC 14580;
STRAINS-ATCC 14580;
RESY M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky B.J.
Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.
Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
Berka R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G.;
"The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential.";
J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Complete genome sequence of the industrial bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bartonellaceae; Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 2; Length 922;
Pred. No. 1.6e+03;
0; Mismatches 1; Indels
                                                                                                                                                  IleS (Isoleucyl-tRNA synthetase).
Name=ileS; ORFNames=BL02267, BL101762;
Bacillus licheniformis DSM 13.
Bacteria; Firmicutes; Bacillales; Bacillus.
                                                       25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
922 AA
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 49882 / Houston 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.3.
PRELIMINARY;
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Aminopeptidase; Glycoprotein; Hydrolase; Metalloprotease;
                                                                              METAL
                                                                                                                                          ACT SITE CARBOHYD
                                                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                      SEQUENCE
                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 86
AT9B HUMAN
                                                                                                                                                                                                                                                                                                                                                                       086G73
                                                                                                                              METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Aminopeptidase N (EC 3.4.11.2) (Microsomal aminopeptidase) (Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=97273974; PubMed=9128148; DOI=10.1016/S0167-4838(96)00204-X; Smith T.S., Graham M., Munn B.A., Newton S.E., Knox D.P., Coadwell W.J., McMichael-Phillips D., Smith H., Smith W.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein Hill).
Haemonchus contortus (Barber pole worm).
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
GO; GO: 0000155; F:two-component sensor molecule activity; IEA.

GO; GO:000160; P:two-component signal transduction system (p. ..;
InterPro; IPR00163; EAL.

InterPro; IPR00160; GOBF.

InterPro; IPR00014; PAS.

InterPro; IPR000014; PAS.

InterPro; IPR000014; PAS.

InterPro; IPR0000019; PAS-assoc_C.

R Pfam; PP00563; EAL; 1.

R MART; SM0052; DUF2; 1.

R SMART; SM0052; DUF2; 1.

R TIGRPAMS; TIGR00229; sensory_box; 1.

R PROSITE; PS50883; EAL; 1.

R PROSITE; PS50883; EAL; 1.

R PROSITE; PS50881; EAL; 1.

R PROSITE; PS50813; EAL; 1.
                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                               Length 961;
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71.4%; Pred. No. 1.6e+03;
.ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                       971 AA.
                                                                                                                                                                                                                                                                                                                                                                      PRT;
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PRINTS; PR00756; ALADIPTASE.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001930; Peptidase_MI.
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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765 VMDLAEF 771
                                                                                                                                                                                                                                                                                 1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                       AMPN HAECO
Q10737;
                                                                                                                                                                                                                               Query Match
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AMPN_HAECO
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043861; 060872;
30-MAY-2000 (Rel. 39, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potential phospholipid-transporting ATPase IIB (EC 3.6.3.1) (HUSSY-
                By similarity.

Cytoplasmic (Potential).

Cytoplasmic (Potential).

Signal-anchor for type II membrane procein (Potential).

Extracellular (Potential).

Zinc (catalytic) (By similarity).

Zinc (catalytic) (By similarity).

Zinc (catalytic) (By similarity).

Procon donor (Potential).

N-linked (GlCMAc...) (Potential).

N-linked (GlCMAc...) (Potential).

N-linked (GlCMAc...) (Potential).

N-linked (GlCMAc...) (Potential).
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GO; GO:0004179; F:membrane alanyl aminopeptidase activity; IEA.
GO; GO:0006508; F:membrane alanyl aminopeptidase activity; IEA.
InterPro; IPR001930; Peptidase_M1.
InterPro; IPR006025; Pept M Zn BS.
Pfam; PF01433; Peptidase M1; 1.
PRINTS; PR00756; ALADIPTASE.
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                                                                                                                                                                                                                                                                                                                                 MW; 95C6A92B5CCA227C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Yan R.F., Li X.R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SEQUENCE 972 AA; 110548 MW; 8DBC651B21D905D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           972 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hidden antigen hll.
Haemonchus contortus (Barber pole worm)
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Name=ATP9B; Synonyms=ATPIIB, NEO1L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                        Query Match 82.8%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 71.4%;
5; Conservative
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                                                                                                          971
378
379
382
461
465
465
98
226
857
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548
857
871 AA;
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Matches 5; Conserv
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Signal-anchor; TINIT MET 0 DOMAIN 1
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RA OLD T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
Sakine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Sekine M., Obayashi M., Kawai Y., Isono Y., Nakamura Y.,
Nagahari K., Murakami K., Yawai Y., Isono Y., Nakamura Y.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Gugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Jamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Tamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Ishida S., Ono Y., Takaguchi S., Watanabe M., Hiraoka S., Chiba Y.,
RA Ishida S., Ono Y., Takaguchi S., Watanabe M., Haraoka S., Chiba Y.,
RA Innose N., Musashino K., Yuuki H., Oshima A., Saaski N., Aotsuka S.,
Nomiyama H., Zatoh N., Takami S., Terashima Y., Sarok S.,
Nomiyama H., Ichihara T., Shiohata N., Sano S.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Ramazaki M., Watanabe T., Sugiyama A., Itakura S., Fukuzumi Y.,
Ramazaki M., Watanabe T., Sugiyama A., Itakura S., Fukuzumi Y.,
Ramadata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RAwabata A., Hikiji T., Kobatake N., Inagaki H., Ishigama K., Pajakan T.,
A Okitani R., Kawakami T., Oyama M., Hata H., Watanabe M., Romatsu T.,
Rawabata A., Hakiji T., Kobatake N., Inagaki H., Masuho Y., Yamashita R.,
A Togashi T., Oyama M., Hata H., Watanabe M., Romatsu T.,
RAWashima Sugano J., Satoh T., Shikai Y., Takahashi Y., Nakagawa K.,
A Matsumura K., Nakajima Y., Milara H., Watanabe M., Komatsu T.,
RAWashima Sugano J., Satoh T., Shikai Y., Takahashi Y., Yamashita R.,
RAWashi K., Yada T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Rompali H., Nakamura N., Nikuchi H., Wasuho Y., Yamashita R., Rompa H., Nakai R., Yada T., Nomura N., Chana C., Isogai T., Sagan S.,
R., Chana M., Raya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A SEQUENCE OF 208-1095 FROM N.A.

Birren B., Linton L., Nusbaum C., Lander E., Ali A., Allen N.,
Adderson S., Barna N., Bastien V., Boguslavkiy L., Boukhgalter B.,
Adderson S., Barna N., Bastien V., Boguslavkiy L., Boukhgalter B.,
A Choepel Y., Colangelo M., Collins S., Collymore A., Cook A.,
Cook A., Cook A., Cook B.,
A Brown A., Camarate J., Campoplano A., Chang J., Farro S., Ferreira P.,
A Bratlano K., Dewar K., Diaz J.S., Dodge S., Faro S., Ferreira P.,
A FitzHugh W., Gage D., Galagan J., Gardyna S., Ginde S., Gord S.,
A Goyette M., Graham L., Grand-Pierre N., Hagos B., Heaford A.,
A Horton L., Hulme W., Iliev I., Johnson R., Jones C., Kamat A.,
A Horton L., Hulme W., Iliev I., Johnson R., Jones C., Kamat A.,
A Horton L., Hulme W., Iliev I., Johnson R., Jones C., Kamat A.,
A Horton L., Hulme W., Iliev I., Johnson R., Jones C., Kamat A.,
A Horton L., Hulme W., Iliev I., Johnson R., Jones C., Karatas A.,
A Horton L., Hulme W., Iliev I., Meness L., Michova T.,
A Morpheeters R., Meldrim U., Meneus L., Mihova T., Mlenga V., Murphy T.,
A Maylor J., Nguyen C., Norbu C., Norman C., Phunkhang P.,
A Pierre N., Pollara V., Raymond C., Retta R., Rieback M., Riley R.,
A Schauer S., Schupback R., Seaman S., Severy P., Spencer B.,
Stange-Thomann N., Stojanovic N., Strauss N., Subramanian A.,
A Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Travis N.,
A Taigilio J., Vassiliev H., Viel R., Vo A., Wilson B., Wu X., Wyman D.,
A Ve W.J., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Multiple members of a third subfamily of P-type ATPases identified by genomic sequences and ESTs."; Genome Res. 8:354-361(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Halleck M.S., Pradhan D., Blackman C.F., Berkes C., Williamson P.L.,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                               PubMed=14702039; DOI=10.1038/ng1285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98217376; PubMed=9548971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [3]
SEQUENCE OF 759-1095 FROM N.A.
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SEQUENCE OF 768-1095 FROM N.A.
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                                                                           SEQUENCE OF 1-420 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:13541; ATPPB.

R GO; GO:0015621; C:integral to membrane; NAS.

GO; GO:00156247; F:aminophospholipid transporter activity; NAS.

GO; GO:0005524; F:aminophospholipid transporter activity; NAS.

GO; GO:0015919; F:atlon-transporting ATPase activity; NAS.

GO; GO:0015917; P:aminophospholipid transport; NAS.

GO; GO:0015917; P:aminophospholipid transport; NAS.

InterPro; IPR001557; ATPASe El-E2 ATPASe reg.

InterPro; IPR005834; Dehal Tike hydro.

InterPro; IPR005839; Flippase.

R InterPro; IPR00539; Flippase.

R Pfam; PF00122; B1-E2 ATPASe.

R Pfam; PF00122; GATPASE.

R Pfam; PF00159; CATATPASE.

R TIGRRAMS; TIGR01652; ATPASE = 1:

R PROSITE; PS00154; ATPASE El-E2; 1.

M ATP-binding; Hydrolase; Magnesium; Multigene family; Phosphorylation;
                                                                                                                                                                                                                                      Unpublished Observations (JUL-2002).
-!- CATALYTIC ACTIVITY: AFP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
             MEDLINE=21064499; PubMed=11124703; DOI=10.1002/1097-0061(200101)18:1x69::AID-YEA647>3.3.CO;2-8; DOI=10.1002/1097-0061(200101)18:1x69::AID-YEA647>3.3.CO;2-8; Stanchi F., Simionati B., Cannata N., Zimbello R., Lanfranchi G., Valle G.; Cannata N., Zimbello R., Lanfranchi G., Valle G.; Characterization of 16 novel human genes showing high similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -aspartylphosphate intermediate (By
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Cytoplasmic (Potential).
Potential.
Extracellular (Potential).
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D -> N (in Ref. 3).
R -> K (in Ref. 3).
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EMBL; AJ006268; CAA06934.1; -.
                                                                                                                                                                                                 CONCEPTUAL TRANSLATION.
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rissum=Brain;
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use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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                                                                                                        MGD; MGI:1354757; Atp3b.
InterPro; IPR001757; Atp3b.
InterPro; IPR001557; ATPage BI-E2.
InterPro; IPR008504; Dehal_Ike_hydro.
InterPro; IPR008505; BI-E2_ATPage_reg.
InterPro; IPR008539; Flippage.
Pfam; PF000122; BI-E2_ATPage; I.
Pfam; PF000122; BI-E2_ATPage; I.
Pfam; PF000129; Hydrolase; I.
PRINTS; PR00119; CATATPASE.
TIGRPAMS; TIGR01652; ATPAGE_Plipid; I.
TIGRPAMS; TIGR01652; ATPAGE_P-LYPE; PROSITE; PS001164; ATPAGE_BI_E2; I.
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                                 entities requires a license agreement ( or send an email to license@isb-sib.ch)
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                                                                               EMBL; AF155913; AAF08476.1; -. EMBL; BC003246; AAH03246.1; -.
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1095 AA; 123546
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71.4%;
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Guery Coal Similarity 71.40,
Ent. Local Similarity 71.40,
Ent. Coal Similarity 71.40,
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VAB1_CAEEL
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SECURANCE OF 658-110-105 FKOM N.A.

MEDLINE=22388257; PubMed=1247-36; Couse L.H., Derge J.G.,

Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McKernan R.J., McKernan R.J., Malke J.A., Gunarate P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakealey B.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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-!- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIPICITY: Found in most tissues except spleen and muscle. Most abundant in testis. Also detected in fetal tissues.
-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IV.
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ICR; TISSUE=Brain;
MEDLINE=20473714; PubMed=11015572;
Halleck M.S., Lawler J.F. Jr., Blackshaw S., Gao L., Nagarajan P.,
Hacker C., Pyle S., Newman J.T., Nakanishi Y., Ando H., Weinstock D.,
Williamson P., Schlegel R. A.;
"Differential expression of putative transbilayer amphipath
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                              .;
0
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P98155; Q99L13;
30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Potential phospholipid-transporting ATPase IIB (EC 3.6.3.1).
                                                                                                                                Length 1095;
S -> I (in Ref. 3).
E -> D (in Ref. 3).
E -> D (in Ref. 3).
R -> K (in Ref. 3).
D -> N (in Ref. 3).
K -> N (in Ref. 3).
K -> N (in Ref. 3).
K -> N (in Ref. 3).
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Pred. No. 1.8e+03;
                                                                                                                                                              1; Mismatches
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71.4%;
                                                                                                 123635
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SEQUENCE
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AT9B MOUSE
ID AT9B MOUSE
ID AT9B MOUSE
DT 30-MAY-
DT 30-MAY-
DT 28-FEB-
DT 05-UED
GN Name-IA
OS BURARY
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noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding; Hydrolase; Magnesium; Multigene family; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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10-0CT-2003 (Rel. 42, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Ephrin receptor 1 precursor (EC 2.7.1.112) (Tyrosine-protein kinase
Eph receptor) (Variable abnormal protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By
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4-aspartylphosphate intermediate similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 1; Length 1095;
Pred. No. 1.8e+03;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW; A0176FEA5DFEA179 CRC64;
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Extracellular (Potential)
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Potential.
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SOLI LILINGA MARKA M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note=No experimental confirmation available,
TISSUE SPECIFICITY: During ventral enclosure of the epidermis,
expression is seen in clusters of presumptive head neuronal cells
and several cells in the tail region. Early larvae show expression
in the nerve ring and ventral nerve cord. Strong expression is
also seen in the procorpus and terminal bulb of the pharynx.
Expression in the nervous system is seen through to adulthood.
SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
sceptor subfamily.
SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98165343; PubMed=9506518; DOI=10.1016/S0092-8674(00)81131-9; George S.E., Slmokat K., Hardin J., Chisholm A.D.; "The VAB-1 Eph receptor tyrosine kinse functions in neural and epithelial morphogenesis in C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  closure of the epidermis.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                    The C. elegans sequencing consortium; denome sequence of the nematode C. elegans: a platform for investigating biology."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MormBase; MSG-100006868; vab-1.

MormBase; MSG-100006868; vab-1.

MormPep; M03A1.1a; CE25060.

MormPep; M03A1.1b; CE25610.

MormPep; M03A1.1b; CE26617.

MormPep; M03A1.1b; CE26617.

MormPep; Monor C. integral to membrane; ISS.

GO; GO:0000739; F:ephrin receptor activity; ISS.

GO; GO:000739; F:ephrin receptor activity; ISS.

MormPep; IPR001090; Ephrin receptor.

MormPep; IPR001090; Ephrin receptor.

MormPep; IPR001090; Ephrin receptor.

MormPep; IPR001090; MormSellike.

MormPep; IPR001099; MormSellike.

MormPep; MormPep; MormSellike.

MormPep; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=061460-2; Sequence=VSP_050207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=O61460-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                              REVISIONS, AND ALTERNATIVE SPLICING.
                                                                                                                                                                         STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF040269; AAC38970.1; -. EMBL; U49956; AAK77620.1; -. EMBL; U49956; AAK77621.1; -. PIR; T42400; T474400.
                                                                                                            Cell 92:633-643(1998)
STRAIN-Bristol N2;
                                                                                                                                                       SEQUENCE FROM N.A.
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R FIRIN; FROUDS; TYRKIASE.

R PRINTS; PRO0109; TYRKIASE.

R PRODOM; PD001495; Ephrin receptor; 1.

R PRODOM; PD001495; Ephrin receptor; 1.

R SMART; SM00615; EPH lbd; 1.

R SMART; SM0060; FN3; 2.

R SMART; SM0019; TYRKC; 1.

R SMART; SM0019; TYRKC; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00109; PROTEIN KINASE LOOM; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; FALSE NEG.

M Alternative splicing; ATP-binding; Developmental protein;

KW Alternative splicing; ATP-binding; Developmental protein;

KW Transmembrane; Tyrosine-protein kinase.

FT SIGNAL
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T-XI: In allele e699; most die as larvae.
E-XK: In allele e856; most die as larvae.
G-E: In allele e2; most die as adults.
C-XF: In allele ju22; most die as adults.
C-XY: In allele e1063; most die as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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.) (Potential).
.) (Potential).
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                                                                                                                                                                                                                                                                                                                                                              Protein kinase.
PDZ-binding motif (Potential).
ATP (By similarity).
ATP (By similarity).
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Pred. No. 1.9e+03;
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                                                                                                                                                                                                                                                Ephrin receptor 1.
Extracellular (Potential)
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                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential).
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                                                                                                                                                                                                                                                                                                                               Fibronectin type-III 1. Fibronectin type-III 2.
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01-MRA-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein Y75B7AL.4.
Name-Y75B7AL.4; ORFNames=Y75B7AL.4;
Caenorhabditis elegans.
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71.4%;
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Pfam; PF00069; Pkinase; 1
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Best Local Similarity
Matches 5; Conserv
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Matches
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                                                                                          "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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SEQUENCE 1130 AA; 123777 MW; FAC055A8A919C8E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC024869; AAK68606.2; -.
                                                                                                                                                                                                                                     "The sequence of C. elegans cosmid Y75B7AL."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                               STRAIN-Bristol N2;
Waterston R.H.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
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WormPep; Y75B7AL.4; CE32278.
                                       STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000198; RhoGAP.
InterPro; IPR008395; Rho GAP.
Pfam; PF00620; RhoGAP; 1.
SMART; SM00324; RhoGAP; 1.
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Submitted (MAY-2002)
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Submitted (NOV-2002)
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Submitted (NOV-2002)
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                                                                              WormBase Consortium
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hes 5; Conserv
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Waterston R.;
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STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.;
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                                                                                                                                                                                                                      Jamar B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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CTRAIN-CSTRIL/6; TISSUE-Brain;

Notable CSTRAIN-CSTRIL/6; TISSUE-Brain;

Rataberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Straueberg R.L., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A picthenko, L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

B stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

R Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

B Dosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sanchez A.,

Muting M., Madan A., Young A.C., Shewchanko Y., Bouffard G.G.,

Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rayminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1146;
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TIGREAMS; TIGRO1494; ATPABE P-type; 4.
PROSITE; PSO154; ATPASE BI_E2; UNKNOWN 1.
SEQUENCE 1146 AA; 129044 WW; FFO7AFD694A1B30E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CS7BL/6; TISSUB=Brain;
Director MGC Project;
Submitted (MGC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC079626; AAH79626.1; -.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 2; I
Pred. No. 1.9e+03;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1173 AA.
PRT; 1146 AA
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InterPro; IPR005834; Dahal like hydro.
InterPro; IPR005139; Plippase.
Pfam; PF00702; Hydrolase; 1.
                                                            Created)
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71.4%;
                                                         25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00119; CATATPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 71.4 es 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequences.
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| ||||
1067 LMVVAEF 1073
                                                                                                                                                                                                               Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                  Atp9b protein.
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2 MXVAEF 7

Gaps

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STRAIN=HKI-227;
PubMed=14700630, DOI=10.1016/j.chembiol.2003.11.009;
He J., Hertweck D.
He J., He J.
He J., He J.
He J., He J.
                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypochetical protein P0453G03.24,
Name=P0453G03.24;
Name=P0453G03.24;
Name=P0453G03.24;
Name=P0453G03.24;
Name=P0453G03.24;
Sharyota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0048037; F:cofactor binding; IEA.
GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
GO; GO:0016748; F:transferase activity; IEA.
GO; GO:000563; P:tosynthesis; IEA.
GO; GO:006633; P:fatty acid biosynthesis; IEA.
InterPro; IPR009081; ACP like.
InterPro; IPR001277; AC_transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=66431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.8%; Score 24; DB 2; Length 2033; 57.1%; Pred. No. 3.3e+03; ive 2; Mismatches 1; Indels
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gramene; Q7X195; -.
InterPro; IPR000413; Integrin alpha.
PROSITE; PS00242; INTEGRIN_ALPHA; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 2033 AA; 221848 MW; 247BFD68BD43562C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clode:P0453G03.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004276; BAC79823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Polyketide synthase type I.
   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2201 AA.
                                                                                                                                                                                                                                                                                                                       PRT; 2033 AA
   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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   5; Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: ||||
1843 ILAVAEF 1849
                                                                                                                                           1173 VLDVÁĚF 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VMXVAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=39947;
                                                                         1 VMXVAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=aurC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                    07XI95
                                                                                                                                                                                                                                                                                                                                                        Q7XI95;
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       Matches
                                                                                                                                                                                                                                                     RESULT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       070KH
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W MEDLINE=22977040; PubMed=14621292;

W MEDLINE=22977040; PubMed=14621292;

W NAKAWILA Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,

A Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,

K A Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,

K A Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,

A Takeuchi C., Yamada M., Tabata S.,

T "Complete genome structure of Gloeobacter violaceus PCC 7421, a

T "Complete genome structure of Gloeobacter violaceus PCC 7421, a

T "Complete genome structure of Gloeobacter violaceus PCC 7421, a

T "Complete genome structure of Gloeobacter violaceus PCC 7421, a

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   Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                       MEDLINE-22531580; PubMed=12644555; DOI=10.1093/molbev/msg031; Kojima K.K., Fujiwara H.; "Evolution of target specificity in R1 clade non-LTR
                                                                                                                                                                                                                                                                                                         EMBL; AB090822; ENA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003764; F:RNA directed DNA polymerase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR005135; Exc endo_phos.
InterPro; IPR005135; Exc endo_phos.
InterPro; IPR000477; RVTse.
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Pred. No. 2.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.8%; Score 24; DB 2; Length 1173; 83.3%; Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF031372; Exo endo phos; 1.
Pfam; PF00178; RVT 1; 2.
PROSITE; PS00904; PPTA; UNKNOWN 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1173 AA; 132166 MW; AF60298E9A9D67B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1566 AA; 172226 MW; 907814D1219662A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gloeobacter violaceus.
Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
NCBI_TaxID=33072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1566 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS; TIGRO1443; intein Cterm; 2.
TIGREAMS; TIGRO1445; intein Nterm; 1.
PROSITE; PS50818; INTEIN C TER; 2.
PROSITE; PS50819; INTEIN ENDONUCLEASE; 2.
PROSITE; PS50817; INTEIN NTER; 2.
                                                                                                                                                                                                                                                                                   Evol. 20:351-361(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                   SEQUENCE FROM N.A.
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MTVAEF 99
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                                        NCBI_TaxID=7165;
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Q7NEB4
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G62 protein (E7 protein) (Fragment)
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57.1%;
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                                                                                                                                                  Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMKIADF 17
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
SUBL; AJ002918; CAA05753.1; -.
GO; GO:000524; F.ATP binding; IEA.
GO; GO:00016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IRR000119; Prot kinase.
Prodom; PD000001; Prot kinase.
Fromom; PD000001; Prot kinase.
Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.8%; Score 24; DB 2; Length 2201; 71.4%; Pred. No. 3.6e+03;
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Pred. No. 2e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Protein tyrosine kinase (EC 2.7.1.112) (Fragment).
Name=DmHD-311;
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Last sequence update)
Last annotation update)
                                                                                   InterPro; IPR006162; Public S. InterPro; IPR001031; Thioseterase. Pfam. PF00698; Acyl_transf.1; 2. Pfam; PF00309; Ketoacyl-synt; 2. Pfam; PF00301; Ketoacyl-synt; 2. Pfam; PF00305; Ptoliding; 2. PROSITE; PS0075; Thioseterase; 1. PROSITE; PS0075; ACP DOMAIN; 2. PROSITE; PS00105; ACP DOMAIN; 2. PROSITE; PS00105; ACP DOMAIN; 2. PROSITE; PS00112; PHOSPHÖPANTETHBINE; 1.
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                             InterPro; IPR008262; Lipase AS.
InterPro; IPR006163; Phsppanteth bind.
   InterPro; IPR000794; Ketoacyl_synth.
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SEQUENCE 2201 AA; 233522 MW;
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nes 5; Conservative
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VMKIADF 14
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Brandil A.W., Kirechner M.W.;

"Molecular cloning of tyrosine kinases in the early Xenopus embryo:
identification of Eck-related genes expressed in cranial neural crest
cells of the second (hyoid) arch.";

Dev. Dyn. 203:119-140(1995).

EMBL; U1723; AAA31286.1;

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004672; F:Protein Kinase activity; IEA.

GO; GO:0004672; F:protein amino acid phosphorylation; IEA.

InterPro; IPRO1009; Kinase_like.

InterPro; IPRO1009; Frot Kinase.

InterPro; PRO0001; Prot_Kinase.

ProDom; PD00001; Prot_Kinase.
                                                                                                                                                                                                                                                                                                                     Brandli A.W., Kirschner M.W.;
"Molecular cloning of tyrosine kinases in the early Xenopus embryo:
identification of Eck-related genes expressed in cranial neural crest
cells of the second (hyoid) arch.";
Dev. Dyn. 203:119-140(1995).
EMBL; Ul1730; AAA91293.1;
HSSP; P11362; 2FGI.
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Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
Probom; PD000011; Prot kinase; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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Pred. No. 2.1e+02;
2; Mismatches 1; Indels
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Pred. No. 2.1e+02;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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MEDLINE=95383727; PubMed=7655077;
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MEDLINE=95383727; PubMed=7655077;
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SEQUENCE
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Q9P166
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MEDLINE-30306484; PubMed=1281307;

A chestier A., wilkinson D.G., Charnay P.;

Thatdi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.G.,

Giladdi-Hebenstreit P., Sieto M.A., Frain M., Mattei M.G.,

That Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain.";

Oncogene 7.2499-2506(1992).

R GO: GO:0006524; F:ATP binding; IEA.

GO: GO:0006472; F:protein kinase activity; IEA.

R GO: GO:0006468; P:protein mino acid phosphorylation; IEA.

InterPro; IPR01009; Kinase like.

InterPro; IPR01009; Kinase like.

InterPro; IPR00019; Prot kinase.

R Probom; PD000001; Prot kinase; 1.

R PROBOM: PROFEIN KINASE DOM; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-NOV-1996 (TrEMBLrel. 101, Last sequence update)
01-NOT-1996 (TrEMBLrel. 25, Last annotation update)
Coturnix coturnix fibroblast growth factor receptor, clone H7
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GO; GO:0004672; F:protein kinase activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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Oncogene 7:2479-2487(1992).
EMBL; X69693; CAA49363.1; -.
HSSP; P11362; 2FGI.
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11 VMKIADF 17
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Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 2.3e+02;
2; Mismatches 1; Indels
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Pred. No. 2.2e+02;
2; Mismatches 1; Indels
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EMBL; AF119881; AAF69635.1; -.
SEQUENCE 61 AA; 7467 MW; 6433950D4657C1D4 CRC64;
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57 57
57 AA; 6523 MW; 8DAA6A71E3F1B45E CRC64;
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01-071-2000 (TrEMBLrel. 15, Last sequence update)
01-071-2000 (TrEMBLrel. 15, Last annotation update)
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InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Proc Kinase.
Probon; PD000001; Prot Kinase; 1.
PROSITE; PS50011; PROTĒIN_KINASE_DOM; 1.
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12 VMKIADF 18
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27 ILKVAEF 33
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Copyright (c) 1993 - 2005 Compugen Ltd.
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This invention, in the area of plant biotechnology, relates to novel polynucleotides comprising a nuclectide sequence encoding a protein which is involved in or associated with the synthesis, metabolism or described in or associated with the synthesis, metabolism or carbobydrates in the plant grain and the expression of which is up-regulated during grain filling. The plant is selected from corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content of the cereal grains. In addition, carbohydrate levels may be modified to a more desirable level using the present invention. The present sequence is the sequence of a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed appecification, but was obtained in electronic format directly from WIPO at tp. wipo.int/pub/publishedpct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New plant genes encoding polypeptides having an activity involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain useful in generating plants having improved nutritional properties.
tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet; wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain; gene; ds; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; SEQ ID NO 238; 130pp; English:
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26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
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Moughamer T; Ricke D;

Cooper B, Goff SA, Kreps J, Provart N,

human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; tranquiliser. Human protein useful for treating neurological disease Seq 3967. ö Score 19; DB 7; Length 146; Pred. No. 9.1e+02; 0; Mismatches 3; Indels Ā ADR10461 standard; protein; 243 86.4%; 57.1%; 04-NOV-2004 (first entry) 4; Conservative Query Match Best Local Similarity Matches 4; Conserv 1 VXXXAEF VAATAEF ADR10461; RESULT 2 ADR10461 \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$

plant biotechnology, carbohydrate synthesis; carbohydrate metabolism; carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;

Rice protein sequence Seq ID238 related to grain filling.

(first entry)

18-DEC-2003 ADC07972;

ADC07972 standard; protein; 146 AA.

RESULT 1 4DC07972

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Gaps

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Candida tropicalis transformation system - using host auxotrophic in an amino acid, purine or pyrimidine pathway as result of mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                      The gene product (and opt. the URA3 B gene product - AAR06640) is used to complement an auxotrophic host to prototrophy. The host may be defective in orotidine-5'-phosphate decarboxylase activity. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytochrome P450 nicotine adenine dinucleotide phosphate oxidoreductase and cytochrome P450 monooxygenase nucleic acids and encoded proteins, useful for overproducing dicarboxylic acids.
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loper JC, Gleeson M;
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57.1%;
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89US-00386837
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Best Local Similarity 57.1.
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Tang M,
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10-MAR-1999;
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23-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to CDNA clones obtained by an oligo-capping method, where none of these clones are identical to any known human mNNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as artibodises, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the ODNA molecules. As such, these can enseful for diagnostic markers or therapeutic targets for molecules are useful for diagnostic markers or therapeutic targets for molecules are useful for diagnostic markers or therapeutic targets for the various disease or morbid states. In particular, they are useful in gene therapy for treating ostcoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintening equilibrium of sense or motor function, and for traating emotional reaction, fear response and panic. Accordingly, they exhibit ostcopathic, neuroprotective, noctropic, antiparkinsonian, cytostatic and tranquiliser activities. This polypeptide is a protein cencoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but and the contained on CD-ROM from the European Patent Office, Vienna Sub-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                      New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                                                                                                                                                                                        Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
Nagai K, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uracil biosynthetic pathway; orotidine-5'-phosphate decarboxylase;
URA3 A gene; auxotrophe; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Orotidine-5'-phosphate decarboxylase encoded by the URA3 A gene.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 8; 1
Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3967; 2686pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR06639 standard; protein; 267 AA.
                                                                                                                                                                                                                                 (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                       14-FEB-2003; 2003JP-00102207. 09-MAY-2003; 2003JP-00131452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.4%;
                                                                                                                                   12-FEB-2004; 2004EP-00003145
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Best Local Similarity 57.1
A; Conservative
                                                                                                                                                                                                                                                                        Isogai T, Yamamoto J,
Wakamatsu A, Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 VATAÄEF 207
                                                                                                                                                                                                                                                                                                                                 WPI; 2004-583265/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADRI0422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 243 AA;
                                                                                                                                                                   14-FEB-2003;
                  Homo sapiens
                                                       EP1447413-A2
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                                                                                                                                                                                                                                                                      Isogai T,
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Gaps

.; 0

3; Indels

Length 267;

Cornett CA;

Example 15; Fig 23; 200pp; English

WO9009449-A

AAR06639;

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The invention relates to 12 novel genomic DNA sequences and proteins which are components of the omega hydroxylase complex of Candida tropicalis ATCC 20366. The DNA sequences (AAA3066-A30577) respectively encode cytochrome P450 NADPH oxidoreductases CPRA and CPRB (AAY90596, AAY90597) and cytochrome P450 monoxygenases CPRSAAA, CYPSAABA, CABABB, CAGABB, CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 267 AA;
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23-APR-2002
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98US-0083798P

01-MAY-1998;

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The present invention relates to the isolation of Candida tropicalis 20336 novel genes (CPRA, CPR2, CYP52ABA, CYP5ABB, CYP5ABBA, CYP5ABB, CYBCABA, CY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding cytochrome P450 and NADPH reductase enzymes of omega-hydroxylase complex of Candida tropicalis, useful for increasing production of dicarboxylic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene; enzyme; yeast; omega oxygenase complex; cytochrome P450 monooxygenase; CYP; NADPH reductase enzymes; CPR; CPRA; CYPS2A1A; CYPS2A2A; CYPS2A3A; CYPS2A3B; CYPS2A3B; CYPS2A5B; CYPS2A5B; CYPS2A5B; CYPS2A5B; CYPS2A5B; CYPS2A5B; CYPS2A5B; CYPS2A5B; CYPS2A5B; CAPSCA5B; CAPSCA5B; dicatboxylic acid; dister; polymer; thermoplastic; plasticising agent; lubricant; hydraulic fluid; agricultural chemical; pharmaceutical; dye; surfactant; adhesive; URA3.
                                                                                                                                                                                                                                                                                                                                            Madduri KM, Cornett CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 5; Length 267; Pred. No. 1.8e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                            Eirich LD, Eshoo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC44987 standard; protein; 267 AA.
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                                                                                                                                                                                                                                                                                                                                                                        Loper JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.4%;
57.1%;
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98US-0103099P.
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                            Craft DL,
Tang M,
                                                                                         CRAFT D L.
EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast URA3A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-138383/18
                                                                  WILSON C R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 267 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABK31897
  05-OCT-1998;
                         10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                     Brenner AA,
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                                                                       (WILS/)
(CRAF/)
                                                                                                                                                                                                                                                                    (LOPE/)
(GLEE/)
                                                                                                                                                                                               (CORN/)
(BREN/)
                                                                                                                                                                                                                                                TANG/)
                                                                                                                                                                        MADD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
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The invention relates to an isolated nucleic acid selected encoding Candida tropicalis omega oxygenase complex enzymes (CPR) designanced PPSO monooxygenase (CYP) and NADPH reductase enzymes (CPR) designated CPRA, CPP52A1A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A3B, CYP52A3B, CYP52A3B, CYP52A3B, CYP52A3B, CYP52A3B, CYP52AB, CYP52ABB or CYP52D4A) or their coding regions. Also included are the CPR/CYP proteins, a vector comprising the nucleic acid cited above, a host cell transfected or transformed with the above nucleic acid, producing the proteins, discriminating members of a gene candidate and production of the production of a dicarboxylic acid and increasing the production of the proteins cited above. The host cell is C. tropicalis is specifically that may be utilised as industrial intermediates in the manufacture of diesters and polymers (e.g. as thermoplastics, plasticishing agents, lubricants, hydraulic fluids, agricultural chemicals, pharmaceuticals, carrying a CYP or CPR gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene; enzyme; yeast; omega oxygenase complex; cytochrome P450 monooxygenase; CYP; NADPH reductase enzymes; CPR; CPRA;
                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding cytochrome P450 and NADPH reductase enzymes (e.g. CPRA, CPRB or CYP52A1A), useful for producing dicarboxylic acids that may be utilized as industrial intermediates in manufacturing
                                                                                                                                                                                                                                                               Madduri KM, Cornett CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.4%; Score 19; DB 7; Length 267
57.1%; Pred. No. 1.8e+03;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                              Eirich LD, Eshoo M,
Loper JC, Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                            Example 15; SEQ ID NO 106; 196pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC45557 standard; protein; 267 AA
            98US-0083798P.
98US-0103099P.
99US-0123555P.
99US-00302620.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 57.1 tes 4; Conservative
                                                                                                                                                                                                                                                              Craft DL,
Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                 diesters and polymers.
                                                                                                                CRAFT D L.
EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast URA3A protein.
                                                                                                                                                                                                                                                                                                        WPI; 2003-777150/73
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                                                                                                    WILSON C R.
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                                                                                                                                                                                                     TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                        N-PSDB; ADC44986.
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                            05-OCT-1998;
10-MAR-1999;
                                                                       12-OCT-2001;
                                                                                                                                                                                                                                                                               Brenner AA,
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                                                           30-APR-1999
                                                                                                                                                                                                                                                               Wilson CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                      (BREN/)
(TANG/)
(LOPE/)
(GLEE/)
                                                                                                                                                           (MADD/)
(CORN/)
                                                                                                    (MILS/)
                                                                                                                   (CRAF/)
                                                                                                                                 (EIRI/)
                                                                                                                                               (ESHO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
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The invention relates to an isolated nucleic acid selected encoding Candida tropicalis omega oxygenase complex enzymes (cytochrome P450 monooxygenase (CYP) and NADPH reductase anzymes (Cytochrome P450 condocated (CYP) and NADPH reductase (CPR) designated CPRA, CYP52A1A, CYP52A2A, CYP52A3B, CYP52A3B, CYP52A5A, CYP52A5B, CYP5A5B, CYP5A5B, CYP5A5BB, CYP5A5B
CPRB; CYP52AlA; CYP52A2A; CYP52A2B; CYP52A3A; CYP52A3B; CYP52A5A; CYP52ABA; CYP52ABA; CYP52ABA; CYP52ABA; Granton Card, diseter; CYP5ABA; CYP5ABB; CYP52ABA; Granton Card, diseter; Polymer; thermoplastic; plasticising agent; lubricant; hydraulic fluid; agricultural chemical; pharmaceutical; dye; surfactent; adhesive; URA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding cytochrome P450 and NADPH reductase enzymes (e.g. CPRA, CPRB or CYP52A1A), useful for producing dicarboxylic acids that may be utilized as industrial intermediates in manufacturing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Loper JC, Gleeson M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loper JC,
                                                                                                                                                                                                                                                                                        98US-0083798P.
98US-0103099P.
99US-0123555P.
99US-00302620.
                                                                                                                                                                                                                                                 03-MAY-2002; 2002US-00139031.
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57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           EIRICH L D.
ESHICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang M,
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                                                                                                                                                                                                                                                                                                                                                                                                                             WILSON C R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                 Candida tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTTTAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADC45556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 267 AA;
                                                                                                                                                           US2003049822-A1.
                                                                                                                                                                                                                                                                                             01-MAY-1998;
                                                                                                                                                                                                                                                                                                                  05-OCT-1998;
10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                              30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brenner AA,
                                                                                                                                                                                                       13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39
                                                                                                                                                                                                                                                                                                                                                                                                                             (WILS/)
(CRAF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TANG/)
(LOPE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORN/)
(BREN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLEE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MADD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIRI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESHO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson
    용
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1 VXXXAEF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \hat{Z}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated nucleic acids encoding cytochrome P450 (CYP) and NADPH reductase (CPR) enzymes of the omega-hydroxylase complex of candida tropicalis. Also included are the CYP and CRP procesins (comprising CPRA, CPRE, CYP52AAA, CYP52AAB, CYP5AAB, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cytochrome P450 and NADPH oxidoreductase, i.e. CPR and CYP, genes and proteins, useful for discriminating members of a gene family by quantifying the amount of target mRNA in a sample, or for omega-oxidation of long chain fatty acids.
                                                                                                                                                                                                                         Yeast, enzyme; cytochrome P450; CYP; NADPH reductase; CPR; omega-hydroxylase complex; omega-oxidation; long chain fatty acid; URA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Madduri KM,
                                                                                                                                                                               Integration vector pURA2in URA3A gene encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Eshoo M,
Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 15; SEQ ID NO 106; 194pp; English
                                            ADES2068 standard; protein; 267 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eirich LD,
Loper JC, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-1998; 98US-0103099P.
10-MAR-1999; 99US-012355P.
30-APR-1999; 99US-00302620.
12-OCT-2001; 2001US-00976800.
                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAY-2002; 2002US-00138916
                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson CR, Craft DL,
Brenner AA, Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRAFT D L.
EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-625522/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WILSON C R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                            Candida tropicalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYP or CPR genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 267 AA;
                                                                                                                                                                                                                                                                                                                                         US2003073220-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADE52067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1998;
                                                                                                                                  29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                   17-APR-2003
                                                                                        ADE52068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EIRI/)
(ESHO/)
(MADD/)
(CORN/)
(BREN/)
(TANG/)
(LOPE/)
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(CRAF/)
RESULT 8
                         ADE52068
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                                                                                                                                                                                                                                                                                                                                                                       CYP52A2B; cytochrome P450; NADH reductase; dicarboxylic acid production; organic substrate oxidation; fatty acid oxidation; gene integration vector; CYP; CPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acids encoding a CYP52A2B protein useful for increasing the production of dicarboxylic acid for oxidizing organic substrates such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated nucleic acid encoding a CYP52A2B protein comprising the fully defined sequence of 522 amino acids, as given in the specification, and comprising a coding region defined by nucleotides 1072-2640 of a fully defined sequence of 3755 base pairs, given in the specification. The nucleic acids encoding the cytochrome P450 and NADH reductase enzymes of Candida tropicalis are useful for increasing the production of dicarboxylic acid for oxidising organic substrates such as fatty acids. This sequence represents a Candida tropicalis associated polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madduri KM,
                                                                                                                                                                                                                                                                                                                      Candida tropicalis associated polypeptide seg id 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eirich LD, Eshoo M, opper JC, Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 106; 188pp; English
                                                                                                                                               ADF72375 standard; protein; 267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Loper JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001; 2001US-00976800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0123555P
                                                                                                                                                                                                                                                                  12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craft DL,
Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WILSON C R.
CRAFT D L.
EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-810780/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida tropicalis
39 VTTTAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS2003077795-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brenner AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fatty acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39
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(TANG/)
(LOPE/)
(GLEE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MADD/)
(CORN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WILS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIRI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESHO/)
                                                                                                                A DE TOUR DE LE COURT DE LE CO
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0; Gaps

Score 19; DB 7; Length 267; Pred. No. 1.8e+03; 0; Mismatches 3; Indels

86.4%;

Query Match
Best Local Similarity 57.1
Matches 4; Conservative

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ADF11815;

RESULT 10

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The invention relates to a new isolated nucleic acid which encodes a CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A3B, CYP52A3B, CYP52ABA, CYP52ABB, CYP52ABB, CYP52ABB, CYP52ABB, CYP52ABB or CYP52D4A protein. The nucleic acid is useful for discriminating between members of a gene family by quantifying the amount of mRNA in a sample. The present sequence represents the amino acid sequence of a Candida tropicalis protein.
                                                                      CPRA; CPRB; CYP52A1A; CYP52A2A; CYP52A2B; CYP52A3A; CYP52A3B; CYP52A5A;
CYP52A5B; CYP52A8A; CYP52A8B; CYP52D4A; gene family; URA3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A, CYP52A5B, CYP52A6B or CYP52D4A gene, useful for discriminating members of a gene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 7; Length 20, Pred. No. 1.88+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madduri KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΣΞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 106; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Eshoo P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä.
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Loper JC, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE64232 standard; protein; 267
                                                                                                                                                                                                                                       01-MAY-1998, 98US-0083798P.
05-OCT-1998, 98US-0103099P.
10-MAK-1999, 99US-0123555P.
310-APR-1999; 99US-00305620.
12-OCT-2001; 2001US-00976800.
                                                                                                                                                                                                               03-MAY-2002; 2002US-00139296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity 57.1%;
4; Conservative
            12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craft DL,
Tang M,
                                                                                                                                                                                                                                                                                                                                                                                              MADDURI K M.
CORNETT C A.
BRENNER A A.
                                                                                                                                                                                                                                                                                                                                                 CRAFT D L.
EIRICH L D.
ESHOO M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-897579/82
                                       C. tropicalis URA3A
                                                                                                                                                                                                                                                                                                                                      WILSON C R.
                                                                                                                      Candida tropicalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 VTTTAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADF11696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 267 AA;
                                                                                                                                                   US2003148486-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                               TANG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brenner AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2004
                                                                                                                                                                                 07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE64232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                    (WILS/)
(CRAF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (TANG/)
(LOPE/)
(GLEE/)
                                                                                                                                                                                                                                                                                                                                                                                               (MADD/)
(CORN/)
(BREN/)
                                                                                                                                                                                                                                                                                                                                                                                   ESHO/)
                                                                                                                                                                                                                                                                                                                                                                    EIRI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a new isolated nucleic acid which encodes a CPRA, CPRB, CPBSAA, CYPS2ASA, CYPS2ASB, CYPS2ASB, CYPS2ASB, CYPS2ASB, CYPS2ASB, CYPS2ASB, CYPS2ASB, CYPS2ASB, CYPS2ASB or CYPS2DAB protein. The nucleic acid is useful for discriminating between members of a gene family by quantifying the amount of mRNA in a sample. The present sequence represents the amino acid sequence of a Candida tropicalis protein.
                                                                                                                                                 CPRA; CPRB; CYP52A1A; CYP52A2A; CYP52A2B; CYP52A3A; CYP52A3B; CYP52A5A; CYP52A5B; CYP52A5B; CYP52A5B; CYP52D4A; gene family; URA3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.4%; Score 19; DB 7; Length 267; 57.1%; Pred. No. 1.8e+03; cive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Madduri KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eirich LD, Eshoo M,
Loper JC, Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 106; 194pp; English.
                           ADF11815 standard; protein; 267 AA.
                                                                                                                                                                                                                                                                                                                   01-MAY-1998; 98US-0083798P.
05-0CT-1998; 98US-0103099P.
10-MAR-1999; 99US-00305620.
12-0CT-2001; 2001US-00976800.
                                                                                                                                                                                                                                                                                         03-MAY-2002; 2002US-00139218.
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craft DL,
Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                                           CRAFT D L.
EIRICH L. D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-897719/82
                                                                                                                      C. tropicalis URA3A
                                                                                                                                                                                                                                                                                                                                                                                                              WILSON C R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VITTAEF 45
                                                                                                                                                                                               Candida tropicalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADF11814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 267 AA;
                                                                                                                                                                                                                            US2003153060-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brenner AA,
                                                                                                                                                                                                                                                           14-AUG-2003
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(CORN/)
(BREN/)
(TANG/)
(LOPE/)

(CRAF/) (EIRI/) (ESHO/) (MADD/) (MILS/)

Cornett CA;

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Gapa

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Integration vector pURA2in URA3A gene encoded protein.

ADF11697 standard; protein; 267 AA.

RESULT 11
ADF11697
ID ADF1
XX
AC ADF1

ADF11697

33

Query Match

Best Loc Matches

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The present sequence is that of the polypeptide encoded by the URA3A selectable marker gene of Candida tropicalis. A claimed C. tropicalis cell has a disrupted chromosomal POX4 and/or POX5 gene in which a portion of the gene(s) is deleted through homologous recombination with a selectable marker gene, especially URA3. This blocks the beta-oxidation pathway of the cell. The size of the delection of the chromosomal gene prevents the strain from reverting to wild-type activity. The cell is used in a claimed process for producing alpha,omega-dicarboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New non-revertible beta-oxidation blocked Candida tropicalis cell having a disrupted chromosomal POX4 and/or POX5 gene(s), useful for producing dicarboxylic acids used in the preparation of perfumes or macrolid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYP; CPRA protein; CPRB protein; dicarboxylic acid; plastic; adhesive;
fragrance; URA3A.
                                                                                                URA3; selectable marker; enzyme; beta-oxidation; dicarboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 86.4%; Score 19; DB 8; Length 267; Local Similarity 57.1%; Pred. No. 1.8e+03; nes 4; Conservative 0; Mismatches 3; Indels
                                                        Candida tropicalis URA3 gene-encoded polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 10; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ26614 standard; protein; 267 AA.
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                                                                                                                                                                                                                                                                                          23-MAY-2002; 2002US-0383332P.
22-MAY-2003; 2003US-0044467.
                                                                                                                                                                                                                                                      22-MAY-2003; 2003WO-US016453
                      11-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                   (COGN-) COGNIS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ^
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                                                                                                                                    Candida tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VXXXAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADG73845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 267 AA;
                                                                                                                                                                        WO2003100013-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003186411-A1
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                                                                                                                                                                                                                04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ26614;
                                                                                                                                                                                                                                                                                                                                                                                           Craft DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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ADJ26614
    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A2B, CYP52A2B, CYP52A2B, CYP52A2B, CYP52A2B, CYP52A2B, CYP52A2B, CYP52A2B, CYP52A4 protein (CYP - cytochrome P450, CPR - NADPH reductase) of the Candida tropicalis omega-hydroxylase complex. Also included are the nucleoic aids encoding the CYP/CPR proteins (including their coding regions), a vector comprising the nucleotide acid, a host cell transfected or transformed with the vector, discriminating members of a gene family by quantifying the amount of target mRNA in a sample and increasing production of a dicarboxylic acid (comprising the host cell having a naturally occurring CPR/CYP protein and culturing the host cell having a naturally occurring of dicarboxylic acid. The CYP and CPR proteins present in higher levels than normal is useful for increasing production of dicarboxylic acids. The present sequence represents a C. tropicalis URA3 protein, used to make the CYP/CPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5B, CYP52A6B or CYP52D4A protein, useful for increasing production of dicarboxylic acid in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Madduri KM, Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19; DB 8; Length 267;
Pred. No. 1.8e+03;
0; Mismatches 3; Indels
Yeast; enzyme; NADPH reductase; CPR; cytochrome P450; CYP; omega-hydroxylase; dicarboxylic acid; URA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eirich LD, Eshoo M, oper JC, Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 15; SEQ ID NO 106; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loper JC,
                                                                                                                                                                                                          01-MAY-1998, 98US-0083798P.
05-0CT-1998, 98US-0103099P.
10-MAR-1999, 99US-0123555P.
30-APR-1999; 99US-0030520.
12-0CT-2001, 2001US-00976800.
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57.1%;
                                                                                                                                                                        03-MAY-2002; 2002US-00138905
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EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
TANG M.
LOPER J C.
GLEESON M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson CR, Craft DL,
Brenner AA, Tang M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-020205/02
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                                                                                                                                                                                                                                                                                                                               WILSON C R.
                                                          Candida tropicalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADE64231
                                                                                            US2003068800-A1
                                                                                                                                  10-APR-2003
                                                                                                                                                                                                                                                                                                                             (WILS/)
(CRAF/)
(EIRI/)
(ESHO/)
(MADD/)
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(BREN/)
(TANG/)
(LOPE/)
(GLEE/)
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Gaps

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03-APR-2003; 2003US-00405660.

ADG73846 standard; protein; 267 AA.

RESULT 13 ADG73846 ID ADG7 XX AC ADG7

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ADG73846

PRESENTATION OF STREET OF

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The invention relates to antisense inhibitors of genes essential to prokaryotic callular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
                                                                                   Candida tropicalis transformation system - using host auxotrophic in an amino acid, purine or pyrimidine pathway as result of mutagenesis.
                                                                                                                                                                 The gene product (and opt. the URA3 A gene product - AAR06639) is used to complement an auxotrophic host to prototrophy. The host may be defective in orotidine-5'-phosphate decarboxylase activity. See also
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic cellular proliferation protein; antibiotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                  86.4%; Score 19; DB 2; Length 268;
57.1%; Pred. No. 1.8e+03;
ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coli cellular proliferation protein #230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; SEQ ID NO 10242; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW,
     ŝ
      Picataggio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU34649 standard; protein; 298 AA.
                                                                                                                                    Disclosure; Fig 4; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-2000; 2000US-0206848P.
26-WAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-02578P.
27-WOV-2000; 2000US-0253655P.
22-DEC-2000; 2000US-0257931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001WO-US009180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-FEB-2001; 2001US-0269308P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
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     Gleeson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-611495/70.
N-PSDB; AAS52508.
                                     WPI; 1990-275138/36.
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                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                   1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                 39 VTTTÄEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                    N-PSDB; AAQ05865
                                                                                                                                                                                                                                                     Sequence 268 AA;
                                                                                                                                                                                                                     AAQ05864-Q05866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2000;
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001
     Cregg JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU34649;
                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises CYP genes from Candida tropicalis which encode CPRA and CPRB proteins. The invention is useful for CPRA and CPRB protein production, the DNA and protein sequences are useful for increasing production of dicarboxylic acid in chemical products, such as: plastics, adhesives and fragrances. The present amino acid sequence represents a Candida tropicalis URA3A protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid encoding a CPRA protein, used to increase production of dicarboxylic acid, for use in chemical products including plastics, adhesives, and fragrances.
                                                                                                                                                                                                                                                                                    Cornett CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uracil biosynthetic pathway; orotidine-5'-phosphate decarboxylase;
URA3 B gene; auxotrophe; mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Orotidine-5'-phosphate decarboxylase encoded by the URA3 B gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.4%; Score 19; DB 8; Length 267; 57.1%; Pred. No. 1.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                  , Eshoo M,
Gleeson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 106; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR06640 standard; protein; 268 AA.
                                                                                                                                                                                                                                                                                  Eirich LD,
                                                                                                                                                                                                                                                                                                     Loper JC,
01-MAY-1998; 98US-0083798P.
05-OCT-1998; 98US-0103099P.
10-MAR-1999; 99US-012555FP.
30-APR-1999; 99US-0030620.
12-OCT-2001; 2001US-00976800.
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les 4; Conservative
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                                                                                                                                                                                                                                                                                  Craft DL,
Tang M,
                                                                                                                               EIRICH L D.
ESHOO M.
MADDURI K M.
CORNETT C A.
BRENNER A A.
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                                                                                                                                                                                                              TANG M.
LOPER J C.
GLEESON M.
                                                                                                    WILSON C R.
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                                                                                                                   CRAFT D L.
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                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADJ26613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-1989;
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27-JUL-1989;
                                                                                                                                                                                                                                                                                                   Brenner AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9009449-A.
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                                                                                                                                                                                                                                                                                  Wilson CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39
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                                                                                                                                                                               (CORN/)
(BREN/)
(TANG/)
(LOPE/)
                                                                                                                  (CRAF/)
(EIRI/)
(ESHO/)
(MADD/)
                                                                                                  (MILS/)
                                                                                                                                                                                                                                                  (GLEE/)
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Matches
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            useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a rokavoric of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell contraining the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding
Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                Score 19; DB 4; Length 298; Pred. No. 2e+03; 0; Mismatches 3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #14234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID NO 56631; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU28707 standard; protein; 298 AA.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362899P.
                                                                                                                                                                                                                                                                                86.4%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-00815242
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                          172 VSTTAEF 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                 Sequence 298 AA;
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Wall
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the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational card drug discovery programs, or for screening homologous nucleic acids credured for proliferation in cells other than S. aureus, S. typhimurium, CC the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained for the interction of the printed specification, but was obtained for the printed specification, but was obtained for the printed format farectly from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19; DB 6; Length 298; Pred. No. 2e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 48228; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #17860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG17869 standard; protein; 305 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-00540217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS82056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed activity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic mino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at (II) and (II) acquences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein, nutritional source, cell proliferation activity, cell differentiation activity, immune stimulant; tissue growth activator, haematopoiesis regulator; anti-inflammatory, tumour invasion suppressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.4%; Score 19; DB 4; Length 305; 57.1%; Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lavallie ER, Racie LA, Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by ARG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW69244 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumour inhibitor; clone CK201 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone CK201_1 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US023224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spaulding V, Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 57.1
nes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 VSTTAEF 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-362424/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 305 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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11-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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New isolated polynucleotides - obtained from human adult testis, human adult ovary, human adult brain and human adult heart cDNA libraries.

N-PSDB; AAV44863

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                                                             invention. The DNA was isolated from a human adult testis cDNA library, and is designated clone CK2011. The DNA sequences and encoded polypeptides can be used as nutritional sources or supplements, or may exhibit e.g. cytokine and cell proliferation/differantiation activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, receptor/ligand activity, anti-inflammatory activity, cativity, chemostatic/chemokinetic activity, cathorises activity, tuned activity, tissue growth activity, tumour inhibition activity or other activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; nutrient; cytokine modulator; proliferation;
differentiation; immune system modulator; tissue growth; chemotactic;
haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids encoding polypeptides, useful for modulating ecytokine and cell proliferation/differentiation activity, the immune system and hematopoiesis regulating activity.
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0
                                                polynucleotide
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Spaulding V, Agostino MJ;
                                                                                                                                                                                                                                                                                 Score 19; DB 2; Length 309;
Pred. No. 2.1e+03;
0; Mismatches 3; Indels
                                              sequence is secreted protein, encoded by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CK201_1 protein sequence SEQ ID 145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 473-474; 557pp, English.
              Claim 27; Page 74-75; 108pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вомшал МК,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB90724 standard; protein; 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-2000; 2000WO-US025135.
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                                                                                                                                                                                                                                                                                   86.4%;
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                                                                                                                                                                                                                                                                                                                       4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            275 VSAAAEF 281
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                        1 VXXXAEF 7
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                                                                                                                                                                                                                                                 Sequence 309 AA;
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gene on which the test compound that inhibits
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are: (1) a vector comprising a promocer operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense ancoding a polypeptide whose expression is inhibited by the antisense polypeptide acid; (2) a host cell containing the vector; (3) an isolated antisense antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies
chemotactic/chemokinetic activity; haemostatic and thrombolytic activity; receptor/ligand activity; anti-inflammatory activity; haematopoiesis activity; cadherin/tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAF98672 which are specific for the CDNA clones encoding the secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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                                                                                                               Length 309;
                                                                                                                                        3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen |
Forsyth |
                                                                                                                                                                                                                                                                                                                             Protein encoded by Prokaryotic essential gene #30241.
                                                                                                              Score 19; DB 4; I
Pred. No. 2.1e+03;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 72638; 1766pp; English.
                                                                                                                                                                                                                                                    ABU44714 standard; protein; 338 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-03628591.
06-MAR-2002; 2002US-0362699P.
                                                                                                               86.4%;
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                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                               Salmonella paratyphi
                                                                                                Query Match
Best Local Similarity
4; Conserve
                                                                                                                                                                                        275 VSAAAÈF 281
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N-PSDB; ACA48584.
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                                                                                                                                                                 1 VXXXAEF
                                                                                       Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       WO200277183-A2
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                                                                                                                                                                                                                                                                              ABU44714;
                                                                 proteins
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Wall D,
                                                                                                                                                                                                                             RESULT 21
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organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed, (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational for displaying proteins or screening for homologous nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence date for this part of form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the
complementary strand of a polynucleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 6; Length 338
Pred: No. 2.3e+03;
0; Mismatches 3; Indels
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, Otsuki
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein sequence SEQ ID NO:12146.
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Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-00248036.
99JP-00300253.
2000JP-00118776.
2000JP-00183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 86.4%;
Local Similarity 57.1%;
les 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; primer;
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11-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB93191;
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09730329-59ed.rag

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of an oligonucle conference of a polynuclectide which comprises a 5-end complementary strand of a polynuclectide which comprises a 5-end sequence and an oligonuclectide comprising a sequence complementary to the camprise and an oligonuclectide comprises a 3'-end sequence, where the polynuclectide which comprises a 1'-end sequence, where the oligonuclectide which comprises a 1'-end sequence, where the combination of the 5'-end sequence, 3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynuclectides, particularly full-length cDNAs. The primers are also useful for the cetection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the countries and the full-length cDNAs are also useful for the countries and any without any specialised methods. Ad403166 to AAH13628 and AAH13633 to AAH13612 represent human amino acid sequences; and AAH13629 to AAH13622 represent coligonucleotides, all of which are used in the exemplification of the
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oligonucleotide comprises at least 15 nucleotides; or (b) a combination
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Pred. No. 5.1e+03;
0; Mismatches 3; Indels
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57.1%;
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Best Local Similarity 57.1.
A; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               present invention
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transaldolase activity; glucose-6-phosphate isomerase; NADH production; target substance manufacture; enzyme; glucose-6-phosphoric acid isomerase. Gluconobacter oxydans glucose-6-phosphoric acid isomerase protein. ADL90006 standard; protein; 957 AA. (first entry) 20-MAY-2004 ADL90006; RESULT 23 ADL90006

ID ADL9

XX

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ADL9

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ADL9

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ADL9

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ADL9

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ADL9

662 VSAAAEF 668

Gluconobacter oxydans

JP2004024140-A.

29-JAN-2004

26-JUN-2002; 2002JP-00186487

26-JUN-2002; 2002JP-00186487.

(AJIN) AJINOMOTO

WPI; 2004-127093/13. N-PSDB; ADL90004 Novel protein having transaldolase activity or glucose-6-phosphate isomerase activity, useful for producing a target substance e.g., xylitol.

Claim 1; SEQ ID NO 18; 89pp; Japanese.

The invention comprises the amino acid and coding sequences of dluconobacter oxydans proteins which possess transationaes activity and/or glucose-6-phosphate isomerase activity. The DNA and protein sequences of the invention are involved in the production of NADH. The DNA and protein sequences of the invention are useful for manufacturing a target substance. The present amino acid sequence represents the Gluconobacter oxydans glucose-6-phosphoric acid isomerase protein.

Sequence 957 AA;

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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
cnocding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
continued or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide or its fragment whose expression is inhibited by the
cartisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
confictation, (7) identifying a gene in an operon required for
crequired for proliferation, or that inhibits cellular proliferation, (8)
identifying a gene required for cellular proliferation or the biological
capathway in which a proliferation-required gene or its gene product lies
corresponded to the test compound that inhibits profiling a
compound's activity, (11) a culture comprising strains in which the gene
compound's activity, (11) a culture comprising strains in which the gene
compound's activity, (11) a culture comprising strains in which the gene
crowpound's activity, (11) a culture comprising strains in which the gene
crowpound's activity, (11) a culture comprising strains in which the gene
crowpound's activity, (11) a culture comprising strains in which the gene
crowpound's activity, (11) a culture comprised
compound's activity, (11) a culture comprised
compound's activity, (12) dentifying the target of a compound that inhibits the
crowpound's are useful for
confidentifying proteins or screening for homologous nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids are sequired
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
                                               Gaps
                                               ö
Length 957;
                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #33272.
Score 19; DB 8; I
Pred. No. 7.2e+03;
0; Mismatches 3;
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 75669; 1766pp; English.
                                                                                                                                                                                                                                             ABU47745 standard; protein; 1266 AA.
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2001; 2001US-00815242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002WO-US009107
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  86.4%;
57.1%;
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Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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Trawick JD,
                                                                                                                                   861 VATAAEF 867
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                                                                                        VXXXAEF
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Wall D,
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               drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at from the published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; antiarteriosclerotic; cerebroprotective; antiparkinsonian; anticonvulsant; anti-HIV; antiallergic; antibacterial; virucide; gene therapy; nucleic acid-associated protein; cancer; atherosclerosis; stroke; Parkinson's disease; epilepsy; Cushing's syndrome; AIDS; allergy; microarray element; protein-protein interaction; drug-target interaction; gene expression; chromosomal mapping; diagnosis.
 cellular proliferation to isolate candidate molecules for rational
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Warren BA, Yang J;
                                                                                                                                                                                                                   Gaps
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Gorvad AE, Griffin JA;
                                                                                                                                                                                                                     ö
                                                                                                                                                                                    Length 1266;
                                                                                                                                                                                                                  3; Indels
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Hafalia AJA, Ison CH, Lal PG, Lee EA, Lee S,
Ramkumar J, Sprague WW, Swarnakar A, Tang YT,
Yue H, Zebazjadian Y,
                                                                                                                                                                                 86.4%; Score 19; DB 6; I
57.1%; Pred. No. 9.9e+03;
iive 0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human nucleic acid-associated protein #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 7; 443pp; English.
                                                                                                                                                                                                                                                                                                                                                                       ADJ80131 standard; protein; 1450 AA.
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01-NOV-2001; 2001US-0335544P.
05-NOV-2001; 2001US-033555P.
09-NOV-2001; 2001US-034650P.
15-NOV-2001; 2001US-0334762P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2002; 2002WO-US034846
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                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004 (first entry)
                                                                                                                                                                                                                   4; Conservative
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                                                                                                                                                                                                                                                                                    895 VSSSAEF 901
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                                                                                                                                                                                                                                                 1 VXXXAEF 7
                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                   Seguence 1266 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                        ADJ80131;
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                                                                                                                                                                                                                                                                                                                                    RESULT 25
ADJ80131
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                                                                                                                                                                                                                     Matches
8888888888888
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The invention relates to novel human nucleic acid-associated proteins and genes encoding them, sequences that have at least 90-99 % identity to the sequences; or biologically active or immunogenic fragments of these. The polypeptides and polymucleotides are useful in diagnosing, treating and preventing disorders associated with aberrant expression of NAAP, such as

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cell proliferative (e.g. cancer or atherosclerosis), neurological (e.g. stroke, Parkinson's disease or epilepsy), developmental (e.g. Cushing's syndrome), autoimmune/inflammatory (e.g. AIDS or allergies), or infections. These may also be used as elements on a microarray which may monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles. The polynucleotide may also be used in chromosomal mapping and in various diagnostic assays. These are also useful in assessing the effects of exogenous compounds on the expression of mucleic acids and amino acid sequences of NAAP, in facilitating discovery process, and in investigating the pathogenesis of diseases or medical conditions. This sequence corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological, antipsoriatic, antiarteriosclerotic, cardiant; vasotropic; angiogenesis; gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis; diabetic retinopathy; cardiovascular disease; atherosclerosis; ischemic limb disease; coronary artery disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the isolation of novel genes (ACF3446-ACF34559) encoding proteins (ABR6410-ABR64281) involved in the process of angiogenesis. The nucleic acid molecules are useful in identifying and/or obtaining full-length human genes involved in an angiogenic process. The
                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New angiogenic genes and polypeptides, useful for diagnosing, prognosticating or treating an angiogenesis-related disorder, cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis cardiovascular diseases.
                                                                                                                                                                                                                                                                           Length 1450;
                                                                                                                                                                                                                                                                         86.4%; Score 19; DB 7; Length 145
57.1%; Pred. No. 1.1e+04;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                    to one of the proteins of the inventions.
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29-OCT-2001; 2001AU-00008532.
13-NOV-2001; 2001AU-00008838.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Angiogenesis protein BNO147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BION-) BIONOMICS LTD
                                                                                                                                                                                                                                                                                                                                                                                      1415 VSAAAEF 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gamble JR, Hahn CN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-354655/33.
                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                         Sequence 1450 AA;
                                                                                                                                                                                                                                                                                                                                                  1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ACF34513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003027285-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001;
27-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR64238;
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 26
ABR64238
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for expression of a polynucleotide encoding a polypeptide from a

microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant

batching an improved property comprises transforming a plant with the recombinant DNA construct and growing the transforming a plant with the recombinant DNA construct is useful for improving plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plant with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or persts, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved lignin production or improved algant growth and development under at least one stress condition, improved lignin production or improved algant growth and development condition in providing in production or improved galactomannan condition, improved lignin production in improved algant growth was earlied polypeptide used in the cope of the invention. Note: The sequence date for this patent did not form part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic

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concleic acid molecule, polypeptides or complexes encoded, cells or genetically modified non-human animals derived from these are useful for the screening of candidate plaramaceutical compounds used in treating angiogenesis-related disorders. They are also useful for diagnosing, prognosticating or treating an angiogenesis-related disorder, which involves uncontrolled or enhanced angiogenesis or is a disorder; which involves uncontrolled or enhanced angiogenesis or is a disorder in which a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis, atherosclerosis), or involves inappropriately arrested or decreased angiogenesis or involves inappropriately arrested or decreased angiogenesis or involves inappropriately arrested or decreased angiogenesis or is a disorder in which an expanding vasculature is of benefit (e.g. ischemic limb disease or coronary artery disease). The modulator of expression or activity of the polypeptide encoded by the treatment of an angiogenesis-related disorder. This sequence corresponds to one of the novel angiogenic protein
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; berbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomanna; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                      86.4%; Score 19; DB 6; Length 1584; 57.1%; Pred. No. 1.38+04; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN24084 standard; protein; 2214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2003; 2003US-00369493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial polypeptide #6737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           1549 VSAAAEF 1555
                                                                                                                                                                                                                                                                                                                                                                                          1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                     Sequence 1584 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN24084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria.
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                          Matches
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Gaps

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86.4%; Score 19; DB 8; Length 2214; 57.1%; Pred. No. 1.8e+04; ive 0; Mismatches 3; Indels

4; Conservative

Local Similarity

Best Loca Matches

Query Match

Sequence 2214 AA;

1770 VTTSAEF 1776

RESULT 28 ABG78424

1 VXXXAEF 7

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New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
                                                                                       Human, memapsin 2, aspartic protease, beta secretase,
degenerative disease, Alzheimer's disease, amyloid precursor protein,
APP, neuroprotective, nootropic, inhibitor;
                                                                   Memapsin 2 substrate specificity determination peptide #30
                                                                                                                                                                                                                                                                                        (OKLA-) OKLAHOMA MEDICAL RES FOUND. (UNII ) UNIV ILLINOIS FOUND.
ABG78424 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 52; 74pp; English.
                                                                                                                                                                                                                                                                                                                            Ghosh AK;
                                                                                                                           substrate side-chain preference
                                                                                                                                                                                                                                                       28-DEC-2000; 2000US-0258705P.
14-MAR-2001; 2001US-0275756P.
                                                                                                                                                                                                                                  28-DEC-2001; 2001WO-US050826
                                             (first entry)
                                                                                                                                                                                                                                                                                                                            rang JJN, Koelsch G,
                                                                                                                                                                                                                                                                                                                                                WPI; 2002-619088/66.
                                                                                                                                                                                   WO200253594-A2.
                                                                                                                                                     sapiens.
                                             15-NOV-2002
                                                                                                                                                                                                           11-JUL-2002.
                                                                                                                                                              Synthetic.
                      ABG78424;
                                                                                                                                                                                                                                                                                                                                                                                    disease
                                                                                                                                                   Homo
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

Goldman BS;

Chen X,

Hinkle GJ, Slater SC,

Cao Y,

WPI; 2004-061375/06.

CHEN X. GOLDMAN B S.

HINKLE G J. SLATER S C.

(HINK/) (SLAT/) (CHEN/)

(CAOY/)

21-FEB-2002; 2002US-0360039P

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to

SEQ ID NO 6737; 122pp; English.

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The invention relates to an inhibitor of catalytically active memapsin 2 (an aspartic protease which can cleave at beta secretase sites), which binds to the active site of memapsin 2 defined by the presence of two catalytic aspartic residues and substrate binding cleft. Also included is memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2 unbertase comprising: (a) reacting a mixture of memapsin 2 unbertases comprising: (a) reacting mixture of memapsin 2 substrates; or (b) preparing a combinatorial intervier of memapsin 2 substrates; or (b) preparing a combinatorial clibrary of memapsin 2 inhibitors containing a base sequence taken from OM99-2 (Glu-val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 which binds to several inhibitors to generate several bound memapsin 2, and detecting the bound memapsin 2 with an antibody raised to memapsin 2 and detecting the bound memapsin 2 with an antibody raised to memapsin 2 and an alkaline phosphatase conjugated secondary antibody. The inhibitors may be used in the manufacture of a medicament for the treatment of Alzheimer's disease since memapsin 2 may be involved in the cleavage of amyloid precursor protein (APP), and for the companiant preference in memapsin 2 sub-sites.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an inhibitor of catalytically active memapsin 2 (an aspartic procease which can cleave at beta secretase sites), which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, memapsin 2, aspartic protease; beta secretase;
degenerative disease; Alzheimer's disease; amyloid precursor protein;
APP; neuroprotective; nootropic; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                   the substrate side-chain preference in memapsin 2 subsequence represents a subsite variant peptide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Memapsin 2 substrate specificity determination peptide #25
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 5; Length 12;
Pred. No. 1.2e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                         determine the substrate specificity of human memapsin 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OKLA-) OKLAHOMA MEDICAL RES FOUND. (UNII ) UNIV ILLINOIS FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG78419 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 52; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ghosh AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               substrate side-chain preference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-DEC-2001; 2001WO-US050826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-2000; 2000US-0258705P.
14-MAR-2001; 2001US-0275756P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
4; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-619088/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNAAAEF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200253594-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                       The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG78419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 29
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catalytic appartic residues and substrate binding cleft. Also included is a method of determination of the substrate side-chain preference in semapsin 2 sub-sites comprising; (a) reacting a mixture of memapsin 2 substrates with memapsin 2, and determining the sub-site preference of memapsin 2 by determining relative initial hydrolysis rates of the mixture of memapsin 2 substrates; or (b) preparing a combinatorial library of memapsin 2 inhibitors containing a base sequence taken from 0M99-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 and addetecting the bound memapsin 2 with an antibody raised to mempsin 2 and an alkaline phosphatase conjugated secondary antibody. The inhibitors may be used in the manufacture of a medicament for the treatment of Alzheimer's disease since memapsin 2 may be involved in the cleavage of amyloid precursor protein (APP), and for determining the substrate side-chain preference in memapsin 2 sub-sites.

The present sequence represents a subsite variant peptide used to
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an inhibitor of catalytically active memapsin 2 dan aspartic protease which can cleave at beta secretase sites), which binds to the active site of memapsin 2 defined by the presence of two catalytic aspartic residues and substrate binding cleft. Also included is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; memapsin 2; aspartic protease; beta secretase; degenerative disease; Alzheimer's disease; amyloid precursor protein; APP, neuroprotective; nootropic; inhibitor; substrate side-chain preference.
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Memapsin 2 substrate specificity determination peptide #24.
                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 5; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.2e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                determine the substrate specificity of human memapsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OKLA-) OKLAHOMA MEDICAL RES FOUND.
(UNII ) UNIV ILLINOIS FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG78418 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 52; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ghosh AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-DEC-2000; 2000US-0258705P.
14-MAR-2001; 2001US-0275756P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-2001; 2001WO-US050826
                                                                                                                                                                                                                                                                                                                                                                                        81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 57.1%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koelsch G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-619088/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNTAÄEF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                   Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200253594-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG78418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang JJN,
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2 substrates with memapsin 2, and determining the sub-site preference of memapsin 2 by determining relative initial hydrolysis rates of the mixture of memapsin 2 substrates; or (b) preparing a combinatorial library of memapsin 2 inhibitors containing a base sequence taken from (oM99-2 (Glu-Val-Asn-Leu-Ala-Ala-Glu-phe), probing the library of inhibitors with memapsin 2 which binds to several inhibitors to generate several bound memapsin 2, and detecting the bound memapsin 2 with an antibody raised to memapsin 2 and an alkaline phosphatase conjugated secondary antibody. The inhibitors may be used in the manufacture of a medicament for the treatment of Alzheimer's disease since memapsin 2 may be involved in the cleavage of amyloid precursor protein (App), and for determining the substrate side-chain preference in memapsin 2 sub-sites.

The present sequence represents a subsite variant peptide used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
determination of the substrate side-chain preference in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lipoprotein; E.coli outer membrane protein (OMP) A signal peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4. .5
/label= signal peptide/ protein junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                determine the substrate specificity of human memapsin 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMP A-2 signal peptide/heterologous protein junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 5; 1
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page ?; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP82869 standard; protein; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83US-00494040.
84US-00607224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86US-00880358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1.
A: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYNY-) UNIV OF NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1988-212802/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VXXXAEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAN80125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUL-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1990
method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US4757013-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP82869;
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AAP8
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Efficiency of expression of lipoprotein expression vectors is improved by introducing the omp A signal peptide from E.coli in place of lipoprotein signal sequence. A fusion protein is produced where the desired protein carries the omp A signal peptide at its N-terminal end. This signal

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The invention relates to annotating a query sequence involving accessing patterns associated with a database comprising annotated sequences, assigning attributes to the patterns based on the annotated sequence assigning attributes to the patterns based on the annotated sequence and using the patterns with assigned attributes to analyse the query sequence. Also included are an apparatus for annotating a query sequence. The method further comprises the step of selecting the accessed patterns that match the query sequence, storing the patterns with assigned attributes, the attribute vector from the patterns with assigned attributes, the attribute vector faracterising portions of the query sequence is a polypeptide sequence comprising amino actific residues and the attribute vector comprises a number of counters (the number of counters is proportional to the number of amino actifications of the query sequence). The assigned attributes are used to contribute values to counters of the attribute vector corresponding to portions of the query sequence matched by the patterns. The method also comprises a plurality of attribute vectors where the plurality of
                                                                                                                                                                                                                                                               ö
          is then cleaved off. No modification of the cleavage site is necessary during the secretion process, unlike for the lipoprotein signal peptide. Synthetic linkers were inserted to ensure the structural gene was in phase with the signal sequence. Proteins encoded by plasmids omp A-1 and comp A-3 demonstrate the other two reading frames. (AAN80124 and AAN80126). See also AAN80118-9 and AAN80128. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Annotating a query sequence e.g. protein sequence involves accessing patterns associated with a database comprising annotated sequences, assigning attributes to the patterns based on the annotated sequence and analyzing the query sequence.
translocation of the product across the cytoplasmic membrane and
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, ubiquitin, annotated sequence, query sequence, database, secondary structure characteristic, bio-dictionary.
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                       Score 18; DB 1; Length 13; Pred. No. 1.3e+02; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IBMC ) INT BUSINESS MACHINES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO52379 standard; peptide; 41 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 4; 28pp; English
                                                                                                                                                                                                                       81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-NOV-2002; 2002US-00305582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-NOV-2002; 2002US-00305582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ubiquitin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-459887/43.
                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                       1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                             1 VAQAAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2004101903-A1
                                                                                                                                                                                 Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rigoutsos I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAY-2004
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                                                                                                                                                                                                                       Query Match
  directs
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Matches
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attribute vectors are ranked, and the top ranking attribute vectors are reported. The method comprises the step of determining a score for the patterns with assigned attributes used to contribute to the attribute vector. The score represents a degree of similarity between the query sequence and the annotated sequences of the database and the score is normalised. The attributes relate to at least one of secondary structure characteristics of the query, presence of known domains, signal peptides, active sites, post-translationally modified sites, cytoplasmic behaviour, extracellular behaviour, and similarity of the query to each of the three phylogenetic domains as a function of amino acid position. The method is used for analysing or annotating query sequence e.g. protein or amino acid sequence, for elucidating properties of protein (including functional, structural and physiochemical properties) directly from corresponding amino acid sequence and for forming a bio-dictionary. The method is also useful for determining cytoplasmic, transmembrane or extracellular region of a query sequence and allows automated elucidation for annotating query sequence and allows automated elucidation for annotating query sequences or complete genomes, quickly, exhaustively previously. The present sequence is a peromen unsiquitin, analysed using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TANGO, MANGO, colon, inflammation, tumor, renal; liver, lung, autoimmune, allergy, cardiovascular, brain, degenerative, placental; pancreatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%; Score 18; DB 8; Length 41; ilarity 57.1%; Pred. No. 4.5e+02; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sharp JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barnes TM, Fraser CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB61451 standard; protein; 44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-2000; 2000WO-US018184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00342687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TANGO 275 TB domain #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (e.g. idiopathic ulcerati
disorders (e.g. jaundice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-050127/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAALAEF 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 4, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                skeletal; muscle
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 275, TANGO 275, TANGO 275, TANGO 275, TANGO 275, TANGO 246, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung

Disclosure, Fig 12, 262pp, English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the preparation of DNA, in a circular vector, that encodes one or more segments of a modular polypeptide. DNA or DNA libraries produced this way are used to produce modular polypeptides, particularly enzymes, which can be used to act on substrates to produce compounds for therapeutic testing. Enzymes of particular interest are those involved in non-ribosomal peptide synthesis or polyketide synthesis, and compounds for testing are particularly macrolide antibiotics, including penicillins, vancomycins or erythromycins, but may also be modular receptors. The present sequence is a peptide used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preparing DNA encoding modular protein for e.g. producing new enzymes for synthesis of polyketide antibiotics, comprises cyclic integration of fragments into a vector.
                                                                                                                                                                                                                                                                                                                                                                               Modular enzyme system; cyclic gene synthesis; repetitive coding sequence; antibiotic; non-ribosomal peptide synthetase; NRPS; PKS; polyketide synthase; actinomycin biosynthase.
disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle disorders
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                   Modular enzyme system related ACP-domain N-terminal peptide MTAD.
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0
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Pred. No. 5.3e+02;
0; Mismatches 3; Indels
                                                                                           Length 44
                                                                                        Score 18; DB 4; ]
Pred: No. 4.9e+02;
0; Mismatches 3
                                                                                                                                                                                                                                                            AAM47175 standard; peptide; 47 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 9; 83pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ACTI-) ACTINODRUG PHARM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-2001; 2001WO-DE001578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-2000; 2000DE-01021267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 57.1%;
4; Conservative
                                                                                         81.8%;
57.1%;
                                                                           12-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Stigmatella aurantiaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-049276/06
                                                                                                                                                                                  35 VYSSAEF 41
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VXXXAEF 7
                                                                                                                                                    1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 47 AA;
                                                               Sequence 44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200181564-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schauwecker F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2001
                                                                                                                                                                                                                                                                                          AAM47175;
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                                                                                                                                                                                                                                RESULT 34
                                                                                                                                                                                                                                               AAM47175
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09730329-59ed.rag

(first entry)

Page 20

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AAY14477 standard, protein; 56 AA.
                                                  17-AUG-1999
                                                                          Fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement.
                                                                                                                                      myeloid cell disorder; lymphoid cell disorder;
bone cartilage tissue growth; tendon tissue growth;
ligament tissue growth; nerve tissue growth; regeneration; wound healing;
tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                      , Wang J;
Wang D;
                                                                                                                           forensic; nutritional source; damaged tissue; diseased tissue;
                                                                                                                                                                                                                                                                                                                                                                    Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; Score 18; DB 7; Length 53; 57.1%; Pred. No. 6e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; SEQ ID NO 957; 156pp; English.
                      ADI21706 standard; protein; 53 AA.
                                                                                                  Novel human polypeptide #185.
                                                                                                                                                                                                                                                                               19-SEP-2002; 2002WO-US029964.
                                                                                                                                                                                                                                                                                                       19-SEP-2001; 2001US-0323739P.
                                                                         (first entry)
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N-PSDB; ADI21486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                              WO2003025148-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 53 AA;
                                                                                                                                                                                                      Homo sapiens.
                                                                         15-APR-2004
                                                                                                                                                                                                                                                     27-MAR-2003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide
                                               ADI21706;
RESULT 35
             ADI21706
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This sequence represents a fragment of a secreted human protein encoded by the nucleic acid molecule detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAX79002) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 53 novel genes and their fragments (nucleic acid sequences: AAX79011-X79064; amino acid sequences AAY1411-Y14464) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 53 polynucleotides, based on which tissues they are most highly expressed in (see AAX79011 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                              Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphom; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; observing stepticis; thyris; testis; lung; thyroid; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrie AM, Florence C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human genes and the secreted polypeptides they encode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 2; Length >0, Pred. No. 6.4e+02;
human secreted protein encoded by gene 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uan R, Ebner R, Re
Greene JM, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 14; 226pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ12304 standard; protein; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0061527P.
97US-0061529P.
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97US-0061536P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMA- HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 57.1%;
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-277587/23.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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Gaps ö

4; Conservative

Matches

27 VRTSÁÉF 33

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RESULT 36 AAY14477

1 VXXXAEF 7

preventing disorders such as cancer, haematopoietic diseases including anaemia and multiple myeloma, reproductive system disorders including prostatitis and inguinal hernia, musculoskeletal diseases including systemic lupus erythematosus and gout, cardiovascular diseases including arrhythmia and hypernatraemia, mixed fetal diseases including detal alcohol syndrome and Down's syndrome, excretory diseases including alcohol syndrome and Down's syndrome, excretory diseases including disease and glomerian mental tis respiratory disease including albebtes and glomerial one pittis, respiratory disease including emphysema and occupational lung disease, endocrine diseases including portal hypertension and irritable bowel syndrome and connective tissue or epithelial diseases including scleroderma and epidermolysis bullosa. As such, there are various activites such as cytostatic, antianemic, antiathmiatory, antispathmatic, antisbaterial, osteopathic, antispathmatory, antispathmatic, menunosuppressive, dermatological, antispatic, antishaterial, osteopathic, dermatological, inmunosupprotective, antispathmatory antispathmatic, menunosuppressive, antispathmatic, menunosuppressive, antispathmatic, notropic, antispendic, inmunosuppricective, antispathmatory antispathmatic, menunosuppressive, antispathmatic, notropic, antispathmatic, antispathmatic, notropic, antispathmatic, notropic, antispathmatic, antispathmatic, notropic, antispathmatic,

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ADJ12304;

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numeni, sectored; cancer; naemalopolect; otherses; anamenia;
multiple myeloma; reproductive system disorder; prostatitis;
multiple myeloma; reproductive system disorder; prostatitis;
muguinal hernia; musculoskeletal disease; systemic lupus erythematosus;
myent; cardiovascular disease; arrhythmia; hypernatraemia; fetal disease;
myent; cardiovascular disease; arrhythmia; hypernatraemia; fetal disease;
myenimer's disease; meningitis; respiratory disease;
myentimer's disease; meningitis; respiratory disease;
myentimery incontinence; renal disorder; neural; sensory disease;
myentimery incontinence; endocrine disease; disbetes;
myenticable bowel syndrome; epithelial disease; scleroderma;
myeritable bowel syndrome; epithelial disease; scleroderma;
mittable bowel syndrome; epithelial disease; scleroderma;
antiathmatic; anti-HIV; immunosuppressive; antiantmatory;
antistemiator; antibacterial; osteopathic; dermatological; antigout;
mimunomodulator; antiarrhythmic; cardiant; nootropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;
methrotropic; uropathic; hypertensive; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acids and polypeptides, useful for diagnosing, treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's
                                                                               secreted; cancer; haematopoietic disease; anaemia;
                                                     Peptide feature of a human secreted protein SegID 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duan RD, Ruben SM,
Yu G, Florence C,
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97US-0061529P.
97US-0061532P.
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99US-00288143
2000US-0244591P
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97US-0071498P
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                             (first entry)
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FLORENCE K A.
GREENE J M.
YOUNG P E.
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Ferrie AM,
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DUAN R D.
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OLSEN H.
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                           20-MAY-2004
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09-OCT-1997
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(FLOR/)
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(FLOR/)
(EBNE/)
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Novel testes-specific gene 22P4F11 which is expressed in human prostate cancer and is useful as a diagnostic marker and/or therapeutic target for prostate cancer.
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Pred. No. 6.4e+02;
0; Mismatches 3; Indels
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57.1%;
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99US-0146584P
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Best Local Similarity 57.1
Matches 4; Conservative
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HUBERT R S.
MITCHELL S C.
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N-PSDB; AAZ94894.
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Greene JM;

Florence KA, Gree Sbner R, Olsen H;

Ebner R,

This invention relates to novel polynucleotides encoding human secreted proteins. Specifically, it refers to the vectors, host cells, recombinant and synthetic methods for producing human polynucleotides, polypeptides and antibodies. Furthermore, it relates to screening methods to identify agonists and antegonists that can be used to inhibit or enhance the production and function of the secreted proteins. The present invention describes these compositions as useful for diagnosing, treating or

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Matches
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                          The present sequence is that of a human 22P4F11 polypeptides, as deduced from an isolated partial CDNA (see AAZ94894). The full-length 22P4F11 sequence is provided in AAY79489. 22P4F11 is a testis-specific gene in normal tissues, and is also expressed in human prostate tumours, in some cases at high levels. The 22P4F11 transcript and/or protein may represent a useful diagnostic marker and/or therapeutic target for prostate cancer. Methods of using 22P4F11 polynucleotides, polypeptides and antibodies for the diagnosis and treatment of cancers expressing 22P4F11, especially prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00101 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                    Score 18; DB 3; Length 69;
Pred. No. 8.1e+02;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ORFX protein sequence SEQ ID NO:12892.
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Example 1; Fig 1B; 54pp; English.
                                                                                                                                                                                                                                        81.8%;
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29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                           development of such cancers
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                                                                                                                                                                                                                                                      Local Similarity 42.9
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                                                                                                                                                                                                         Sequence 69 AA;
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Best Local S
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syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosia of liver, psoriaais, benign tumours, keloid, degenerative disorders, haemorrhage, careoarthritis, neurodegenerative disorders, disorders, haemorrhage, cransplantation, cardiovascular diseases, disbetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune disorders such as multiple sclerosis, rheumatoid disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from conficient part of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic cormat directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leotides and polypeptides, useful for drug screening assays and monitoring of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alloiococcus otitidis, antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 5; Length 73; Pred. No. 8.6e+02; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alloiococcus otitis antigenic protein SEQ ID NO:3718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Alloiococcus otitidis polynucleotides treating and diagnosing diseases, drug screffects during drug clinical trials.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB09905 standard; protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%;
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18-NOV-2002; 2002US-0426742P.
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N-PSDB; ADB09908.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 73 AA;
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Claim 1; SEQ ID NO 10066; 122pp; English.

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host cell, transfected, transformed or infected with the vector of (2);

(4) an antibody specific for the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide, its complement, biological equivalent or fragment, or the polymorlectide that is comprised in the expression vector; (6) a pharmaceutical composition comprising the polypeptides of (1) and a carrier; (7) a protein chip comprising the polypeptides of (1), their biological equivalent or fragment; (8) immunogenic composition; (9) detecting and/or identifying Alloicoccus cutitidis in the biological sample; (10) a kit comprising a container containing the novel polymucleotide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polypeptide by culturing the polymetically engineered host cell under conditions suitable to produce the polymetical form the culture. (1) can be used in gene therapy. The polymucleotides, antibodies and compositions of the present invention can be used for treating and diagnosing diseases, drug creening assays and monitoring of effects during drug clinical trials. The present sequence represents an Alloicoccus otitidis and the present sequence represents an Alloicoccus otitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%; Score 18; DB 6; Length 83; 57.1%; Pred. No. 9.9e+02; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                          antigen protein from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADS21033 standard; protein; 93 AA.
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GOLDMAN B S.
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SLATER S C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 83 AA;
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Matches
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ADS21033
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant such as maize or soybean. The method of producing a transformed plant such as maize or soybean. The method of producing a transformed plant cach having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme semultions, pathogens or peets, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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57.1%; Pred. No. 1.18+03;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  format from USPTO at segdata.uspto.gov/seguence.html.
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29-AUG-2000; 2000US-0228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 93 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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Matches
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                                                                                                                                                                         The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1) in the specification). ABN15762 to ABN27525 encode the human ORFX proteins given in ABP00100 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, cateoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular disorders, disbetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage diseases, various immune deficiencies and disorders, infectious diseases, autoimmune disorders sullippe sclerosis, rheumatoid arthritis, autoimmune inflammatory eye disease. Open transplantation burne inflammatory eye disease. Open diseases, desting are also set of the set of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                         Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                              preventing and treating cardiovacular disease, neurodegenerative hyperproliferative disorders and autoimmune disorders.
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                                                                                                                                          Disclosure; SEQ ID NO 11030; 1037pp; English.
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20-JAN-2000; 2000US-0177050P.
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Matches 3; Conservative
WPI; 2002-106308/14
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                       N-PSDB; ABN21276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 112 AA;
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The invention relates to the isolation of genes AAC63410-C63458 encoding the human secreted proteins AAB29802-B29850. This sequence represents a cragment of the protein encoded by the gene given in the descriptor line. The sequence is used as a query sequence for doing BLASTX searches to determine homologous sequence to the protein. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tisques disclosed in the specification. The nucleic acids, proteins, c.g. by protein or gene therapy. The genes are isolated from a range of human tisques disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal crack, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune crickyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, thematoid arthritis and ulcerative colitis; (c) cardiovascular disorders cue as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases cue as viral, bacterial, fungal and parasitic infections
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                                                                                                                                   Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor-ligand interaction; cytostatic; chondrocyte; tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 3; Length 121;
Pred. No. 1.5e+03;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                     Disclosure; Page 479; 495pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADF76715 standard; protein; 137 AA.
   Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hunte B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.9
Matches 3; Conservative
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, Wood WI,
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Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-721702/68.
N-PSDB; ADF76714.
                                                                WPI; 2000-647424/62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 121 AA;
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Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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   Rosen CA,
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in the formation, differentiation and maintenance of multicellular corganismes, remaining the formation, differentiation and maintenance of multicellular corganismes. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information.

Corganismes. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information.

Corganismes. The fate of many individual cells (for example mitogenic factors, such the cells and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins of the invention may have cytostatic activities through the strimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a cumman. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present
                                                                                                                                                This invention relates to novel nucleic acids encoding human PRO secreted
                 New PRO polypeptides, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soybean, protein phosphatase 2A; protein phosphorylation modulation, transgenic plant, gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soybean partial protein phosphatase 2A regulatory subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 18; DB 7; Length 137; 57.1%; Pred. No. 1.7e+03; ive 0; Mismatches 3; Indels
                                                                                                             Claim 10; SEQ ID NO 390; 918pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY99815 standard; protein; 139 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US029823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 138
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                                                                          diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 137 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
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Gaps

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In present sequence to soprom process, the present sequence are coding this protein was identified in clone src2c.pk023.19 of a cDNA library made from soybean eight-day-old root infected with cyst nematode. BLAST analysis showed that the sequence encodes protein phosphatase 2A regulatory subunit B. The nucleotide sequence may be used for the recombinant production of the protein in vivo, e.g. via a gene therapy protocol, or in vitro, e.g. in fermentation culture. The protein may then be used to modulate the process of reversible protein phosphorylation in plants. It may be used directly to supplement a plant's own production of the enzyme or to rectify mutations that result in the expression of inactive protein. The protein may also be used to test for modulators of protein phosphorylation which may be used to alter the activity of the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                              The present sequence is soybean protein phosphatase 2A regulatory subunit
                                                  Polynucleotides encoding plant protein phosphatase useful for modulating reversible protein phosphorylation in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
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Pred. No. 1.8e+03;
0; Mismatches 3; Indels
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                                                                                                        Claim 12; Page 48-49; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%;
57.1%;
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26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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WPI; 2000-431599/37.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VXXXAEF
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                 N-PSDB; AAA48570
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 139 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 46
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           expressing the proteins are an aregonized for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and calls genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55521). The nucleic acid sequence, is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-0CT-2001) which is available in electronic format directly from WIPO at
identifying agents (agonists and antagonists) that bind to them. Cells
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide sequence useful in the identification or Lactococcus
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                                                                                                                                                                                                                                                                                         4; Length 144;
                                                                                                                                                                                                                                                                                       Score 18; DB 4; Length 144
Pred. No. 1.8e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Renault P, Ehrlich SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; SEQ ID NO 2081; 2504pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB55379 standard; protein; 148 AA.
                                                                                                                                                                                                                     secreted proteins of the invention
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                                                                                                                                                                                                                                                                                          81.8%;
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(first entry)
                                                                                                                                                                                                                                                                                                                           4; Conservative
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                              1 VXXXAEF 7
                                                                                                                                                                                                                                                       Sequence 144 AA;
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16-MAY-2002
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standardise Os field)

Sequence 148 AA

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The invention relates to the isolation of genes AAC59624-C59669 encoding the human secreted proteins AAB14439-B34448. This sequence represents a peptide fragment homologous to the protein encoded by the gene isolated in the present invention. The sequence is a search result from a BLASTX homology search. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and in the specification. The nucleic acids, proteins, antibodies and in the specification. The nucleic acids, proteins, antibodies and in the specification of:

(ant) agonists are useful in the diagnosis, treatment and prevention of:

(a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders end outlements, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid and parestive colitis; (c) cardiovascular disorders such as myccardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, because in the found and parasitic infections
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                                                                                                                                                                                                                                                                                                                                                                Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuleer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
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                                      Gaps
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                                                                                                                                                                                                                                                                                                                              Human secreted protein BLAST search protein SEQ ID NO: 141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 3; Length 155; Pred. No. 2e+03;
  Length 148;
                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
Score 18; DB 5; I
Pred. No. 1.9e+03;
                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 373; 384pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                              AAB34523 standard; protein; 155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preventing, treating or ameliorat
Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2000; 2000WO-US006828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0125358P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 57.1%;
4; Conservative
  81.8%;
57.1%;
                                                                                                                                                                                                                                                                                        (first entry)
  Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM,
                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-602216/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                  VSTLAEF
                                                                              1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200056767-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-1999;
                                                                                                                                                                                                                                                                                          02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA,
                                                                                                                                                                                                                                                      AAB34523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ношо
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                                                                                                                                                                          RESULT 48
                                                                                                                                                                                              AAB34523
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Gaps

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Length 159; 3; Indels

DB 8;

Score 18; DB 8; Pred. No. 2e+03; 0; Mismatches

81.8%; 57.1%;

Query Match Best Local Similarity

Sequence 159 AA;

4; Conservative

Matches

7

1 VXXXAEF

8

142 VAAEAEF 148

format from USPTO at segdata.uspto.gov/seguence.html

VXXXAEF 7

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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance;
                                                                                                                                                            cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                              Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 16932; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                              Chen X,
                                                  ADS27899 standard; protein; 159 AA.
                                                                                                                                                                                                                                                                                                                                                                            Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                            20-FEB-2003; 2003US-00369493.
                                                                                                                                                                                                                                                                                               21-FEB-2002; 2002US-0360039P.
                                                                                                             Bacterial polypeptide #16932
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                CAO Y.
HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                CHEN X.
GOLDMAN B S.
 44 VATLAEF 50
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-061375/06
                                                                                                                                                                                                                                     US2003233675-A1.
                                                                                         02-DEC-2004
                                                                                                                                                                                                                                                        18-DEC-2003.
                                                                                                                                                                                                                  Bacteria.
                                                                     ADS27899;
                                                                                                                                                                                                                                                                                                                                     (SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                         GOLD/)
                                                                                                                                                                                                                                                                                                                                                                            Cao Y,
                                                                                                                                                                                                                                                                                                                  CAOY/)
                                                                                                                                                                                                                                                                                                                             HINK/)
                                                   셤
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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uvaitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes.

Propionibacterium acnes immunogenic protein #28527.

27-FEB-2002 (first entry)

AAU67631;

AAU67631 standard; protein; 162 AA

RESULT 50 AAU67631

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conjugations and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by practices. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypercosis and osteomyellitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with a cne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The plypeptides may be used as antigens in the production of antibodies percipit for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and cherefore treat P. acnes infections. The antibodies may also be used as antigens. The antibodies may also be used as enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitcham JL, Wang SS, Bhatia A; Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 28826; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                 20-APR-2001; 2001WO-US012865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS59604.
                                                                                                                                                                                                                                                                       WO200181581-A2.
                                                                                                                                                                                                                                                                                                             01-NOV-2001.
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to prowoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant the excombinant DNA construct and growing the transformed plant with the aving an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the comprised or polypeptide is useful for producing plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scome part of the printed specification but was obtained in electronic

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Gaps

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Length 162; 3; Indels

Score 18; DB 6; Pred. No. 2.1e+03; 0; Mismatches

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sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynuclectides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                     81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 VAVTAEF 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 VYSSÁÉF 57
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                    Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200052165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB28213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                 Matches
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           88888888
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cenceding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynuclectides (BMM35624-ABM64536) and to immunogenic fragments of by a canes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a continuous comprising a polypeptide of the invention; antibodies against polypeptides of the invention; a method for sthmulating an immune response specific for a P. acnes in composition (comprising P. acnes polypeptides, polypeptides, and an isolated T cell population comprising T cells prepared via this method; a vaccine composition proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit continuous conti
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Propionibacterium acnes polypeptides and polynucleotides encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes predicted ORF-encoded polypeptide #28826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                            Length 162;
                                                                                                                                                    Score 18; DB 4; Length 162
Pred. No. 2.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 28826; 1481pp; English.
       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM64150 standard; protein; 162 AA.
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Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2001; 2001US-00978825.
                                                                                                                                                        81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                       Local Similarity 57.1
es 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              100 VAVTAEF 106
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                                                                                                                                                                                                                                                                                                         1 VXXXAEF 7
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                                                                                Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003033515-A1.
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                                                                                                                                                        Query Match
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Breast tumor antigen polypeptides and polynucleotides, useful for manufacturing vaccines and compositions for treating, diagnosing, and monitoring breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                           Cytostatic; vaccine; human; breast tumour; antigen; breast cancer.
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AAB28213 standard; protein; 169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Fig 2; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00272886.
99US-00396313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-FEB-2000; 2000WO-US005431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00262505
                                                                                                                                                     (first entry)
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(first entry)

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Streptococcus polypeptide SEQ ID NO 8518.
                         ABP29671 standard; protein; 193 AA
                                                                          02-JUL-2002
                                                 ABP29671;
 RESULT 54
ABP29671
                                      ****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of novel lactic acid bacteria (Lactobacillus rhamnosus strain HN001) polynucleotide sequences, and the proteins encoded by them. Also disclosed are oligonucleotide probes and primers, and genetic constructs comprising the polynucleotide sequences of the invention. The polynucleotide sequences are useful for preparing a vaccine against bacterial infections or for improving the properties of microbes used in the manufacture of milk-derived products, food products, food additives, nutritional supplements, bloactive substances or probiotic supplements, and for modifying the flavour, aromatic and intrinsial value of foods. They are also useful for identifying microorganisms having a trait associated with the polynucleotide. The present sequence represents a novel L. rhamnosus polynucleotide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at segdata.uspto.gov.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide from Lactobacillus rhamnosus HN001 strain, useful for preparing a vaccine against bacterial infections or for modifying the flavor, aroma or nutritional benefits of a bioactive or probiotic supplement product.
                                                                                                                        Lactic acid bacteria; vaccine; bacterial infection; microbe; mik-derived product; food product; food additive; nutritional supplement; bloactive substance; probiotic supplement; flavour; aroma; texture; nutritional value; food; microorganism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 179;
                                                                                                  Lactobacillus rhamnosus polypeptide sequence #78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18; DB 8; I
Pred. No. 2.3e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                        Glenn M, Havukkala IJ, Lubbers M, Dekker J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 21; SEQ ID NO 199; 54pp; English.
                                                                                                                                                                                                     Lactobacillus rhamnosus; strain HN001.
                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD.
                         ADI67204 standard; protein; 179 AA.
                                                                                                                                                                                                                                                                                                                                              01-SEP-1999; 99US-0152032P. 08-AUG-2000; 2000US-00634238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                   99US-0147853P.
                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2001; 2001US-00971536.
                                                                                                                                                                                                                                                                                03-OCT-2002; 2002US-00264213
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-090459/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADI67079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 179 AA;
                                                                                                                                                                                                                               US2004009490-A1.
                                                                                                                                                                            antibacterial.
                                                                                                                                                                                                                                                                                                                                  01-SEP-1999;
01-SEP-1999;
                                                                          22-APR-2004
                                                                                                                                                                                                                                                                                                         09-AUG-1999;
                                                                                                                                                                                                                                                        15-JAN-2004.
                                                                                                                                                                                                                                                                                                                      09-AUG-1999
                                                 ADI67204;
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RESULT 5
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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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Pred. No. 2.5e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masignani V, Margarit Y RosI, Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 3962; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2001; 2001GB-00005640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 81.8%;
Similarity 57.1%;
4; Conservative (
                                                                                                                                                                                                                                                                                                                                                                     29-OCT-2001; 2001WO-GB004789
                                                                                                                                                  Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-352536/38.
N-PSDB; ABN70302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 193 AA;
                                                                                                                                                                                                                      WO200234771-A2.
                                                                                                                                                                                                                                                                                              02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Telford J,
Tettelin H;
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VTSIAEF 47

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Gaps

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3; Indels

Local Similarity 57.1 les 4; Conservative

Matches

162 VSTIAEF 168

1 VXXXAEF

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RESULT 55

ABP25742

09730329-59ed.rag

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AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34381 to AAX34583. AAX91802 to AAX91899 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivalis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                             Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigenic Porphorymonas gingivalis peptides for preventing gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 2; Length 204;
Pred. No. 2.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agius CT,
                                                                                                          Porphorymonas gingivalis protein PG64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO66356 standard; protein; 214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patterson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 524; 588pp; English
                                                                                                                                                                                                                                                                                                                                                                                        98AU-00001546.
98AU-00002264.
98AU-00002911.
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98AU-00003338.
98AU-00003654.
98AU-00004917.
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57.1%;
                                                                                                                                                                                                                                                                                                                  98WO-AU001023
                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 57.1 es 4; Conservative
                                                                                                                                                                                                       Porphyromonas gingivalis
                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barr IG, Pa
I, Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-385613/32.
N-PSDB; AAX91751.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSLC-) CSL LTD
                                                                                                                                                                                                                                        WO9929870-A1
                                                                                                                                                                                                                                                                                                                  10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1998;
                                                  20-MAR-2003
25-AUG-1999
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                                  27-AUG-2003
                                                                                                                                                                                                                                                                               17-JUN-1999
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09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAY-1998
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                                                                                                                                                                  antigenic.
AAY34533;
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                                                                                                                                                                                                                                                                                                                                                                          31-DEC-
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ABO66356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5481 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a streptococcus mapped (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity characteristy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                               Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Masignani V, Margarit Y RosI, Grandi G, Fraser C;
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Pred. No. 2.6e+03;
0; Mismatches 3; Indels
                                                                                                                            Streptococcus polypeptide SEQ ID NO 660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 3219; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY34533 standard; protein; 204 AA.
             ABP25742 standard; protein; 197 AA
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24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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57.1%;
                                                                                                                                                                                                                                                                                                                                                   29-OCT-2001; 2001WO-GB004789
                                                                                       (first entry)
                                                                                                                                                                                                                                          Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-352536/38.
N-PSDB; ABN66373.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 197 AA;
                                                                                                                                                                                                                                                                           WO200234771-A2.
                                                                                       02-JUL-2002
                                                                                                                                                                                                                                                                                                                02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relford J,
                                                ABP25742;
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Margetts MB;

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Gaps

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RESULT 56 AAY34533 ID AAY3 XX

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Margetts MB;

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Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAY34583. AAX91802 to AAX91989 represent PCR primers used in the AAY34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                        Antigenic Porphorymonas gingivalis peptides for preventing gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment; prevention; disease; diagnosis; gene therapy; screening; bacterial; antimicrobial; antibiotic; pathogenesis; infection.
                                                                                                                                                                                                                                                                                                                                        AAX91536 to AAX91801 encode two hundred and sixty six antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 2; Length 221; Pred. No. 2.9e+03; 0; Mismatches 3; Indels
                                                                                                                                                                   Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lonetto MA,
                                                                                                                                                                   Agius CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY85820 standard; protein; 225 AA.
                                                                                                                                                                    Patterson MA,
                                                                                                                                                                                                                                                                                                         Claim 1; Page 371; 588pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP.
               98AU-00003128.
98AU-00003338.
98AU-00003654.
                                                               98AU-00004917.
98AU-00004963.
98AU-00005028.
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98AU-00002911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae
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                                                                                                                                                                      Barr IG, Pa
I, Webb EA;
                                                                                                                                                                                                                    WPI; 1999-385613/32.
N-PSDB; AAX91618.
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N-PSDB; AAZ96199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 221 AA;
                                                                                                                                    (CSLC-) CSL LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9806734-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-2000
                                                                 29-JUL-1998;
                                                                                                   04-AUG-1998;
                                                                                                                                                                    Ross BC, Ba
Hocking DM,
                   23-APR-1998;
                               05-MAY-1998;
                                                   22-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY85820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY85820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                 Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%; Score 18; DB 7; Length 214; 57.1%; Pred. No. 2.8e+03; cive 0; Mismatches 3; Indels
 Klebsiella pneumoniae polypeptide segid 12873
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 12873; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphorymonas gingivalis protein PG64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY34400 standard; protein; 221 AA.
                                                                                                                                                                                                                                                        (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97AU-00000839.
97AU-00001182.
98AU-00001546.
98AU-00002264.
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                                                                                                                                                                                      27-JAN-2000; 2000US-00489039
                                                                                                                                                                                                                        99US-0117747P
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(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gingivalis
                                                                                                                                                                                                                                                                                           Osborne M;
                                                                                   Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVSTAEF 192
                                                                                                                                                                                                                                                                                                                           WPI; 2003-895346/82.
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                                                                                                                                                                                                                                                                                                                                           N-PSDB; ACH99907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-DEC-1997;
30-JAN-1998;
10-MAR-1998;
                                                                                                                      US6610836-B1
                                                                                                                                                                                                                        29-JAN-1999;
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                                                                                                                                                      26-AUG-2003
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25-AUG-1999
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                                                                                                                                                                                                                                                                                           Breton GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigenic
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Matches

RESULT 58 AAY34400

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THE SECTION OF SECTION

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Gaps

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This invention describes novel isolated Streptococcus pneumoniae polymucleotides (see AAZ96173-256494) and their encoded proteins (see AAX95792-Y86182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of such a polypeptide. They can also be used to expression or activity of interact with and inhibit or activate such a polypeptide. The polypeptide for DNA encoding them, via agene therapy) are also useful for inhibit such bacterial polypeptides. The polypeptides to inhibit such bacterial polypeptides. The polypeptides are particularly useful to identify antimicrobial compounds and antibiotics. They are also useful to determine their role in pathogenesis of infection, dysfunction and disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
Streptococcus pneumoniae proteins and related DNA - useful for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 24570; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 2; Length 225;
Pred. No. 3e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 24570.
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                                                  Claim 5; Page 338-339; 640pp; English
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                  compounds for antibacterial activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB65926 standard; protein; 225 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                  81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VMSAAEF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VXXXAEF
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                                                                                                                                                                                                                                                                                                                                               Sequence 225 AA;
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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insecticides, therapeutics and pharmaceutical drugs. The invention

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      gene; transgenic; enhanced seed oil; vegetable oil.
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                                                                                                                     Length 225
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                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ledeaux JR,
                                                                                                                     Score 18; DB 4;
Pred. No. 3e+03;
                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Oil-associated gene related protein #1093.
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                                                                                                                                                                                                                                                                                     Ā
                                                                                                                                                                                                                                                                                     ADJ49593 standard; protein; 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2002; 2002US-0365301P.
26-JUN-2002; 2002US-0391786P.
26-JUN-2002; 2002US-0392018P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2003; 2003US-00389566
                                                                                                                      81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                             (first entry)
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Matches 4; Conservative
                                                                                                                                                  4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAURIE C C.
RAVANELLO M.
SAVAGE T.
LEDEAUX J R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-142683/14.
                                                                                                                                                                                                           7 VITAÄËF 13
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                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                               7
                                                                                                                                                                              1 VXXXAEF
                                                                                           Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2004025202-A1
                                                                                                                                                                                                                                                                                                                                                                                                        oil-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant seed
                                                                                                                                                                                                                                                                                                                 ADJ49593;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RAVA/)
(SAVA/)
(LEDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROGE/)
                                                                                                                                                  Matches
                                                                                                                                                                                                                                                        RESULT 61
                                                                                                                                                                                                                                                                       4DJ49593
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The sequence is that of the polypeptide encoded by a region isolated from S. pneumoniae which shows homology to serine protease HtrA. The protein, or agonists of it, may be useful as an antibacterial for treatment or prevention of infection, specifically caused by S. pneumoniae (particularly meningitis) but possibly also Helicobacter pylori (ulcers and gastric cancer). It may be of particular use before insertion of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding it, can also be used in vaccines to induce a cellular and/or humoral immune response, or to screen for other antibacterials. The DNA may also contain flanking sequences that are potential sources of control elements for bacterial gene expression. Detecting a sequence encoding the protein can be used diagnostically, e.g. to detect a mutation for serotyping or classifying infectious agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soybean, protein phosphatase 2A, protein phosphorylation modulation, transgenic plant, gene therapy.
                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acids from Streptococcus pneumoniae - useful, for identifying anti-bacterial(s) for treatment and prevention of
                                          coding region; ORF; open reading frame; antibacterial; infection; prevention; meningitis.
                                                                                                                                                                                                                                                                                       Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean partial protein phosphatase 2A regulatory subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 2; Length 231;
Pred. No. 3.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                       Black MT, Hodgson JE, Knowles DJC, Lonetto MA,
               Streptococcus pneumoniae encoded polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY99822 standard; protein; 236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 85; 130pp; English.
                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                97WO-US019226.
                                                                                                                                                                                                             96US-0029930P
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57.1%;
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                                                                                          Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                     Zarfos PN;
                                                                                                                                                                                                                                                                                                                                     WPI; 1998-286586/25
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 231 AA;
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                                                                                                                                                                                27-OCT-1997;
                                                                                                                                                                                                              01-NOV-1996;
                                                                                                                    WO9819689-A1
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                                                                                                                                                                                                                                                                                                                                                                                                               meningitis.
                                                                                                                                                                                                                                                                                                        Reid RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY99822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene. The construct is useful for transgenic plant seed which has in its genome the construct, that is functional in the plant to transcribe the oil-associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents the amino acid sequence of an oil-associated gene related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                           oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rogers JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 8; Length 228; Pred. No. 3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Savage T, Ledeaux JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                Oil-associated gene related protein #1077.
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                                                                                                     ADJ49577 standard; protein; 228 AA
                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2002; 2002US-0365301P.
26-JUN-2002; 2002US-0391786P.
26-JUN-2002; 2002US-0392018P.
                                                                                                                                                                                                                                                                                                                                                   14-MAR-2003; 2003US-00389566.
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                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laurie CC, Ravanello M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAVANELLO M.
SAVAGE T.
LEDEAUX J R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SAVA/) SAVAGE T.
(LEDE/) LEDEAUX J R
(ROGE/) ROGERS J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-142683/14
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                            VEAAAEF 47
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VXXXAEF 7
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                                                                                                                                                                                                                                                                                       US2004025202-A1.
                                                                                                                                                                  06-MAY-2004
                                                                                                                                                                                                                                                                                                                     05-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant seed
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                                                                                                                                    ADJ49577;
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AAG27923 standard; protein; 239 AA.
                                             Example 2; Fig 8; 48pp; English
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99US-0123180P.
99US-0125788P.
99US-012654P.
99US-0126788P.
99US-012678P.
99US-0128734P.
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99US-0134256P.
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99US-0132487P.
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                     167 VTTVAEF 173
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                1 VXXXAEF 7
                                                                                                                                                            therapeutic agents
                                                                                                                                                                                 Sequence 236 AA;
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                                                                                                                                                                                                     The present sequence is soybean protein phosphatase 2A regulatory subunit
                                                                                                                                             Polynucleotides encoding plant protein phosphatase useful for modulating reversible protein phosphorylation in plants.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease; HtrA; protein removal; periplasm; virulence factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Hultgren SJ, Hruby DE, Franke CA, Evans AK;
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                                                                                         Klein TM;
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57.1%; Pred. No. 3.1e+03;
ive 0; Mismatches 3; Indels
                                                                                        Rafalski JA,
                                                                                        Lee J,
                                                                 (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB61537 standard; protein; 236 AA.
                                                                                                                                                                               Claim 12; Page 62; 73pp; English
                                                                                        Sakai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SIGA-) SIGA TECHNOLOGIES INC (UNIW ) UNIV WASHINGTON.
                      99WO-US029823
                                            98US-0112541P
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nes 4; Conservative
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                                                                                        Famodu OO, Miao G,
                                                                                                              WPI; 2000-431599/37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalytic domain.
                                                                                                                          N-PSDB; AAA48577
                                                                                                                                                                                                                                                                                                                                                           Sequence 236 AA;
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                    15-DEC-1999;
                                            16-DEC-1998;
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22-JUN-2000
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AAB61537
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Assay for DegP protease inhibitors useful as therapeutic agents, involves mixing inhibitor of DegP activity with DegP and major pilin subunit of Pap pilus as substrate and detecting changes in DegP activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%; Score 18; DB 4; Length 236; 57.1%; Pred. No. 3.1e+03; ive 0; Mismatches 3; Indels
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99US-0145276P. 99US-0145913P. 99US-0145918P. 99US-014591P. 99US-014538P. 99US-014638BP. 99US-014638P. 99US-0147304P. 99US-0147204P.	99US-0147260P. 99US-0147303P. 99US-0147416P. 99US-0147935P. 99US-01481319P. 99US-0148684P. 99US-0148684P. 99US-0149668P. 99US-0149668P. 99US-0149175P. 99US-0149175P. 99US-0149722P. 99US-0149722P.	990S-0150864P- 990S-0150884P- 990S-0151066P- 990S-0151080P- 990S-015130P- 990S-015303P- 990S-015303P- 990S-015378B- 990S-015378B- 990S-015403P- 990S-015403P- 990S-015403P- 990S-015403P- 990S-015403P- 990S-015403P- 990S-015408P- 990S-015408P-	990S-015711779 990S-0157865P 990S-0158029P 990S-0158232P 990S-0158293P 990S-0158293P 990S-0158293P 990S-0158231P 990S-0159331P 990S-0159331P 990S-0159638P 990S-016976P 990S-016076P 990S-016076P 990S-016076P 990S-016076P 990S-016076P 990S-016076P 990S-016076P
26-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 02-AUG-1999; 03-AUG-1999; 04-AUG-1999; 04-AUG-1999; 04-AUG-1999; 04-AUG-1999; 06-AUG-1999;	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	25-AUG-1999; 26-AUG-1999; 27-AUG-1999; 27-AUG-1999; 31-AUG-1999; 31-AUG-1999; 01-SEP-1999; 13-SEP-1999; 15-SEP-1999; 16-SEP-1999; 16-SEP-1999; 22-SEP-1999; 24-SEP-1999; 24-SEP-1999; 28-SEP-1999; 28-SEP-1999; 28-SEP-1999; 28-SEP-1999;	04-00T-1999; 06-00T-1999; 08-00T-1999; 12-00T-1999; 13-00T-1999; 13-00T-1999; 14-00T-1999; 14-00T-1999; 14-00T-1999; 14-00T-1999; 14-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999; 21-00T-1999;
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908-01 908-01 908-01 908-01 908-01 908-01 908-01 908-01	908-01 908-01 908-01 908-01 908-01 908-01 908-01 908-01 908-01 908-01 908-01 908-01 908-01	900S-01 900S-01 900S-01 900S-01 900S-01 900S-01 900S-01 900S-01 900S-01 900S-01 900S-01 900S-01	99US-01435242F. 99US-01443624P. 99US-0144085P. 99US-0144085P. 99US-0144332P. 99US-0144332P. 99US-0144332P. 99US-0144332P. 99US-0144332P. 99US-0144332P. 99US-0144332P. 99US-0144332P. 99US-0144332P. 99US-0144884P. 99US-0145088P. 99US-0145088P. 99US-0145088P. 99US-0145088P. 99US-0145088P.
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Matches

RESULT 67 AAR9719

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The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (IMTR) polypeptide activity. The method comprises contacting an NIMR polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the midliators. NIMR mucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIMR expression and activity. These modulators can be used to reduce the infection infection a surface, and the virulence of a microbe in a subject suffering from an infection. AAU29129-AAU291379 represent Escherichia coli NIMR amino acid sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bscherichia coli, major nitroreductase protein, NfsA, Vibrio harveyi, NADH oxidoreductase Frp; flavin reductase P; enzyme; antibacterial; antituberculostatic, vulnerary; antiinflammatory; virucide; auditory; antitubsive; litholytic; nephrotropic; gastrointestinal; antilocer; bacterial growth inhibitor; bacterial infection; microbial infection; tuberculosis; respiratory infection; prondhitis; sinualtis; pneumonia; sore throat; diphtheria; acute epiglottitis; influenza; ottis media; bronchopneumonia; Legionnaire's disease; whooping cough; urethritis; cystitis; pyelonephritis; colitis; enteritis; gastric ulcer; cholera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound.
                                                                                                       mar regulated polypeptide; NIMR; microbial infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   major nitroreductase protein NfsA amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%; Score 18; DB 4; Length 240
57.1%; Pred. No. 3.2e+03;
.ive 0; Mismatches 3; Indels
                                                                    Novel mar regulated protein (NIMR) #51.
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                                                                                                                                                                                                                                                            08-MAR-2001; 2001WO-US007478.
                                                                                                                                                                                                                                                                                                 10-MAR-2000; 2000US-0188362P
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                                 18-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                           Barbosa TM,
                                                                                                                                                                                                                                                                                                                                      (TUFT ) TUFTS COLLEGE
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                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-602769,
N-PSDB; AAS46278
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                                                                                                                                                                                  WO200170776-A2.
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                                                                                                                                                                                                                                                                                                                                                                           Levy SB,
AAU29379;
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Matches
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ABP57429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of the nitroreductase enzyme ncoded by the E.coli nfsA gene. The gene was isolated as given in Kumar and Jayaraman, (1991) J.Bioscence, 16, 145-159, and was subcloned to produc the plasmid pAJ102. The gene can be used to generate strains of E.coli which are senstive to mutagenic and carcinogenic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E. coli nitro:reductase gene - useful to produce mutagen or carcinogen sensitive strain, using E. coli host.
                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                      Length 239;
                                                                                                                                                                                                                                           3; Indels
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Pred. No. 3.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E.coli nitroreductase protein.
                                 99US-0161406P.
99US-0161359P.
99US-0161360P.
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                                                                                                                            99US-0161992P.
                                                                                                                                                                                                      81.8%;
57.1%;
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                 99US-0161405P
                                                                                                                                                                 99US-0162142P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                   191 VITRAEF 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHCC ) CHISSO CORP.
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                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT32986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 240 AA;
             25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP08131176-A
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                                                                                                                            28-OCT-1999
28-OCT-1999
                                                                                                                                                                 29-OCT-1999
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Gaps

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RESULT 68 AAU29379 ID AAU29 XX

Matches

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Length 240;

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                                                                                                                                                                                                                                                                                                heterocyclic compounds (I) to their salts. (I) has antibacterial, antituberculostatic, vulnerary, antiinflammatory, virucide, auditory, antituberculostatic, nephrotropic, gastrointestinal and antiulcer activities, and can be used as a bacterial growth inhibitor. (I) can be used for treating bacterial or microbial infection and tuberculosis in wound cleaning methods (e.g. wipes or gavage); for treating upper and in wound cleaning methods (e.g. wipes or gavage); for treating upper and lower respiratory tract infections (e.g. bronchitis, sinualis, consented plates). The consented is a similar, chronic streptococcal infections dipthheria, acute epiglotitis, influenza, chronic bronchitis, middle ear infections (ctitis media) bronchopneumonia, regionnaire's disease, atypical pneumonia or whooping cough), urinary tract infections (e.g. urethritis, cystitis, pyelonephritis (kidney infection), asymptomatic bacterial cystitis, acute urethral syndrome or recurrent urinary tract infections or infections (e.g. tood consenting), asymptomatic bacterial uresticis, pastrointestinal infections, cholera or typhus). (I) can be used for inhibiting bacterial growth in a non-living system. The present sequence represente an E. coli major nitroreductase protein NfaA which is given in comparison with a NADH oxidoreductase protein NfaA which is communishing acute inventive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                   nitrofuran containing heterocyclic compounds useful in treating e.g.
                                                                                                                                                                           Clement JJ;
                                                                                                                                                                                                                                                                                            present invention describes nitrofuran compounds substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 240;
                                                                                                                                                                           Ali J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                         Magee AS, Roy A, Moe ST, Griffith JP, Ala PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 6;
Pred. No. 3.2e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention
duodenal ulcer; pancreatitis; typhus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP57430 standard; protein; 240 AA.
                                                                                                                                        (ESSE-) ESSENTIAL THERAPEUTICS INC.
                                                                                                                                                                                                                                                                     Disclosure; Page 23; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                          25-JUN-2002; 2002WO-US020387.
                                                                                                                  25-JUN-2001; 2001US-0300636P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 5/...
4; Conservative
                                                                                                                                                    (PLIV ) PLIVA DD ZAGREB
                                                                                                                                                                                                         WPI; 2003-201374/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VXXXAEF 7
                        Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 240 AA;
                                             WO2003000255-A1.
                                                                                                                                                                                                                                               tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-APR-2003
                                                                    03-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP57430;
                                                                                                                                                                                     Navia M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 70
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Escherichia coli; major nitroreductase protein; NFsA; Vibrio harveyi; NADH oxidoreductase Frp; flavin reductase P; enzyme; antibacterial;

NADH oxidoreductase Frp (flavin reductase P) amino acid sequence.

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The present interactions distributed by the conception of the present interpresent in present interacts and the concording of the conceptions of the conceptions of the conceptions of the conception of the conce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nitrofuran containing heterocyclic compounds useful in treating e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clement JJ;
antitussive; litholytic; nephrotropic; gastroinfestinal; antiulcer; bacterial growth inhibitor; bacterial infection; microbial infection; tuberculosis; respiratory infection; bronchitis; sinusitis; pneumonia sore throat; diphtheria; acute epiglottitis; influenza; otitis media; bronchoneumonia; leggionnaire s disease; whooping cough; urethritis; cystitis; pyelonephritis; colitis; enteritis; gastric ulcer; cholera; duodenal ulcer; pancreatitis; typhus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes nitrofuran compounds substituted with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 3.2e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ali J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Griffith JP, Ala PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ESSE-) ESSENTIAL THERAPEUTICS INC. (PLIV ) PLIVA DD ZAGREB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 23; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-2002; 2002WO-US020387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Magee AS, Roy A, Moe ST,
Navia M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1-
---a 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-201374/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 VAQAAEF 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003000255-A1.
                                                                                                                                                                                                                                                                                                                                                                                   Vibrio harveyi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2003
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomybilitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies polypeptides may acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by curryen linked immunosorbent assay (ELISA). Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes predicted ORF-encoded polypeptide #28230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.8%; Score 18; DB 4; Length 247; 57.1%; Pred. No. 3.3e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                      Mitcham JL, Wang SS,
                                                                  dermatological; osteopathic; neuroprotectant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 28230; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABM63554 standard; protein; 247 AA.
                                                                                                                                                                                                                           21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                             20-APR-2001; 2001WO-US012865
                                                                                                                                                                                                                                                                                                                    Persing DH, M;
e J, Zhang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                 Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                      2001-616774/71.
                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                       L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS59774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 247 AA;
                                                                                                                              WO200181581-A2.
                                                                                                                                                             01-NOV-2001
                                                                                                                                                                                                                                                                                                                      Skeiky YAW,
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                                                                                                             Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patterson MA, Agius CT, Rothel LJ, Margetts MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigenic Porphorymonas gingivalis peptides for preventing gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes immunogenic protein #27931.
                                                                               gingivalis protein PG65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 524-525; 588pp; English.
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98AU-00003654.
98AU-00004917.
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98AU-00002264.
98AU-00002911.
98AU-00003128.
                                                                                                                                                                                                                                                         98WO-AU001023
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              (revised)
(revised)
(first entry)
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                                                                                                                                                            Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ross BC, Barr IG, Pa
Hocking DM, Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-385613/32.
N-PSDB; AAX91752.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CSLC-) CSL LTD.
                                                                               Porphorymonas
              27-AUG-2003
20-MAR-2003
25-AUG-1999
                                                                                                                                                                                          WO9929870-A1
                                                                                                                                                                                                                                                         10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1998;
                                                                                                                                                                                                                         17-JUN-1999
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23-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1998
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                                                                                                                                                                                                                                                                                                                                       LO-MAR-1998
                                                                                                                               antigenic.
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Bhatia A;

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Gaps

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AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAX34883. AAX91802 to AAX91898 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                          Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigenic Porphorymonas gingivalis peptides for preventing gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agius CT, Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 2; Length 248
Pred. No. 3.3e+03;
0; Mismatches 3; Indels
                                                                                                   Porphorymonas gingivalis protein PG65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patterson MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 372; 588pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB69168 standard; protein; 249
                                                                                                                                                                                                                                                                                                                                                                                            97AU-00001182.
98AU-00001546.
98AU-00002264.
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Similarity 57.1%;
4; Conservative
                                                          (first entry)
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                                                                                                                                                                                                         Porphyromonas gingivalis
                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-385613/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barr IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VXXXAEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX91619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSLC-) CSL LTD.
                                                                                                                                                                                                                                                W09929870-A1.
                 27-AUG-2003
20-MAR-2003
25-AUG-1999
                                                                                                                                                                                                                                                                                                                                10-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                           10-DEC-1997
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30-JUL-1998
                                                                                                                                                                  antigenic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ross BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB69168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding a Propionibacterium acres protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acres polypeptides. The invention additionally encompasses expression vectors and host cells comprising a ddittionally encompasses expression vectors and host cells comprising a polypeptide of the invention; antibodies against polypeptides of the invention; polypeptide of the invention; antibodies specific for a P. acres invention; accine composition (comprising T cells prepared via this method; a vaccine composition (comprising T cells prepared via this method; a vaccine composition (comprising P. acres polypeptides, polymeric presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acres in a patient; and a method for inhibiting the development of P. acres in a patient; The P. acres polypeptides, polymericating cells that express the polypeptides are useful for antigen-presenting cells that express the polypeptides are useful for adiagonsing, preventing or treating acre polypeptides are useful for adiagonsing, preventing or treating acre vulgaris, or for stimulating an immune response specific for a P. acres protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulating a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acres polymerication, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                     Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                Maisonneuve JL;
Jones R, Carte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                   Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 247;
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                                                                                                                                                                                                                                                                                                                                Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 6; I
Pred. No. 3.3e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 28230; 1481pp; English.
                                    immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                              Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY34401 standard; protein; 248 AA
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                                                                                                                                                                                                                                                                                                                           Mitcham JL, Skeiky YAW, Persi
Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                    11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.8%;
57.1%;
                                                                                                                                                                                                                                             15-OCT-2001; 2001US-00978825
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Best Local Similarity 57.1.
A; Conservative
                                                                             Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-381789/36.
N-PSDB; ACF64703.
                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 VAVTAEF 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 247 AA;
                                                                                                                    WO2003033515-A1
                                                                                                                                                             24-APR-2003
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Margetts MB;

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Gaps

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Drosophila melanogaster polypeptide SEQ ID NO 34296.

AAY34401

RESULT 74 AAY34401 ID AAY: XX AC AAY:

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Length 248;

Piraee M;

Farnet CM,

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Zazopoulos E,
                                    (ECOP-) ECOPIA BIOSCIENCES INC
07-AUG-2003; 2003US-0492997P.
10-NOV-2003; 2003US-0518286P.
                                                                                                                                                                                                                                                                                                                              81.8%;
57.1%;
                                                             Mcalpine JB,
                                                                                     WPI; 2004-593481/57.
N-PSDB; ADR01210, ADR01256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.1
Best A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osborne M;
                                                                                                                                                                                                                                                                                                                                                                                                      123 VAVAAEF 129
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                                                                                                                                                                                                                                                                              dibenzodiazepinone
                                                                                                                                                                                                                                                                                                                                                                              1 VXXXAEF
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                                                                                                                                                                                                                                                                                                      Sequence 253 AA
                                                             Bachmann BO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB063928;
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                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA equences (ABL16175) and the encoded proteins (ABB57277-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic, Antibacterial, Antiinflammatory, Cancer cell growth inhibitor, Lipooxygenase inhibitor, farnesyl dibenzodiazepinone, cancer, bacterial infections, inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.
                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Farnesyl dibenzodiazepinone biosynthetic ORF23 protein HYDK, SEQ ID
          Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 34296; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%; Score 18; DB 4; Length 249; 42.9%; Pred. No. 3.3e+03; cive 1; Mismatches 3; Indels
                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Micromonospora sp.; strain 046-EC011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR01255 standard; protein; 253 AA.
                                                                                                                                                                                                               PWD,
                                                                                                                          23-MAR-2001; 2001WO-US009231
                                                                                                                                                23-MAR-2000; 2000US-0191637P.
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Best Local Similarity 42.99,
E.ahes 3; Conservative
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                                                                                                                                                                                                               검
                                               Drosophila melanogaster.
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                                                                                                                                                                                                                                       2001-656860/75
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ISASAEF 53
                                                                                                                                                                                      (PEKE ) PE CORP NY.
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N-PSDB; ABL13271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 249 AA;
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                       pharmaceutical
                                                                        WO200171042-A2
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                                                                                                 27-SEP-2001
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                                                                                         The present invention relates to novel farnesyl dibenzodiazepinone compounds. The compounds can be obtained by cultivation of a novel strain of Micromonospora sp., i.e. 046-EC011 or [S01]046. The compounds are excellent tumour growth inhibitors as well mammalian lipooxygenase inhibitors and so are useful for treating cancer, pre-cancerous conditions, bacterial infections and inflammation in mammal. The present sequence is a protein involved in the biosynthetic pathway for a farnesyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for
  ð
                                                                                                                                                                                                                                                                                                                                                      Gaps
    the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding a Klebsiella pneumoniae polypeptide, preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                 Length 253;
                                                                                                                                                                                                                                                                                             Score 18; DB 8; Length 252.
Pred. No. 3.4e+03;
New farnesyl dibenzodiazepinone compounds useful for e.g. cancer, bacterial infections and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klebsiella pneumoniae polypeptide segid 10445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 10445; 932pp; English
                                                           Claim 53; SEQ ID NO 46; 269pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABO63928 standard; protein; 255
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AAG92053 standard; protein; 258 AA.
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                    carbohydrates or enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                       B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organic acid synthesis.
                                       Pompejus M, Kroeger
                                                                          WPI; 2001-061975/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                           N-PSDB; AAF71659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 258 AA;
   (BADI ) BASF AG
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AAG92053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diapty acid; compound; vitamin; cofactor; polyketide; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                 Gaps
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                                                                                                                           81.8%; Score 18; DB 7; Length 255; 57.1%; Pred. No. 3.4e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                 AAB79542 standard; protein; 258 AA.
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99DE-01042123.
99DE-01042125.
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99DE-01031413.
99DE-01031419.
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99US-0143208P.
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99DE-01042087.
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99DE-01031562.
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99DE-01031428
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                       VAQAAEF 91
                                                                                                                                                                                                   1 VXXXAEF 7
                                                                                                                                            Best Local Similarity
                                                                                         Sequence 255 AA;
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
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09-JUL-1999;
14-JUL-1999;
14-JUL-1999;
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                                                                                                                             Query Match
                                                                                                                                                                 Matches
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ID AAB778
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AAB77842
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DA AAB7787
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AAP71360 to AAF71750 encode the Corynebacterium glutamicum sugar metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 co. AAB 79633 which are involved in carbon metabolism and energy production. The C. glutamicum SMP gene can be used in vectors [II] for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a coloyketide, or an enzyme. The presonce of [I] or SMP proteins [III] encoded by them are used for diagnosing the presence or activity of corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to C. glutamicum, identify and localise C. glutamicum sequences of interest, in thunction, in modulating SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production in a cell (i.e. ATP, NADPH)
                                                                                                                                                                                                                                                                              New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids,
Haberhauer G;
      Schroeder H, Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 1004-1005; 1246pp; English.
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Score 18; DB 4; Length 258; Pred. No. 3.5e+03; 0; Mismatches 3; Indels

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Gaps

; 0

C glutamicum protein fragment SEQ ID NO: 5807.

Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

Yokoi H; Ochiai K, Hayashi M, Mizoguchi H, Ando S, Hayash Senoh A, Ikeda M, Ozaki A; Nakagawa S, Tateishi N,

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21-MAR-2000 (first entry)
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(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petersen J, Pizza M, I
Tettelin H, Venter JC;
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N-PSDB; AAZ54505.
                                                                                                                                                                                                                                                                                                                          39 VASNAEF 45
                                                                                                                                                                                                                                                                                                   1 VXXXAEF 7
N-PSDB; AAZ54506.
                                                                                                                                                                                                                                    Sequence 266 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                      AAY75743;
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                                                                                                       The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria and organic acids, nucleact acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent electronic form part directly from the European Patent Offlice
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                                        Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
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antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Masignani V, Mora M;
Scalato E, Scarselli M;
                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis ORF 981 protein sequence SEQ ID NO:2960.
                                                                                    Claim 17; SEQ ID NO 5807; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                             / Match 81.8%; Score 18; DB 4; Length 258; Local Similarity 57.1%; Pred. No. 3.5e+03; nes 4; Conservative 0; Mismatches 3; Indels
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Ratti (
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Tettelin H, Venter JC;
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98US-0094869P.
98US-009904P.
98US-0103749P.
98US-0103749P.
98US-0103794P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis.
          2001-376931/40
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          WPI; 2001-376931/
N-PSDB; AAH67272.
                                                                                                                                                                                                                                                         Sequence 258 AA;
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02-SEP-1998;
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09-OCT-1998
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                                                                                                                                                                                                                                                                              Query Match
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY5941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ5457 to AAZ5456 and AAZ54616 to AAZ5437 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols
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antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
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Scalato E, Scarselli M;
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Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics.
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, Pizza M, Rappuoli R, Ratti G,
                                                                                                           Claim 2; Page 1384; 1453pp; English.
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98US-0098994P.
98US-009662P.
98US-0103749P.
98US-0103744P.
98US-0103766P.
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Best Local Similarity 57.1%;
Matches 4; Conservative
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polypurcleotides of the invention may also be used in gene therapy protocols. (Updated on 12-SBP-2003 to standardise OS
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                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 3; Length 266; Pred. No. 3.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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                                  Claim 2; Page 1383; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY95653 standard; protein; 268 AA.
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99GB-0000952
99GB-0001946
99GB-00001048
99GB-00002074
99GB-00002078
99GB-0000208
99GB-00002879
99GB-00002879
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57.1%;
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vaccines and diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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N-PSDB; AAA50077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                              Sequence 266 AA;
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23-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
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                                                                               AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neiseeria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54571 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisesria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
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Scalato E, Scarselli M;
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Novel Neisserial polypeptides predicted to be useful antigens for
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                                                                                                                                                                                                                                                                                                                                                                                81.8%; Score 18; DB 3; Length 266; 57.1%; Pred. No. 3.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                   Page 1383; 1453pp; English
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   Pizza M, Rappuoli R,
   Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY75742 standard; protein; 266 AA.
                                                                                                                                                                                                                                                                                                              used in gene therapy protocols
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98US-0098994P.
98US-0099062P.
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98US-0103796P.
99US-0121528P.
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(GENO-) INST GENOMIC RES.
                 vaccines and diagnostics
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                                                                                                                                                                                                                                                                                                                                              Sequence 266 AA;
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Tettelin H,
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21-MAR-2000
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25-FEB-1999
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                                                   Claim 2;
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Matches
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                                                The present sequence is that of the protein product of the BASB071 gene (see AAA50077) of Neisseria meningitidis ATCC 13090. The protein contains aleader sequence, characteristic of a lipoprotein signal sequence, and aleader sequence, and shows significant similarity to the Neisseria gonorrhoeae His protein. The invention provides novel N. meningitidis BASB051, BASB057, BASB060, BASB061, BASB065, BASB066, BASB066, BASB067, DAYSP646 and the polynucleotides (see AAA50070-77) encoding them. These polypeptides and polynucleotides are used to produce medicaments, especially vaccines, to generate immune responses in an animal (claimed). Antibodies directed against the polypeptides are used in the treatment of N. meningitidis disease (claimed). The polypeptides and polynucleotides can also be used as diagnostic reagents for the diagnosis or staging of N. meningitidis disease, and for the detection of an infectious organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a peptide (I) encoded by an operon (II) of Neisseria meningitidis including virulence genes, or a related molecule having a 40% sequence similarity at the peptide or nucleotide level in a Gram-negative bacterium, or its functional fragment, for therapeutic or diagnostic use. (I) and (II) are useful in the manufacture of a mandicament for treating or preventing a condition (e.g., meningatis) associated with infection by Neisseria or Gram-negative bacteria. The product is useful for veterinary treatment and in a screening assay for
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU72995 standard; protein; 268 AA.
                   Claim 1; Page 110; 127pp; English.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                   response to a drug
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                                                                                                                                                                                                                                                                                                                                        Sequence 268 AA;
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The invention relates to an isolated nucleic acid comprising any one of the fall antisanse sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid conformation of a cell antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide, (5) inhibiting cellular proliferation or the activity of a gene in an operor required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological dentifying a gene required for cellular proliferation or the biological continuation and product or the thest compound that inhibits proliferation of an or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
the identification of an antimicrobial drug. The vaccines have prophylactic applications. AAU72911-AAU73014 represent N. meningitidis virulence proteins of the invention
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Xu HH;
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                                                                                                              Score 18; DB 5; Length 268;
Pred. No. 3.6e+03;
0; Mismatches 3; Indels
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                            ABU37163 standard; protein; 268 AA
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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57.1%;
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Trawick JD,
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Best Local Similarity
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                                                                                Sequence 268 AA;
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Wall D,
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compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent CC to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required CC for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids cequired for proliferation in cells other than S. aureus, S. typhimurium, CC required for proliferation in cells other than S. aureus, S. typhimurium, CC required for proliferation genes. Note: The sequence data for this parent did not form part of the printed specification, but was obtained con electronic format directly from WIPO at CC in electronic format directly from WIPO at CC standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                            81.8%; Score 18; DB 6; Length 268; 57.1%; Pred. No. 3.6e+03; ive 0; Mismatches 3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #23623.
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Yamamoto R,
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Matches 4; Conservative
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Trawick JD,
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                                                                                                                                                                                                                                                                                                           Sequence 268 AA;
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25-OCT-2001;
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polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding cle the polypeptide; (5) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gnee product or that has an activity against a biological pathway consideration, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids frequired for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in alloration forms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 6; Length 268;
Pred. No. 3.6e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; infection; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. gonorrhoeae amino acid sequence SEQ ID 6550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monaci E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 664; 815pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP80010 standard; protein; 269 AA.
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57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  format
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 268 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wla NK, Khare R;
Baughn MR, Gietzen KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; thyromimetic; gene therapy; cell proliferative disorder; cancer; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; immune disorder; inflammatory disorder; AIDS; allergy; developmental disorder; Hypothyroidism; Cushing's syndrome; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a human kinase and phosphatase protein designated KPP-16. Human KPP sequences have cytostatic, anticonvulsant, nootropic, neuroprotective, creebroprotective, anti-HIV, antiallergic, antiinflammatory and thyromimetic activities, and can be used in gene therapy. The human KPP polypeptides and polypuls of the invention are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of KPP, such as cell
antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABPP76736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                                                  Gaps
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J, Gururajan R, Baughn MR, Gietz
Jero KD, Becha SD, Richardson TW;
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                                                                                                                                                             Score 18; DB 6; Length 269;
Pred. No. 3.6e+03;
                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; kinase; phosphatase; enzyme; KPP; cytostatic;
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Yue H, Lee EA, Marquis JP;
                                                                                                                                                                                                0; Mismatches
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Elliott VS, Tran UK, Ramkumar J,
                                                                                                                                                                                                                                                                                                                                                            ADN61450 standard; protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human KPP-16 protein SEQ ID NO:16.
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26-NOV-2002; 2002US-0429766P.
11-FEB-2003; 2003US-0447043P.
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                                                                                                                                                             81.8%;
                                                                                                                                                                            57.18;
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                                                                                                                                                                                                  4; Conservative
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Jin P, Hawkins PR,
                                                                                                                                                                                                                                                                       48
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                                                                                                                                                                                                                                  1 VXXXAEF 7
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Best Local Similarity
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                                                                                                                                                                                                                                                                     VASNAEF
                                                                                                                            Sequence 269 AA;
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                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neglected target tissue antigen; NTTA; autoimmunity; autoimmune response; immunotherapeutic agent; insulin dependent diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
proliferative (e.g. cancer, atherosclerosis), neurological (e.g. AIDS, epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome) disorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of KPP. The KPP sequences or their fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Administration of neglected target tissue antigens to modulate immune
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Pred. No. 3.6e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY57069 standard; protein; 271 AA
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                                                                                                                                                                                                                                                                                 81.8%;
57.1%;
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     1 VXXXAEF
                                                                                                                                                                                                                                          Sequence 269 AA;
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                                                                                                                                                                                                  polypeptide
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target determinants used as agents promoting tolerance agents have failed to induce an effective regulatory T cell response. NTTAs as agents promoting tolerance are anticipated to be safer than use of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomolatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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Wang ZW;
                                                                                                                                              Gaps
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J, Zhang J, Ren F, Chen R,
Goodrich R;
                                                                                                           81.8%; Score 18; DB 3; Length 271; 57.1%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                       AAM78464 standard; protein; 271 AA.
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20-JUN-2000; 2000US-00560875.
19-JUL-2000; 2000US-00654936.
01-SEP-2000; 2000US-00654936.
20-CCT-2000; 2000US-00663561.
20-CCT-2000; 2000US-0069325.
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                                                                                                                                                                                                                                                                                                                                                                                    Human protein SEQ ID NO 1126.
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                                                                                                                                            4; Conservative
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                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                          1 VXXXAEF
                                                                               Sequence 271 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157190-A2
                                                determinants
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Ma Y, Zh
Xue AJ,
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                                                                                                                               Best Loc
Matches
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The present invention describes a method (M1) for diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, or determining the prognosis or outcome of a cancer patient. M1 involves providing a set of genes that are differentially expressed in cancerous or non-cancerous conditions, determining the expression levels of the set of genes and calculating a ratio of the expression levels of the differentially expressed genes. M1 is useful for diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, where the cancer is malignant pleural mesothelioma (MPM), lung adenocarcinoma, squamous carcinoma, medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell lymphoma, follicular lymphoma and ovarian cancer, and for determining prognosis or outcome of a cancer patient. The ratio of expression levels cancer class, and/or cancer prognosis, all of which are useful for determining a course of treatment of a patient. The present sequence
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 relevant pages from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing cancer cells in tissue sample, or determining prognosis or outcome of cancer patient, by calculating ratio of expression levels of genes that are differentially expressed in cancer and non cancer tissues.
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer, malignant pleural mesothelioma; MPM; lung adenocarcinoma; squamous carcinoma; medulloblastoma; prostate cancer; breast cancer; diffuse large B-cell lymphoma; follicular lymphoma; ovarian cancer;
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                                                                                        Length 271;
                                                                                        Score 18; DB 4; Length 271
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
(AAK52582) and 3666 (AAM80020) are omitted as the releval sequence listing were missing at the time of publication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                    Calretinin (calbindin 2) SEQ ID NO:16.
                                                                                                                                                                                                                                                                                       ADB70324 standard; protein; 271 AA.
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                                                                                      h 81.8%;
Similarity 57.1%;
4; Conservative
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                                                                                                                                                                                                 VGSSAEF 112
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                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                           1 VXXXAEF 7
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                                                      Sequence 271 AA;
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Sequence 271 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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Score 18; DB 7; Length 271;
Pred. No. 3.7e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                      ADE63979 standard; protein; 271 AA.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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         Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                          1 VXXXAEF 7
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The invention discloses a composition comprising two or more isolated rat

or human polynucleotides or a polynucleotide which represents a fragment,

derivative or allelic variation of the nucleic acid sequence. Also

claimed are a vector comprising the novel polynucleotide, a host cell

comprising the vector, a method for identifying a nucleotide sequence

which is differentially regulated in an animal subjected to pain and a

tito perform the method, an array, a method for identifying an agent

that increases or decreases the expression of the polynucleotide sequence

that is differentially expressed in neuronal tissue of a first animal

subjected to pain, a method for identifying a compound which regulates

the expression of a polynucleotide sequence which is differentially

compound that regulates the activity of one or more of the

polynucleotides, a method for producing a pharmaceutical composition, a

method for identifying a compound or small molecule that regulates the

compound that regulates the activity of one or more of the

specification, a method for identifying a compound useful in treating

copyreptides or their antibodies. The polynucleotide or the compound

plan and a pharmaceutical composition comprising the one or more

polyneptides or their antibodies. The polynucleotide or the compound

modulates its activity is useful for preparing a medicament for treating
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specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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                                                                                                                                                                                      81.8%; Score 18; DB 7; Length 271; 57.1%; Pred. No. 3.7e+03; ive 0; Mismatches 3; Indels
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                    Sequence 271 AA;
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a fit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound or small molecule that regulates the activity of one or more of the method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the
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pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. 3.7e+03;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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Best Local Similarity 57...
A; Conservative
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                                                                                                                                                            Sequence 271 AA;
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specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypoptides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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Best Local Similarity
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polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the method for identifying a compound or small molecule that regulates the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of diagnosing the presence of cancer cells or non-cancer cells in a tissue sample, determining prognosis or outcome of a cancer patient, selecting a course of treatment for a subject having or suspected of having malignant pleural mesothelioma (MPM) and evaluating treatment of MPM comprising determining the ratio of the expression level of a set of genes differentially expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, malignant pleural mesothelioma, MPM; tumour, lung adenocarcinoma, squamous carcinoma, medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell lymphoma, follicular lymphoma, ovarian cancer,
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that regulates the activity of one or more of the
                                                                                                                                                                                                                                                                                                                                                         81.8%; Score 18; DB 7; Length 271; 57.1%; Pred. No. 3.7e+03; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human malignant pleural mesothelioma (MPM) protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gullans SR, Bueno R;
                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 77; SEQ ID NO 16; 53pp; English.
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                                                                                                                                                                                                                                                                                                                    Sequence 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS2003219760-A1
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squamous carcinoma, medulloblastoma, prostate cancer, breast cancer, diffuse large B-cell lymphoma, follicular lymphoma and ovarian cancer. The method is useful for diagnosing MPM in a subject suspected of having MPM which involves obtaining a tissue sample suspected of being cancerous from a subject and determining the expression of nucleic acid markers or its expression products in the tissue sample. This sequence represents a human MPM protein of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridiaation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
cancer tissue. The cancer is chosen from MPM, lung adenocarcinoma,
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99US-0132485P.
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99US-0134218P.
99US-0134219P.
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57.1%;
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Matches 4; Conserv
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16-APR-1999
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19-MAY-1999
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated oplypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a gene in an operon required for required for that has an activity against a biological pathway in which a proliferation or the tinhibites cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibition; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene
                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                        Gaps
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                                                                                                Score 18; DB 3; Length 284;
Pred. No. 3.9e+03;
0; Mismatches 3; Indels
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Forsyth RA,
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Yamamoto R,
                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                         ABU44257 standard; protein; 288 AA
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Carr GJ,
99US-0161361P.
99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
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06-SEP-2001; 2001US-00948993.
25-GCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                     81.8%;
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                                                                                                                                      Conservative
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Trawick JD,
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N-PSDB; ACA48127.
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29-OCT-1999;
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28-OCT-1999
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to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fite.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, avaccine composition (comprising P. acnes polypeptides) and this method; a vaccine composition (comprising P. acnes polypeptides).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
product is overexpressed or underexpressed; (12) determining the extent
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Jones R, Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                      Score 18; DB 6; Length 288;
Pred. No. 3.9e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic polypeptide #29488.
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Lodes MJ, Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; SEQ ID NO 29488; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM64812 standard; protein; 290 AA.
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Barth B, Vallieve-Douglass J;
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57.1%;
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Best Local Similarity 57.10,
Best Local 4; Conservative
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ng S, Jen S,
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                                                                                                                                                                                                                                                                                                 Sequence 288 AA;
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9905-0145088P
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contigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynuclectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the collopeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynuclectides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the catimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a specifically claimed P. acnes polypeptide which is this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                  81.8%; Score 18; DB 6; Length 290; 57.1%; Pred. No. 3.9e+03; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                 AAG49548 standard; protein; 294 AA
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99US-0123548P.
99US-0125788P.
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Best Local Similarity 57.1
Matches 4; Conservative
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25-MAR-1999;
01-APR-1999;
06-APR-1999;
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30-APR-1999;
06-MAY-1999;
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RR 27-JUL-1999; 99US-0145231P.
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RR 23-AUG-1999; 99US-015563P.
RR 23-AUG-1999; 9
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PR 22-OCT-1999; 99US-0160989P.
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PR 28-OCT-1999; 90US-0161932P.
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Search completed: June 13, 2005, 13:55:56 Job time : 131 secs

135, App 158, App 23, Appl

Title: Perfect score:

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Sequence 158, Apples equence 23, Apples equence 2, Appli Sequence 2, Appli Sequence 11504, Apples equence 115076 Patent No. 5187076 Patent No. 5187076
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Sequence 89, Appl
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Sequence 24, Appl
Sequence 12, Appl
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                                                                                                                                                                    Sequence 106, Apple Sequence 24, Apple Sequence 24, Apple Patent No. 5204252 Patent No. 5204252 Patent No. 5204252 Sequence 158, Apple Sequence 296, Apple Sequence 12873, Apple Sequence 14188, Apple Sequence 14188, Apple Sequence 16718, Apple Sequence 262, Apple Sequence 18326, Apple Sequence 250, Apple Sequence 18326, Apple Sequence 2400, Apple Sequenc
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Copyright (c) 1993 - 2005 Compugen Ltd
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0S-09-22-991A-16774
0S-09-111-16-346
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Sequence 203: Sequence 242: Sequence 255: Sequence 126:			Sequence 8, Appli Sequence 8, Appli																																																					
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-09-270-767-43252 Sequence -09-248-796A-15773 Sequence -09-328-352-4431 Sequence -07-741-940-6 Sequence	S-08-289-548A-6 Sequence S-08-452-654-6 Sequence	S-08-452-65555-6 S-08-865-336-3 Sequence	S-08-865-336-4 Sequence S-08-450-582-6 Sequence	S-08-449-731-6 Sequence S-07-956-700B-8 Sequence	S-08-476-537-8 Sequence	S-08-485-607-8 Sequence S-08-475-879-8 Sequence	S-09-433-043B-8 Sequence	S-09-248-796A-19854 Sequence S-08-779-764A-29 Semience	S-09-563-456-29 Sequence	Sequence	S-09-328-352-6184 Sequence S-09-270-767-58211 Sequence	S-07-741-940-4 Sequence	S-08-289-548A-4 Sequence	S-08-452-654-4 Sequence	Sequence	S-08-430-382-4 Sequence S-08-449-731-4 Semience	-09-543-681A-6648 Sequence	-07-956-700B-21 Sequence	-08-476-537-21 Sequence	-08-485-607-21 Sequence	Sequence	-09-433-043B-21 Sequence	-09-489-039A-13347 Sequence	-09-10/-332A-4412 Sequence	Sequence	-09-540-236-2107 Sequence	-09-265-585C-126 Sequence	Sequence	-03-270-707-33337 Sequence	-09-107-433-3575 Seguence	-09-252-991A-22212 Sequence	-09-270-767-44034 Sequence	-09-46I-920F-4 sequence	S-10-253-016E-4 S-09-253-9918-30991 Sequence	S-08-858-2072-331 Semience	S-09-252-991A-18196 Semience	S-09-583-110-4372 Seguence	S-09-902-540-10278 Sequence	S-09-543-681A-8270 Sequence	S-09-583-110-4236 Sequence	S-09-489-039A-9274 Sequence	S-09-107-433-3706 Sequence	Sequence	8-09-10/-53ZA-544Z Sequence	2-03-110-213-10 2-09-543-6813-5469 Sequence	-03-343-001A-3439 Sequence	Seguence	-08-403-866-9 Sequence	-09-270-767-44219 Sequence	-09-270-767-40279 Sequence	-09-270-767-55495 Sequence	S-09-328-352-7671 Sequence	S-09-489-039A-12539 Sequence	Sequence	S-09-583-110-3285 Sequence	Sequence
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RESULT 3

US-10-400-902-24

Sequence 24, Application US/10400902

Sequence 24, Application US/10400902

Patent No. 6790640

GENERAL INFORMATION:
APPLICANT: Carfet, David L.
APPLICANT: Exich, Dudley
APPLICANT: Exich, Dudley
TITLE OF INVENTION: USE OF CYPEZAZA PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
TITLE OF INVENTION: USE OF CYPEZAZA PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
FILE REFERENCE: U0012 OS/OAAP (1010-49)
CURRENT APPLICATION NUMBER: US/10/400,902

CURRENT FILING DATE: 2003-03-31

PRIOR PILING DATE: 2001-07-24

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/09911781
Factor No. 6673613
GENERAL INFORMATION:
APPLICANT: Craft, David L.
APPLICANT: Elrich, Dudley
APPLICANT: Elrich, Dudley
APPLICANT: Elrich, Dudley
APPLICANT: Birich, Dudley
APPLICANT: SAGO 10 NOS: 34
SGOTWARE: PatentIn version 3.1
SEQ ID NO 24
EBNGTH: 267
TYPE: PRT.
APPLICANT: APPLICANT
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APPLICANT: Gleeson, Martin

TITLE OF INVENTION: CYTOCHROME P450 MONOXYGENASE AND NADPH CYTOCHROME P450

TITLE OF INVENTION: CYTOCHROME P450 MONOXYGENASE AND NADPH CYTOCHROME P450

TITLE OF INVENTION: CYTOCHROME GENES AND PROTEINS RELATED TO THE OMEGA

TITLE OF INVENTION: RELATING THERETO

FILE REFERENCE: 1010-16.seq

CURRENT PAPLICATION NUMBER: U5/99/302,620B

CURRENT PAPLICATION NUMBER: 1999-04-30

NUMBER OF SEQ ID NOS: 109

SOFTWARE: PATENTING DATE: 2.1

SEQ ID NO 106

LENGTH: 267

TYPE: PRT
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Pred. No. 4.7e+02;
0; Mismatches 3; Indels
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Pred. No. 4.7e+02;
0; Mismatches 3; Indels
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Best Local Similarity 57.1%;
Matches 4; Conservative
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4; Conservative
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US-09-302-620B-106
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US-09-911-781-24
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Matches
                                      Sequence 912, App
Sequence 118, App
Sequence 119, App
Sequence 753, Ap
Sequence 22, Appli
Sequence 21567, A
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Sequence 2911, Ap
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US-09-538-022-932
US-09-433-043B-119
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US-09-433-043B-119
US-09-433-043B-119
US-09-433-043B-119
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US-09-128-325-6123
US-09-128-326-24
US-09-129-366-24
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US-09-949-016-5971
US-09-949-016-5971
US-09-949-016-5971
US-09-949-016-5971
US-09-579-181-2
US-09-578-366-67
US-09-578-366-67
US-09-578-368-67
US-09-724-566A-73
US-09-724-566A-83
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US-09-302-620B-106
Sequence 106, Application US/09302620B
Parent No. 6331420
GENERAL INFORMATION:
APPLICANT: Wilson, C. Ron
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Eshoo, Mark
APPLICANT: Cornett, Cathy A.
APPLICANT: Banner, Alfred A.
APPLICANT: Loper, John C.
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39 VTTTAEF 45
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Best Local Similarity
Matches 4; Conserv
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TITLE OF INVENTION: CANDIDA TROPICALIS TRANSFORMATION SYSTEM
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                          TITLE OF INTERNATION: CANDIDA TROPICALIS TRANSFORMATION SYSTEM NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/386,837
FILING DATE: 27-JUL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 308,481
FILING DATE: 08-FEB-1989
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Patent No. 5204252

PAPLICANT: CREGG, JAMES M.; GLEESON, MARTIN A.; HAAS, LISA

PICATAGGIO, STEPHEN

TITLE OF INVENTION: CANDIDA TROPICALIS TRANSFORMATION SYSTEM

NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

PILING DATE: 27-JUL-1989

PRIOR APPLICATION NUMBER: 308,481

FILING DATE: 08-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 86.4%; Score 19; DB 6; Length 267; Similarity 57.1%; Pred. No. 4.7e+02; 4; Conservative 0; Mismatches 3; Indels
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                                                                                Length 267;
                                                                                                                 3; Indels
                                                                                                                                                                                                                                                       ;Patent No. 5204252
; APPLICANT: CREGG, JAMES M.;GLEESON, MARTIN A.;HAAS, LISA
;PICATAGGIO, STEPHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Patent No. 5204252; AMES M.; GLEBSON, MARTIN A.; HAAS, LISA;
                                                                                Score 19; DB 4; I
Pred. No. 4.7e+02;
                                                                                                               0; Mismatches
                                                                              86.4%;
             ; TYPE: PRT
; ORGANISM: Candida tropicalis
US-10-400-902-24
                                                               Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                              39 VTTTAEF 45
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Best Local Similarity
Matches 4; Conserv
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LENGTH: 267
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5204252-2
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| CURRENT ADDITIONTON NUMBER: US/7/186, 937 |
| PRINCE ADDITION NUMBER: US/7/186, 937 |
| PRINCE ADDITION NUMBER: US/7/186, 937 |
| PRINCE ADDITION NUMBER: US/8/186, 938 |
| PRINCE ADDITION NUMBER: US/8/186, 938 |
| PRINCE ADDITION NUMBER: US/9/2/886, 143 |
| PRINCE ADDITION NU
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PINCUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 2709, 2004001
CURRENT FILLING DATE: 2000-01-27
PRIOR RAPLICATION NUMBER: US 60/117,747
PRIOR FILLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Holland, Ross
APPLICANT: Holland, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: O'Toole, Paul W.
APPLICANT: Colbear, Timothy
ITILE OF INVENTION: Polynucleotides, materials incorporating
ITILE OF INVENTION: them and methods for using them.
FILE REFERENCE: 11000.1043U1
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 296
INVENTION OF SEQ ID NOS: 472
CORPANISM: Lactobacillus rhamnosus
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Pred. No. 7.4e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%; Score 18; DB 4; Length 179; 57.1%; Pred. No. 6.1e+02; ive 0; Mismatches 3; Indels
                                            Length 89;
                                         Score 18; DB 4; 1
Pred. No. 2.8e+02;
0; Mismatches 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12873, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                              US-09-634-238-296
; Sequence 296, Application US/09634238
Patent No. 6544772
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         Glenn, Matthew
Havukkala, Ilkka J.
Bloksberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
Christensson, Anna C.
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; ORGANISM: Klebsiella pneumoniae
;US-09-489-039A-12873
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57.1%;
                                            Query Match 81.8%;
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 VSTIAEF 168
                                                                                                                                                                                        82 VSNTAEF 88
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US-09-489-039A-12873
US-09-949-016-9298
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patent No. 6812339

GENERAL INPORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TUTLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLLING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastsEQ for Windows Version 4.0

SEQ ID NO 9298
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                                                                                        . LOCATION: (55)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-288-143-158
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APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
TITLE OF INVENTION: NOVEL GENE EXPRESSED IN PROSTATE CANCER TITLE OF INVENTION: NOVEL GENE EXPRESSED IN PROSTATE CANCER FILE REFERENCE: 1703-021.US1
CURRENT APPLICATION NUMBER: US/09/410,132
CURRENT FILING DATE: 1999-09-30
EARLIER APPLICATION NUMBER: 60/102,572
EARLIER FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN DATE: 1999-07-28
SOFTWARE: PATENTIN DATE: 1999-07-28
IEARLIER PLING DATE: 1999-07-28
SOFTWARE: PATENTIN DATE: 1999-07-28
IEARLIER PLING DATE: 1999-07-28
IEARLIER PLING DATE: 1999-07-28
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Pred. No. 2.2e+02;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                  0; Mismatches
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
                 ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                             36 VAARAEF 42
                                                                                                                                                                                                                                                                                 1 VXXXAEF 7
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ORGANISM: Human
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US-09-949-016-9298
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US-09-410-132-4
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ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-16774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-16774
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Patent No. 6610836
GENERAL INFORMATION:
Patent No. 6610836
GENERAL INFORMATION:
TITLE OF INVENTION:
FILLE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
SEQUENCE OF US CONTROL OF U
                                                                                                                                                                                                   Sequence 34, Application US/09605858

Patent No. 6306619

GENERAL INFORMATION:
APPLICANT: LIU, Christopher
APPLICANT: LIU, Christopher
APPLICANT: HULTOREN, Scott J.
APPLICANT: HURBY, Dennis E.
APPLICANT: HURBY, Dennis E.
TITLE OF INVENTION: DEGP PERIPLASMIC PROTEASE, A NEW ANTI-INFECTIVE TARGET
TITLE OF INVENTION: DEGP PERIPLASMIC PROTEASE FUNCTION
TITLE OF INVENTION: AND AN IN VITRO ASSAY FOR DEGP PROTEASE FUNCTION
CURRENT FILING DATE: 2000-06-29
CURRENT FILING DATE: 2000-06-29
CURRENT FILING DATE: 2000-06-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%; Score 18; DB 4; Length 255; 57.1%; Pred. No. 9e+02; ive 0; Mismatches 3; Indels
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Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Ver. 2.0
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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186 VVSTAEF 192
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GRGANISM: SpneumhtrA
US-09-605-858-34
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US-09-902-540-14188
                                                                                                                                              RESULT 13
US-09-605-858-34
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LENGTH: 236
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Sequence 100, Application US/09583110

Sequence 100, Application US/09583110

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Parloo-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR APPLICATION NUMBER: US 60/081,533

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR APPLICATION NUMBER: US 60/051,553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16774, Application US/09252991A
Sequence 16774, Application US/09252991A
Sequence 16.551795
GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OP INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OP INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OP INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PLILNG DATE: 1999-02-18
PRIOR PLILNG DATE: 1998-02-18
PRIOR PLILNG DATE: 1998-02-18
PRIOR PLILNG DATE: 1998-07-27
SEQ ID NO 16774
SEQ ID NO 16774
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APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
FILE REFERENCE: 38-10(15849)B
CURRENT PPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR RPPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14188
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0
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APPLICANT: FORSYth, R. Allyn
APPLICANT: Chisen, Kari
APPLICANT: Chisen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
FILE REFERENCE: ELITRA, 106A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT APPLICATION NUMBER: US 60/164415
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-9
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 346
LENGTH: 347
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18326
LENGTH: 360
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81.8%; Score 18; DB 4; Length 338;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels
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Pred. No. 1.3e+03;
1; Mismatches 3;
                   PRIOR APPLICATION NUMBER: DE 19941390.8
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941391.6
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 442
SEQ ID NO 262
LENGTH: 338
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                                                                                                                                                                                                                                                                                            , ORGANISM: Corynebacterium glutamicum
US-09-602-777A-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 346, Application US/09711164
Patent No. 6589738
GENERAL INFORMATION:
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Best Local Similarity 42.9:
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US-09-711-164-346
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                                                                                                                                                                                                                                                                      TYPE: PRT
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PRIOR FLILING DATE: 1999-07-10
PRIOR FLILING DATE: 1999-07-14
PRIOR PRIOR PRILING DATE: 1999-07-14
PRIOR PRILING DA
                                                                                                                                                                                                                   Gaps
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                                                                                                                                                        Score 18; DB 4; Length 335;
Pred. No. 1.2e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Detent No. 6831165
                                                  TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-09-583-110-5099
                                                                                                                                                             81.8%;
57.1%;
                                                                                                                                                        Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                         224 VMSAAEF 230
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US-09-602-777A-262
SEQ ID NO 5099
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US-09-107-433-4600
Sequence 4600, Application US/09107433
Sequence 4600, Application US/09107433
Patent No. 6800744
Setuence 4600, Application US/09107433
Sequence 4600, Application US/09107433
Sequence 4600, Application US/09107433
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
THERAPEUTICS
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Pred. No. 1.5e+03;
0; Mismatches 3; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: CURNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
PILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown:
OPERATING SYSTEM: «Unknown:
SOFTWARE: «Unknown:
                                                                                                           Sequence 4402, Application US/09583110 Patent No. 6699703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pneumoniae
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TELEFAX: (781)893-8277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
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Best Local Similarity 57.1%;
Matches 4; Conservative
    211 ISTTAEF 217
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                                                                                                                                                                                                                                                                                              Sequence 15437, Application US/09902540
; Sequence 15437, Application US/09902540
; Patent No. 683347
; GENREAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION: UN/095, 902, 540
; CURRENT PLING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217, 883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15437
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Sequence 2, Application US/09410132

Sequence 3, Application US/09410132

GENERAL INFORMATION:

APPLICANT: Afar, Daniel E.

APPLICANT: Mitchell, Stephen C.

TITLE OF INVENTION: NOVEL GENE EXPRESSED IN PROSTATE CANCER

FILE REFERENCE: 1703-021. US1

CURRENT APPLICATION NUMBER: US/09/410,132

CURRENT APPLICATION NUMBER: 60/102,572

EARLIER FILING DATE: 1999-09-30

EARLIER FILING DATE: 1999-09-30

EARLIER FILING DATE: 1999-07-28

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO. 2

LENGTH: 387
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                                                                 Score 18; DB 4; Length 360;
Pred. No. 1.3e+03;
                                                                                                             3; Indels
                                                                                                           0; Mismatches
                                                              Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Myxococcus xanthus
; ORGANISM: Candida albicans
US-09-248-796A-18326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1
Lange 4; Conservative
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                                                                                                                                                                                                 112 VITSAEF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 VAAGAEF 224
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FOR DIAGNOS GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
APPLICANTON: NUCLEIC Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: PREMER: US/09/583,110
CURRENT APPLICANTON NUMBER: US 60/985,131
PRIOR PILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION UNMBER: US 60/051,553
NUMBER OF SEQ ID NOS: 5322
LENGTH: 397

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Sequence 4, Application US/08973275B
; Sequence 4, Application US/08973275B
; Patent No. 5958706
; GENERAL INFORMATION:
    APPLICANT: MAMINA, Shinji
; APPLICANT: NAMINA, Shinji
; APPLICANT: NAMINA, Shinji
; APPLICANT: NAMINA, Shinji
; TITLE OF INVENTION: FINE MAGNETIC PARTICLES CONTAINING USEFUL PROTEINS
; TITLE OF INVENTION: BOUND THERETO, PROCESS FOR PRODUCING THE SAME, AND USE
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: UNBER: US/08/973,275B
; CURRENT TAPLICATION NUMBER: US/09/701043
; EARLIER APPLICATION NUMBER: 1987-03-27
; EARLIER FILING DATE: 1997-03-27
; EARLIER FILING DATE: 1996-03-28
; EARLIER FILING DATE: 1996-03-28
; EARLIER FILING DATE: 1996-05-16
; EARLIER FILING DATE: 1996-05-16
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57.1%; Pred. No. 1.6e+03;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence 2, Application US/09122632 | Patent No. 6033878 | GENERAL INFORMATION: | GENERAL INFORMATION: | APPLICANT: Tadashi MATSUNAGA | TITLE OF INVENTION: PROTEIN-BOUND MAGNETIC PARTICLES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: TRANSMEM
LOCATION: (7)..(380)
OTHER INFORMATION: Membrane bound region of mag A protein.
                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 2; Length 434 Pred. No. 1.6e+03; 0; Mismatches 3; Indels
                      18-SEP-1995
                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/529,600D
FILING DATE: 18.5EP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-248700
FILING DATE: 16-SEP-1994
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Magnetospirillum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-529-600D-2
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Matches 4; Conserv
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US-09-122-632-2
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA;
TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA;
TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA;
TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA;
CURRENT REFERENCE: 2709.2004001
CURRENT PILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10042
LENGTH: 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.8%; Score 18; DB 4; Length 403; 57.1%; Pred. No. 1.5e+03; tive 0; Mismatches 3; Indels
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Patent No. 5861285

GENERAL INFORMATION:
APPLICANT: Tadashi MATSUNAGA
TITLE OF INVENTION: PROTEIN-BOUND MAGNETIC PARTICLES AND TITLE OF INVENTION: PROCESS OF PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
                                                                                                                                                                                        ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...400
SEQUENCE DESCRIPTION: SEQ ID NO: 4600:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                            LENGTH: 400 amino acids TYPE: amino acid
INFORMATION FOR SEQ ID NO: 4600:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                        SEQUENCE CHARACTERISTICS
                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 VrtvaEF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VAESAEF 187
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Matches 4; Conserv
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US-09-489-039A-10042
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US-08-529-600D-2
                                                                                                                                                                                                              PEATURE
                                                                                                                                                                                                                                                                                                                                                          Query Match
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Sequence 158, Application US/09684855
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Best Local Similarity 57.1%;
Matches 4; Conservative
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US-09-684-855-158
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US-09-328-352-7566
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US-09-488-265B-23
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57.1%; Pred. No. 1.6e+03;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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Patent No. 6599735

GENERAL INFORMATION:
APPLICANT: F. HOFFMATION:
CURRENT EDITION CONTINUOUS FERMENTATION PROCESS
TILE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
CURRENT APPLICATION NUMBER: US/09/684,855
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: EP 90121663.9
PRIOR FILING DATE: 1999-10-11
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PATENTIN OF: 2.0
SEQ ID NO 135
LENGTH: 440
    PROCESS OF PRODUCING THE SAME
TITLE OF INVENTION: PROCESS OF PRODUCING THE S. NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P. STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                          STATE: D.C.
COUNTRY: U.S.A.
ZID: 20005-391B
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122,632
FILING DATE: 18-SEP-1995
APPLICATION NUMBER: US/08/529,600
FILING DATE: 16-SEP-1995
APPLICATION NUMBER: US/68/529,600
FILING DATE: 16-SEP-1995
APPLICATION NUMBER: US/68/529,600
FILING DATE: 16-SEP-1995
APPLICATION NUMBER: US/68/529,600
FILING DATE: 16-SEP-1994
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acide
TYPE: amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.12
Best Local 4; Conservative
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-122-632-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: T. lanuginosa
US-09-684-855-135
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US-09-684-855-158

RESULT 30

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Sequence 7566, Application US/09328352

Batent No. 6562958

GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE REFERENCE: GTC99-03P8

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7566

LENGTH: 443
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Pred. No. 1.6e+03;
0; Mismatches 3; Indels
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PARENT NO. 6599735
GREMEAL INFORMATION:
APPLICANT: F. Hoffmann-La Roche AG
TITLE OF INTENTION: CONTINUOUS FERMENTATION PROCESS
FILE REFERENCE: C38435/111692
CURRENT APPLICATION NUMBER: US/09/684,855
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: EP 90121663.9
PRIOR FILING DATE: 1999-10.11
NUMBER OF SEQ ID NOS: 169
SQOTUMARE: PARENT NOS: 169
SQOTUMARE: PARENTIN VET. 2.0
SQOTUMARE: PARENTIN VET. 2.0
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TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESSE:
CITY: New York
STREET: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COUNTRY: U.S.A.
ZIP: 10174-6401
COUNTRY: U.S.A.
MEDIUM TYPE: Diskette
COMPUTER: NEW COMPUTER: Diskette
COMPUTER: NEW COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISK CO
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Pred. No. 1.8e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCETAMARE: FastSEG for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,642
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: US/08/819,825
FILING DATE: 18 **MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Phytase Variants
TITLE OF INVENTION: Phytase Variants
FILE REFERENCE: 5618.500-02
FILE REFERENCE: 5618.500-03
CURRENT APPLICATION NUMBER: US/09/273,871A
CURRENT FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: PA 1998 00407
PRIOR APPLICATION NUMBER: PA 1998 00407
PRIOR FILING DATE: 1998-03-13
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1998-06-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/09273871A Patent No. 6514495 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFRENCE/DOCKET NUMBER: 4758.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 VIASAEF 167
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SEQ ID NO 14
LENGTH: 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Berka, Randy M.
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
                                                                                                                                                  Gaps
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                                                                              Length 443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New TOTK
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
CORTANT: APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 4758.200-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 212 867 0238
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                              Score 18; DB 4; I Pred. No. 1.6e+03; 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 81.8%; Score 18; DB 2; I
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09163642
Patent No. 6221644
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides F.
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-819-825-2; Sequence 2, Application US/08819825; Patent No. 5865118; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 475 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                          Ouery Match
Best Local Similarity 57.1

4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-819-825-2
                                                                                                                                                                                                                                                                                  351 VAGTAÈF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 VIASAEF 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VXXXABF 7
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          US-09-328-352-7566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-163-642-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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Gaps

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Length 507;

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APPLICANT: JONES, WILLIAM K
APPLICANT: TUCKER, RONALD F
APPLICANT: RUBGER, DAVID C
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZEAYNAK, ENGIN
APPLICANT: ACUBERASAMPATH, THANGAVEL
APPLICANT: NUBRASAMPATH, THANGAVEL
APPLICANT: OZININGN: NOVEL MORPHOGENIC PROTEIN COMPOSITIONS
TITLE OF INVENTION: OF MATTER
                                                                                                                                                      Score 18; DB 4; Length 507
Pred. No. 1.9e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES,
ADDRESSEE: INC.
STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,335
FILING DATE: 04-MAR-1993
PRIOR APPLICATION NUMBER: US 07/971,091
FILING DATE: 03-NOV-1992
PRIOR APPLICATION NUMBER: US 07/946,235
FILING DATE: 16-SEP-1992
PRIOR APPLICATION NUMBER: US 07/946,235
FILING DATE: 16-SEP-1992
PRIOR APPLICATION NUMBER: US 07/938,336
FILING DATE: 08-AUG-1992
PRIOR APPLICATION NUMBER: US 07/923,780
FILING DATE: 31-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: 27,829
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             US-08-459-346-19; Sequence 19, Application US/08459346; Patent No. 5834179; GENERAL INFORMATION:
                                                                                                                                                      Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  513 amino acids
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                                                                                                                                                                                                                                                                                                            288 VITAAEF 294
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STRANDEDNESS: Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                          1 VXXXAEF 7
                          ; LENGTH: 507
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01748
     SEQ ID NO 11504
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Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

NUMBER OF SEQ ID NOS: 207012
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                                                                                                    Query Match 81.8%; Score 18; DB 4; Length 475; Best Local Similarity 57.1%; Pred. No. 1.8e+03; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
81.8%; Score 18; DB 4; Length 475;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 3: Indels
                                                                                                                                                                                                                                                                                                                                                                      US-10-1083-452-11

US-10-1083-452-14

US-10-1083-452-14

Patent No. 6689368

GENERAL INFORMATION:

TITLE OF INVENTION: Phytase Variants

FILE REFERENCE: 5618-560-03

CURRENT FILING DATE: 2002-02-26

PRIOR APPLICATION NUMBER: US/09/273,871

PRIOR PILING DATE: 1999-03-22

PRIOR APPLICATION NUMBER: PA 1998 00407

PRIOR PILING DATE: 1999-03-22

PRIOR PILING DATE: 1999-03-22

PRIOR PILING DATE: 1999-03-22

PRIOR PILING DATE: 1999-03-22

PRIOR PILING DATE: 1999-01-18

PRIOR FILING DATE: 1998-06-19

PRIOR PILING DATE: 1998-06-19

PRIOR PILING DATE: 1998-01-18

PRIOR PILING DATE: 1999-01-22

PRIOR PILING DATE: 1998-01-31

PRIOR PILING DATE: 1998-01-31

PRIOR PILING DATE: 1998-01-31

PRIOR PILING DATE: 1998-06-25

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 14

SEQ ID NO 14

SEQ ID NO 14
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosa
US-09-273-871A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Thermomyces lanuginosa
                                                                                                                                                                                                                                                       161 VIASAEF 167
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APPLICANT: Israel, David
Wolfman, Neil M.
TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
Heterodimers, Compositions and Methods of Use.
NUMBER OF SEQUENCES: 30
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                                          APPLICANT: JONES, WILLIAM K
APPLICANT: TUCKER, RONALD F
APPLICANT: RUEGER, DAVID C
APPLICANT: OPPERNANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: NUBERASAMPATH, THANGAVEL
TITLE OF INVENTION: OF MATTER
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 3; Length 513;
Pred. No. 1.9e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MCDIUM TYPE: Floppy disk
MCDUUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin DATA:
APPLICATION NUMBER: US/08/889,419
FILING DATE: 08-7UL-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/459,346
FILING DATE: O2-JUN-1995
ATTORNEY/ARENT INFORMATION:
NAME: MEYERY THOWAS C.
REGISTRATION NUMBER: 36,989
REFERENCY DOCKET NUMBER: CRP-081DVCN
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
FENTING TATA ACTION OCTORS
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..513
OCTHER INFORMATION: /note= "PRE-PRO-BMP6 (HUMAN)"
PUBLICATION INFORMATION:
AUTHORS: CELESTE,
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Parent Administrator, Testa, Hurwitz
ADDRESSEE: Thibeault, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08469411
Patent No. 6190880
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein
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DATE: 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                      USA
      Patent No. 6071708
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-469-411-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/07989847

Sequence 8, Application US/07989847

Sequence 8, Application US/07989847

GENERAL INFORMATION:

APPLICANT: Israel, David

APPLICANT: Wolfman, Neil M.

TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein

TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Legal Affairs, Genetics Institute, Inc.

STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                       DB 2; Length 513;
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                                              /note= "PRE-PRO-BMP6 (HUMAN)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02140-2387
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,847
                                                                                                                                                                                                                                     Score 18; DB 2; I
Pred. No. 1.9e+03;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.9e+03;
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NAME/KEY: Protein
LOCATION: 1..513
OTHER INFORMATION: /note= "PRE-PRO-BMP
PUBLICATION INFORMATION:
AUTHORS: CELESTE,
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: KADINOS, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE DOCKET NUMBER: GI-5192B
TELECOMMINICATION INFORMATION:
TELEPANE: 617-876-1170
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 19, Application US/08889419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 513 amino acide
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-07-989-847-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                   250 VVTAAEF 256
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                                                                                                                                            ; PAGES: 9843-9847
; DATE: 1991
US-08-459-346-19
                                                                                                                                                                                                                                                                                                                           1 VXXXAEF 7
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US-08-889-419-19
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US-07-989-847-8
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LOCATION: 1..513
OTHER INFORMATION: /note= "PRE-PRO-BMP
OTHLCATION INFORMATION:
PUBLICATION INFORMATION:
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                  ALLING DATE:
PELLING DATE:
PELLING DATE:
PRIOR APPLICATION NUMBER: US 08/029,335
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,091
FILING DATE: 03-NOV-1992
PRIOR APPLICATION NUMBER: US 07/946,235
FILING DATE: 16-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,336
FILING DATE: 08-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,780
FILING DATE: 31-JUL-1992
ATTORNEY/AGBNT INFORMATION:
NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: CRP-081CP
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
APPLICATION NUMBER: US/08/040,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                          FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 VVTAAEF 256
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DATE: 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VXXXAEF 7
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Matches
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APPLICANT: JUNES, WILLIAM K
APPLICANT: JUNES, WILLIAM K
APPLICANT: TUNCKER, DAVID C
APPLICANT: RUBERS, DAVID C
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: CARAYNAK, ENGIN
APPLICANT: KUBERSASMPATH, THANGAVEL
TITLE OF INVENTION: NOVEL MORPHOGENIC PROTEIN COMPOSITIONS
TITLE OF INVENTION: OF MATTER
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: INC.
STREET
STREET
STREET
CITY: HORKINTON
STREET
             ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                              COUNTRY: USA

ZIP: 01140-2187

COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,411
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 81.8%; Score 18; DB 3; Length 513; Best Local Similarity 57.1%; Pred. No. 1.9e+03; Matches 4; Conservative 0; Mismatches 3; Indels
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ZIP: 01748
COUNTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,542
FILING DATE:
FLILING DATE:
FLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI-5192B-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8622
TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-08-469-411-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-402-542-19
; Sequence 19, Application US/08402542
; Patent No. 6395883
; GENERAL INFORMATION:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 VVTAÄEF 256
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Gaps
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Factor No. 6533109

GENERAL INFORMATION:

APPLICANT: Israel, David

APPLICANT: Wolfman, Nell M.

TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein

TITLE OF INVENTION: Heterodimers, Compositions and Methods of Use.

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Legal Affairs, Genetics Institute, Inc.

STREET: 87 Cambridge

CITY: Cambridge

CITY: Ambridge

CITY: Ambridge
                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                    Match 81.8%; Score 18; DB 3; Length 513; Local Similarity 57.1%; Pred. No. 1.9e+03; les 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02140-2387
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: DEM PC Compatible
COMPUTER: Path PC COMPASS: SOFTWARE: PATHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/780,601A
FILING APTE:
/note= "PRE-PRO-BMP6 (HUMAN)"
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APPLICATION NO. 5187076

APPLICANT: WOZNEY, JOHN M.; WANG, ELIZABETH A.; ROSEN, VICKI A.;

CELESTE, ANTHONY J.

TITLE OF INVENTION: DNA SEQUENCES ENCODING BMP-6 PROTEINS

NUMBER OF SEQUENCES: 16

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 10/07/490,033

FILING DATE: 07-MAR-1990

PRIOR APPLICATION NUMBER: 370,544

FILING DATE: 03-JUN-1989

APPLICATION NUMBER: 329,610

FILING DATE: 04-MAY-1989

APPLICATION NUMBER: 329,610

FILING DATE: 08-MAR-1989

APPLICATION NUMBER: 179,100

FILING DATE: 08-MAR-1989

APPLICATION NUMBER: 179,100

FILING DATE: 08-MAR-1989

APPLICATION NUMBER: 179,101
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Pred. No. 1.9e+03;
0; Mismatches 3; Indels
                                                                                                  COMPUTER TEADABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NDATA:
APPLICATION NUMBER: PCT/US93/07189
FILING DATE: 19930729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..513
OTHER INFORMATION: /note= "PRE-PRO-BMPOUBLICATION INFORMATION:
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                        CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-(
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE GHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-APR-1988
APPLICATION NUMBER: 179,197
FILING DATE: 08-APR-1988
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57.1%;
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APPLICATION NUMBER: 28,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
STREET: 35 SOUTH STREET CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
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                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 6118, Application US/09949016
; Patent No. 6812339
; GENERAL INDORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CLOO1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR PELING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-00-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFFWARE: FastSEQ for Windows Version 4.0
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CORRESPONDENCE ADDRESS: ADDRESSE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                            1.9e+03;
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Pred. No. 1.9e+03
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/469,411
FILING DATE: 06-Jun-1995
ATTORNEY/AGENT INPORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI-5192B-CON
TELEPHONE: 617-498-8622
TELEPHONE: 617-498-8622
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application PC/TUS9307189 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 44
US-09-949-016-6118
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PCT-US93-07189-19
                                                                                                                                                                                                                                                                                                                                                                             US-09-780-601A-8
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LENGTH: 513
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CURRENT APPLICATION NUMBER: US/09/949,016
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                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
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Fatent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: C1001307
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;Patent No. 5187076
; APPLICANT: WOZNEY, JOHN M.;WANG, ELIZABETH A.;ROSEN,VICKI A.;
;CELESTE, ANTHONY J.
;CELESTE, ANTHONY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TABLE OF INVENTION: DNA SEQUENCES ENCODING BMP-6 PROTEINS
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/490,033
FILING DATE: 07-WAR-1990
APPLICATION NUMBER: 347,559
FILING DATE: 04-WAY-1989
APPLICATION NUMBER: 329,610
FILING DATE: 28-WAR-1989
APPLICATION NUMBER: 179,100
FILING DATE: 08-ARR-1988
APPLICATION NUMBER: 179,101
FILING DATE: 26-ARR-1988
APPLICATION NUMBER: 31,346
FILING DATE: 26-MAR-1987
APPLICATION NUMBER: 31,346
FILING DATE: 36-MAR-1987
                                                                                                                                                                                                                                                                                            81.8%; Score 18; DB 6; Length 513; 57.1%; Pred. No. 1.9e+03; ive 0; Mismatches 3; Indels
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FILING DATE: 20-MAR-1987
APPLICATION NUMBER: 31,346
FILING DATE: 26-MAR-1987
APPLICATION NUMBER: 943,322
FILING DATE: 17-DEC-1986
APPLICATION NUMBER: 880,776
FILING DATE: 01-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-JUL-1986
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity
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US-09-949-016-10103
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                                                                                                                                                                                                               LENGTH: 513
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Gequence 12, Application US/09828302
| Sequence 12, Application US/09828302
| Patent No. 6818805
| GENERAL INFORMATION:
| APPLICANT: COSTA E SILVA, OSWALDO DA
| APPLICANT: COSTA E SILVA, OSWALDO DA
| APPLICANT: GINAL, ROUYING
| APPLICANT: GINAL, ROUYING
| APPLICANT: GINAL, ROUYING
| TITLE OF INVENTION: PHOSPHATAASE STRESS-RELATED PROTEINS AND METHODS OF USE
| TITLE OF INVENTION: IN PLANTS
| FILE REFERENCE: 16333-0029
| CURRENT APPLICATION NUMBER: 60/196,001
| PRIOR APPLICATION NUMBER: 60/196,001
| PRIOR FILING DATE: 2000-04-07
| NUMBER OF SEQ ID NOS: 46
| SEQ ID NO 12
| LENGTH E DATE OF LENGTH E SASE OF THE SASE OF
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Patent No. 6812339
Facent No. 6812339
Facent No. 6812339
Facent No. 6812339
Facent No. 6812339
FACENTIAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION UNDER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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Pred. No. 2e+03;
0; Mismatches 3; Indels
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CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10103

LENGTH: 522
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Sequence 75, Application US/09268347

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

FILE REPERENCE: 1038-860

CURRENT APPLICATION NUMBER: US/09/268,347

CURRENT PILING DATE: 1999-03-16

NUMBER OF SEQ ID NOS: 54

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 45

LENGTH: 660
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| Sequence 46, Application US/09268347
| Sequence 46, Application US/09268347
| Patent No. 6335182
| General Information:
| APPLICANT: Loosmore, Sheena M. |
| TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS |
| FILE REFERENCE: 1038-860 |
| CURRENT APPLICATION UNBER: US/09/268,347 |
| CURRENT FILING DATE: 1999-03-16 |
| NUMBER OF SEQ ID NOS: 54 |
| SEQ ID NO 46 |
| LENGTH: 659 |
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                                                                                                                    Score 18; DB 4; Length 637;
Pred. No. 2.4e+03;
0; Mismatches 3; Indels
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Pred. No. 2.5e+03;
0; Mismatches 3; Indels
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Pred. No. 2.5e+03;
0; Mismatches 3; Indels
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; Sequence 31488, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Haemophilus influenzae
US-09-268-347-46
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                        Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                           TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                     213 VALSAEF 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   573 VASNAEF 579
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                                                                                 US-09-543-681A-5869
    SEQ ID NO 5869
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                         LENGTH: 637
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Patent No. 6605709
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF PALLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Construction of the construction of applicant: Applicant: Applicant: Johnson, Jerry L. APPLICANT: Allied, Carolyn C. APPLICANT: Allied, Carolyn C. APPLICANT: Extland, Beth C. APPLICANT: Will applicant: Waterials and Methods for the Alteration of Enzyme and TITLE OF INVENTION: Materials and Methods for the Alteration of Enzyme and TITLE OF INVENTION: Acetyl CoA Levels in Plants TITLE OF INVENTION: Acetyl CoA Levels in Plants CURRENT APPLICATION NUMBER: US/09/344,882 CURRENT APPLICATION NUMBER: US 60/090,717 PRIOR APPLICATION NUMBER: US 60/090,717 PRIOR PRIOR FILING DATE: 1999-06-25 NUMBER OF SEQ ID NOS: 38 SOOFWARE: PatentIn Ver: 2.2 SEQ ID NO 18 SEQ ID NO 18
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                                                                                                                                                                                                            DB 4; Length 563;
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                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                          81.8%; Score 18; DB 4; I
57.1%; Pred. No. 2.1e+03;
tive 0; Mismatches 3;
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11259
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 18, Application US/09344882; Patent No. 6764851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nikolau, Basil J
Wurtele, Eve S
Oliver, David J
Behal, Robert
Schnable, Patrick S
Ke, Jinshan
Johnson, Jerry L
Allred, Carolyn C
Fatland, Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Arabidopsis Thaliana
                                                                                                                                                                                      Ouery Match
Best Local Similarity 57...
4; Conservative
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Matches 4; Conservative
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                                                                                                                                              ; ORGANISM: Human
US-09-949-016-11259
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US-09-543-681A-5869
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US-09-344-882-18
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US-09-083-587-2
; Sequence 2, Application US/09083587
; Sequence 2, Application US/09083587
; Patent No. 6492138
; GENERAL INFORMATION:
; APPLICANT: Schmandt, et al.
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; NOVBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 233 SOUTH Wacker Drive/6300 Sears Tower CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 60606-6402 COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: BATENIT Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/083,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34451
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-6448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
DESCRIPTION: /desc = "hPAL peptide"
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40 King Street West
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TYPE: amino acid
STRANDEDNESS: not releva
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Matches 4; Conservative
471 VRTSAEF 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
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US-08-772-270A-12
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                  APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31488

LENGTH: 669
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| Sequence 2, Application US/09363708 |
| TITLE OF INVENTION: NOVEL SHC BINDING PROTEIN |
| TITLE OF INVENTION: NOVEL SHC BINDING PROTEIN |
| NUMBER OF SEQUENCES: 12 |
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun |
| STREET: 233 South Wacker Drive/6300 Sears Tower |
| CITY: Chicago |
| STARE: Illinois |
| COUNTRY: United States of America |
| COUNTRY: United States of America |
| CONDUTER: ISADBLE FORM: MEDIUM TYPE: ISADBLE FORM: MEDIUM TYPE: ISADBLE FORM: |
| COMPUTER: ISADBLE FORM: |
| COMPUTER: ISADBLE FORM: |
| REDIUM TYPE: ISADBLE FORM: |
| COMPUTER: ISADBLE FORM: |
| SOFTWARE: Patentin Release #1.0, Version #1.30 |
| CURRENT APPLICATION DATA: |
| PATENT ON DATA: |
| PATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 81.8%; Score 18; DB 4; Length 669; Best Local Similarity 57.1%; Pred. No. 2.6e+03; Matches 4; Conservative 0; Mismatches 3; Indels
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ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/34451
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6310
TELEPKX: (312) 474-6448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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DESCRIPTION: /desc = "hPAL peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
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57.1%;
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TYPE: amino acid
STRANDEDNESS: not releva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-09-363-708-2
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                                            Gaps
                                                                                                                                                                                                                               Sequence 12, Application US/08772270A

Parent No. 6019984

GENERAL INFORMATION:
APPLICANT: MacInnes, Janet
APPLICANT: Ricciati, Paul
APPLICANT: Rosendal, Soren
TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR
TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                            ö
81.8%; Score 18; DB 4; Length 672; 57.1%; Pred. No. 2.6e+03;
                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Beresh
STREET: 40 King 5
CITY: TOTONTO
STATE: ONLARIO
COUNTRY: Canada
ZIP: MSH 3Y2
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Redmond, Mark J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 VSSDAEF 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-248-796A-16379
                                                                                                                                                                                                                                                                            94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-603-133B-12
                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jackson, Stephen P
APPLICANT: Jackson, Stephen P
APPLICANT: Gell, David A
TITLE OF INVENTION: Interactions of Ku polypeptides and applications
TITLE OF INVENTION: Lhereof
FILE REFERENCE: 620-100
CURRENT APPLICATION NUMBER: US/09/569,037
CURRENT PILING DATE: 2000-05-11
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%; Score 18; DB 4; Length 728; 57.1%; Pred. No. 2.8e+03; tive 0; Mismatches 3; Indels
                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/772,270A
FILING DATE: December 23, 1996
CLASSIFICATION: 424
ATTONEY/AGENT INPORMATION:

NAME: Gravelle, Micheline
REGISTRATION NUMBER: 6580-81
FELERENCE/DOCKET NUMBER: 6580-81
TELECOMMULCATION INFORMATION:

TELECOMMULCATION INFORMATION:

TELEFACOMMULCATION INFORMATION:

TELEFACOMMULCATION INFORMATION:

TELEFACOMMULCATION INFORMATION:

TELEFACOMMULCATION INFORMATION:

TELEFACOMMULCATION OF SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 711 amino acids

TYPE: Amino acid

STRANDEDNESS: aingle

TYPE: Amino acid

STRANDEDNESS: aingle

TOPOLOCY: Incar
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/07603133B Patent No. 5298244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 59
US-09-569-037-8
; Sequence 8, Application US/09569037
; Patent No. 6753151
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-569-037-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 57.1
Matches 4, Conservative
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 VLSAÄEF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             718 VANAAEF 724
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US-07-603-133B-12
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Sequence 16379, Application US/09248796A

Facert No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
CURRENT FILING DATE: 1998-02-13
PRIOR PEDICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16379
LENGTH: 1010
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Pred. No. 4e+03;
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 1; Length 775; Pred. No. 3e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RODINS, RODERTE J.
REGISCHATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                           ADDRESSEE: Morrison & Poerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 775 amino acida
TYPE: AMINO ACID
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 327-295
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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81.8%; Score 18; DB 1; Length 1252; 57.1%; Pred. No. 5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,780
FILING DATE: 18-FEB-1994
CLASSIFICATION: 5.14
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David
REFERENCE/DOCKET NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMIC:002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 320-7200
TELEFRAME (512) 34-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
'.DMCTH: 1252 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:

COUNTRY:

ZIP:
77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 30.5EP-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/199,780
FILLING DATE: 30.5EP-1994
CLASSIFICATION NUMBER: US 08/199,780
FILLING DATE: 30.5EP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08316650
| Patent No. 5542496
| GENERAL INFORMATION:
| APPLICANT: Roessler, Bake J. APPLICANT: Roessler, Bake J. APPLICANT: Lin, Wushan | TITLE OF INVENTION: METHODS AND COMPOSITIONS | TITLE OF INVENTION: PER STIMULATING BONE CELLS | NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 15
CORRESSEONDENCE ADDRESS:
ADDRESSEB: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     941 VYSSAEF 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Best Local Similarity
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                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Texas
                                                                                                                     COUNTRY: USP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-316-650-3
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    Gaps
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    3; Indels
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Patent No. 5763416
GENERAL INFORMATION:
APPLICANT: Bonadio, Jeffrey
APPLICANT: Goldstein, Steven A.
TITLE OF INVENTION: Gene Transfer Into Bone Cells
TITLE OF INVENTION: And Tissues
                                                                                                                                                                                                                                                                                                                                                                                             STATE: DOUBLY:
STATE: TRABBLE
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02251
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION:
APPLICATION NUMBER: US 08/199,780
FILING DATE: 18-FEB-1994
CLASSIFICATION:
APPLICATION NUMBER: UNCO09P--
TELEFRANCE DOCKET NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 31,165
REFERENCE/DOCKET NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 32,165
REFERENCE/DOCKET NUMBER: 31,165
REFERENCE/DOCKET NUMBER: 32,165
REFERENCE/OFFET STATES
TELEFAX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LFNNTTH: 1251 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%; Score 18; DB 5;
57.1%; Pred. No. 5e+03;
tive 0; Mismatches
  0; Mismatches
                                                                                                                                                                                                                  GENERAL

APPLICANT:

TITLE OF INVENTION: METHOUS ....

TITLE OF INVENTION: CELLS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

CTREET: P.O. Box 4433
                                                                                                                                                RESULT 62
PCT-0895-02251-3
PSequence 3, Application PC/TUS9502251
; GENERAL INFORMATION:
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           940 VYSSAEF 946
                                                                                    621 VITEAEF 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
GY: linear
                                          1 VXXXAEF 7
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US-08-199-780-3
  Matches
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57.1%; Pred. No. 5e+03;
tive 0; Mismatches 3; Indels
                          Score 18; DB 3; Length 1253;
Pred. No. 5e+03;
                                                                                                                                                                                                                                                                                                               Ablicant: Defirey
APPLICANT: Bondio, Jeffrey
Yin, Wushan
TITLE OF INVENTION: LATENT TGF( BINDING PROTEIN (LTBP)
GENES, COMPOSITIONS AND METHODS
                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/592,685
FILING DATE: 12-Jun-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: 4100.000500/FUS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/479,722B
APPLICATION NUMBER: US/08/479,722B
APPLICATION NUMBER: US PCT/US95/02251
FILING DATE: 21-FEB-1995
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: US 08/199,780
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Williams, Morgan & Amerson
STREET: 7676 Hillmont, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 67
US-09-077-098A-7
; Sequence 7, Application US/09077098A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 77040
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1253 amino acids
                                                                                                                                                                                                                                                            Sequence 4, Application US/09592685 Patent No. 6774105 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (713) 934-7011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS
                          Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                941 VYSSAEF 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-592-685-4
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                                                                                                                                                                                                                                                                                                                             81.8%; Score 18; DB 2; Length 1252; 57.1%; Pred. No. 5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LATENT TGF ( BINDING PROTEIN (LTBP) GENES, COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTY: 1628

ZIP: 77040

COMPUTER READALE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,722B
FILING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fussey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: 4100.000500/FUS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US95/02251
FILING DATE: 21-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/199,780
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Williams, Morgan & Amerson
7676 Hillmont, Suite 250
                      REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMIC:008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08479722B
Patent No. 6074840
GENERAL INCORMATION:
APPLICANT: Bonadio, Jeffrey
APPLICANT: Yin, Wushan
TITLE OF INVENTION: LATENT TGF( BIN
TITLE OF INVENTION: GENES, COMPOSIT
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                          TELECHONDA.,
TELEPHONE. (5.-
TELEFAX: (713) 789-..
TELEX: 79-0924
; INPORMATION FOR SEG ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1252 amino acids
"VPE: amino acids
"VPE: amino acids
"VPE: amino acids
"VPE: amino acids
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
Parker, David L.
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                   TOPOLOGY: linear; MOLECULE TYPE: protein US-08-316-650-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-479-722B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                          941 VYSSAEF 947
                                                                                                                                                                                                                                                                                                                                                                                                                1 VXXXAEF 7
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STREET: 7676 Hi
CITY: Houston
STATE: Texas
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US-08-479-722B-4
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Sequence 6978, Application US/09949016

Sequence 6978, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTHARE: PSELSEQ for Windows Version 4.0

SEQ ID NO 6978

LENGTH: 4377
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Pred. No. 1.9e+04;
1; Mismatches 3; Indels
                                                                                                                                                                                         Length 3913;
                                                                                                                                                                                       Score 18; DB 4; Length 391
Pred. No. 1.7e+04;
1; Mismatches 3; Indels
                           ; NUMBER OF SEQ ID NOS: 207012
; SCPTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10933
; LENGTH: 3913
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27, Application US/09604608 Patent No. 6545127
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                                                                                                                                                                                           81.8%;
                                                                                                                                                                                       Query Match
Best Local Similarity 42.9
Matches 3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                2933 IATTAEF 2939
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APPLICANT: Tang, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                US-09-949-016-6978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-949-016-6978
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-09
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                                                                                                         MATSUO, Kazuo
HAWADA, Fukusaburo
TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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WEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,098A
FILING DATE: 19-May-1998
PRIOR APPLICATION NUMBER: PCT/JP97/03222
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: PCT/JP97/03222
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INPORMATION:
NAME: RORNBAU, Anne M.
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSES: BROWNY AND NEIMARK
STREET: 624 Winth Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 4; I
Pred. No. 8.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 10933, Application US/09949016
; Patent No. 6812339
Patent No. 6544519
GENERAL INFORMATION:
APPLICANT: TOKUNAGA, Eiji
SAKAGUCKI, Magaghi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2039 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%;
                                                                                                                                                                                                                                                                                                                                                      ZIP: 20001
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1
                                                                                                                                                                                                              NUMBER OF SEOUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 VAAGAEF 428
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US-09-949-016-10933
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Gaps

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APPLICANT: Tung, Jay
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConloque, Lisa
APPLICANT: McConloque, Lisa
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US/09/501,708
PRIOR PRILING DATE: 2000-02-10
PRIOR PILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
SOFTWARE: PSEC for Windows Version 4.0
SEQ ID NO 87
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, John P.
APPLICANT: Basi, Guirdpal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Pohn, Varghese
APPLICANT: Power, Michael
APPLICANT: Sower, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09724566A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: APP fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.3
Best Local Similarity 57.1
Matches 4; Conservative
                         atsuno, Gwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VXXXAEF 7
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; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Catalytically Active Recombinant Memapsin and Methods
; TILE OF INVENTION: Of Use Thereof
; PRIOR FILING DATE: 1999-06-28
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/140, 368
; PRIOR PILING DATE: 2000-01-25
; PRIOR PILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/170, 336
; PRIOR PILING DATE: 2000-01-25
; PRIOR FILING DATE: 2000-01-25
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                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-604-608-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Inhibitors
US-09-604-608-28
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                                                                                                                                                                                                                                                                                                                    3; Indels
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Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Frigon, Varghese
APPLICANT: Power, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
PRIOR FILING DATE: 2000-06-08
                                           PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1°
                    NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                  1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                 1 VNLAAEF 7
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US-09-724-566A-87
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US-09-604-608-28
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Gaps
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APPLICANT: Tung, Jay
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConJoque, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWS.
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/119,51
PRIOR FILING DATE: 2000-02-10
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 88
77.3%; Score 17; DB 4; Length 9; 57.1%; Pred. No. 4.1e+05; ive 0; Mismatches 3; Indels
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Gaps
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## APPLICANT: Tung, Jay
## APPLICANT: Tung, Jay
## APPLICANT: Tung, Jay
## APPLICANT: McConlogue, Lisa
## TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
## TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
## TITLE OF INVENTION: McMeds
## TITLE OF INVENTION: McMeds
## TITLE OF INVENTION: McMeds: 108/09/724,566A
## CURRENT FILING DATE: 2000-11-28
## PRIOR APPLICATION NUMBER: US/09/10-72
## PRIOR APPLICATION NUMBER: US/0119,571
## PRIOR FILING DATE: 1999-02-10
## PRIOR FILING DATE: 1999-02-10
## PRIOR FILING DATE: 1999-06-15
## NUMBER OF SEQ ID NOS: 104
## SOFTWARE: FastSEQ for Windows Version 4.0
## LENGTH: 9
## CONTROL OF THE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.3%; Score 17; DB 4; Length 9; Best Local Similarity 57.1%; Pred. No. 4.1e+05; Matches 4; Conservative 0; Mismatches 3; Indels
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      CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR FILING DATE: 2000-02-10
PRIOR PILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOUTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 93
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Boast, Guriqbal
APPLICANT: Boast, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Frigon, No. 6627739mand
APPLICANT: Frigon, No. 6827739mand
APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
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US-09-724-566A-94
; Sequence 94, Application US/09724566A
; Patent No. 6627739
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: APP fragment
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ORGANISM: Artificial Sequence
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APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
APPLICANT: Tatsuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Beta-Secretase
TITLE OF INVENTION: WINBER: US/09/724,566A
CURRENT APPLICATION NUMBER: US/09/501,708
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR PILING DATE: 1999-02-10
PRIOR PILING DATE: 1999-06-15
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APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
      Pred. No. 4.1e+05;
0; Mismatches 3; Indels
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SOFTWARE: PattSEQ for Windows Version 4.0
SEQ ID NO 89
LENGTH: 9
                                                                                                                                                                                                                                                              RESULT 74
US-09-724-566A-89
i Sequence 89, Application US/09724566A
i Patent No. 6627739
i GENERAL INFORMATION:
i APPLICANT: Anderson, John P.
APPLICANT: Basi, Guriqbal
i APPLICANT: Esti, Guriqbal
i APPLICANT: Frigon, No. 6627739mand
i APPLICANT: John, Varghese
i APPLICANT: John, Varghese
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PABERAL INFORMATION:
APPLICANT: Anderson, John P. APPLICANT: Dane, Minh Tam
APPLICANT: Dane, Minh Tam
APPLICANT: Prigon, No. 6627739mand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: APP fragment US-09-724-566A-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
57.1%;
   Best Local Similarity 57.1
Matches 4; Conservative
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Matches 4; Conservative
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Sinha, Sukanto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tatsuno, Gwen
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US-09-724-566A-93
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APPLICANT:
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: APP fragment
US-09-471-669A-88
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PRIOR FILING DATE: 1998-12-31
PRIOR PILING DATE: 1999-02-10
PRIOR PILING DATE: 1999-02-10
PRIOR PILING DATE: 1999-06-15
PRIOR PILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Basi, Guriqbal
Doane, Minh Tam
Frigon, No. 6830918mand
John, Varghese
Power, Michael
Sinha, Sukanto
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 89, Application US/09471669A
Patent No. 6830918
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Tung, Jay
Wang, Shuwen
McConloue, Lisa
Elan Pharmaceuticals, J
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57.1%;
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57.1%;
                    SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 88
LENGTH: 9
                                                                                                                                                                                            Query Match
Best Local Similarity 57.2.
4; Conservative
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NUMBER OF SEQ ID NOS: 108
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                    1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                               3 VNLAAEF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT: Wang, Shuwen
APPLICANT: Blan Pharmaceuticals, Inc.
TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
FILE REPERBENE: 05270-006430US
CURRENT APPLICATION NUMBER: US/09/471,669A
CURRENT APPLICATION NUMBER: US 60/114,408
PRIOR PRING DATE: 1998-12-34
PRIOR PILING DATE: 1998-12-10
PRIOR APPLICATION NUMBER: US 60/119,571
PRIOR APPLICATION NUMBER: US 60/119,571
PRIOR APPLICATION NUMBER: US 60/139,172
PRIOR PILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PATENTIN VOT: 2.1
SEQ ID NO 87

TENGTH: 9
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US-09-471-669A-87
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TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
FILE REPERENCE: 015270-006430US
CURRENT APPLICATION NUMBER: US/09/471,669A
CURRENT FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: US 60/114,408
PRIOR PLILING DATE: 1999-12-31
PRIOR PLILING DATE: 1999-12-31
PRIOR APPLICATION NUMBER: US 60/119,571
PRIOR APPLICATION NUMBER: US 60/119,172
PRIOR PLING DATE: 1999-02-10
PRIOR PLING DATE: 1999-06-15
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APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6830918mand
APPLICANT: John, Varghese
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuno, Gwen
                                                                                                  APPLICANT: Anderson, John P.
APPLICANT: Basi, Guriqbal
APPLICANT: Basi, Guriqbal
APPLICANT: Frigon, No. 6830918mand
APPLICANT: Proper, Michael
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Sukanto
                                      ; Sequence 87, Application US/09471669A; Patent No. 6830918; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-471-669A-88
; Sequence 88, Application US/09471669A
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ORGANISM: Artificial Sequence
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Wang, Shuwen
McConlogue, Lisa
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Best Local Similarity
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS FILE REFERENCE: 015270-006430US
CURRENT APPLICATION NUMBER: US/09/471,669A
CURRENT FILING DATE: 1999-12-24
PRIOR APPLICATION TOWNER: US/09/471,669A
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                                           3; Indels
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    Length 9;
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Score 17; DB 4; I
Pred. No. 4.1e+05;
0; Mismatches 3;
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; Sequence 93, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basi, Guriqbal
; APPLICANT: Doane, Minh Tam
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Sequence 12, Application US/08415751
Patent No. 564372
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: POLYPEPTIDES BII
TITLE OF INVENTION: CRYPTOSPORIDIUM
TITLE OF INVENTION: WETOR AND TRAN
TITLE OF INVENTION: WETOR AND TRAN
TITLE OF INVENTION: WETORS FOR INM
TITLE OF INVENTION: DIAGNOSIS AND K
NUMBER OF SEQUENCES: SO
CORRESPONDENCE ADDRESS:
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United States of America
                                                                                                                                                                                                                                                               Sequence 24, Application US/09634955B Patent No. 6511834
GENERAL INFORMATION:
                                          77.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1.
                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: Californi
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3 VNFAAEF 9
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                                                                                                                       1 VXXXAEF 7
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STREET: 389
  US-09-471-669A-94
                                                                                                                                                                                                                                                  US-09-634-955B-24
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US-08-415-751-12
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APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: Wang, Shuwen
APPLICANT: Mang, Shuwen
APPLICANT: Elan Pharmaccuticals, Inc.
TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
FILE REFERENCE: 015270 006430US
CURRENT FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: US 60/114,408
PRIOR FILING DATE: 1999-12-31
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 108
SOFFWARE: PATENTIN VOICE: 1209-06-15
NUMBER OF SEQ ID NOS: 108
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OTHER INFORMATION: Description of Artificial Sequence: APP fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: APP fragment
38-09-471-669A-93
                                                                                                                                                               APPLICANT: Elan Phármaceuticals, Inc.
TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
FILE REFERENCE: 015270-006430US
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                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/471,669A
CURRENT FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: US 60/114,408
FRIOR FILING DATE: 1998-12-31
PRIOR FILING DATE: 1998-02-10
PRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 94, Application US/09471669A Patent No. 6830918 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson, John P.
APPLICANT: Basi, Guriqbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6830918mand
APPLICANT: John, Varghese
Frigon, No. 6830918mand
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                      Tung, Jay
Wang, Shuwen
McConlogue, Lisa
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Sinha, Sukanto
Tatsuno, Gwen
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Best Local Similarity 57.1
Matches 4; Conservative
                                        Power, Michael
Sinha, Sukanto
                     John, Varghese
                                                                                Tatsuno, Gwen
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APPLICANT:
APPLICANT:
APPLICANT:
  APPLICANT:
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APPLICANT: Meyers, Rachel
APPLICANT: Cook, William James
TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL HUMAN DEHYDROGENASE
TITLE OF INVENTION: MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-134
CURRENT APPLICATION NUMBER: US/09/634,955B
CURRENT FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.

SEQ ID NO 24
LENGTH: 23
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                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.3%; Score 17; DB 4; Length 23; 57.1%; Pred. No. 1.38+02; tive 0; Mismatches 3; Indels
Score 17; DB 4; Length 9; Pred. No. 4.1e+05; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRYPTOSPORIDIUM ANTIBODIES, DNA AND RNA ENCODING THEM, HYBRID VCTCOR AND TRANSFORMED HOST AND METHODS FOR IMMUNOTHERAPY AND DIACNOSIS AND KIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage COMPUTER: PC OPERATING SYSTEM: DOS SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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APPLICANT: GARY BRETON
TITLE OF INVENTION: DIGGISCLE ACID AND ANINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR REPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
SRO ID NO 7973
LENGTH: 68
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; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH;
; LENA; HELDIN, CARL-HENRIN,
TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 53
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
FILING DATE: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSON-WELSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENA, HELDIN, CARL-HENRIK

TITLE OF INVENTION: ISOLATED NUCLECTIDE SEQUENCE EXPRESSING
HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
NUMBER OF SEQUENCES: 5
CURRENT APPLICATION DATA:
PELICATION NUMBER: 27-FEB-1990
                                                                                                                                                                                                                                                                                                                                                  Length 68;
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Pred. No. 4.3e+02;
0; Mismatches 3;
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Pred. No. 4.3e+02;
0; Mismatches 3.
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57.1%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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US-09-543-681A-7973
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity
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US-09-246-796A-24127, Application US/09248796A

Sequence 24127, Application US/09248796A

Sequence 24127, Application US/09248796A

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANT:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196-132

CURRENT APPLICATION NUMBER: US 60/094,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR PELLING DATE: 1998-02-13

PRIOR PELLING DATE: 1998-02-13

NUMBER: US 60/096,409

NUOS PLING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 24127
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Pred. No. 2.9e+02;
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57.1%; Pred. No. 4.1e+02;
tive 0; Mismatches 3,
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APPLICATION: 435

FILING DATE: 03-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: May 29, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY,AGENT INFORMATION:
NAME: Hana Dolezalova
REGISTRATION NUMBER: 480.19-
TELEPONE: (415) 324-1677
TELEPONE: (415) 324-1677
TELEPAX: (415) 324-1677
TELEPAX: (415) 324-1677
TELEPAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
TYPE: mino acid
TYPE: mino acid
TYPE: mino acid
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; Sequence 7973, Application US/09543681A
; Patent No. 6605709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.3%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 VKIAAEF 60
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Matches 4; Conserv
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Sequence 27, Application US/08479078
| Sequence 27, Application US/08479078
| Patent No. 584446
| GENERAL INFORMATION:
| APPLICANT: Pawson, Anthony | TITLE OF INVENTION: Method for Assaying for a Substance that | TITLE OF INVENTION: Method for Assaying for a Substance that | TITLE OF INVENTION: Method for Assaying for a Substance that | TITLE OF INVENTION: Method for Assaying for a Substance that | TITLE OF INVENTION: Method for Assaying for a Substance that | TITLE OF INVENTION: 27 | TITLE OF INVENTION: 27 | TOTONION | TO
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Sequence 185, Application US/08311731A

Patent No. 6583266

TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                Length 95;
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                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 77.3%; Score 17; DB 2; Le Best Local Similarity 57.1%; Pred. No. 6.2e+02; Matches 4; Conservative 0; Mismatches 3;
                                                                                                                                          Score 17; DB 4; 1
Pred. No. 6.1e+02;
0; Mismatches 3.
                     ORIGINAL SOURCE:
CREANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                          Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                          36 VRDAAEF 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 VKDAAEF 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VXXXAEF 7
                                                                                                                                                                                                                                                                   1 VXXXAEF
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-08-479-078-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-479-078-27
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 90
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                                                                                   Sequence 16636, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN.

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

FRICE REPERIONCE: 107196.132

PRIOR PELLICATION NUMBER: US 60/074,725

PRIOR PELLICATION NUMBER: US 60/074,725

PRIOR PELLICATION NUMBER: US 60/074,725

PRIOR PELLING DATE: 1998-02-13

PRIOR PELLING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 79. Application US/08311731A

Patent No. 6583266

GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS

APPLICANT: MAO, JEN-I

ITILE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 411
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COMPUTER READABLE FORM:
MEDIUM TYPEM FOODDATIBLE
COMPUTER: IS PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C. STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFRENCE/DOCKET NUMBER: C004.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.1%;
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 57.1 Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 VMKAAEF 41
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CITY: BOSTON
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US-08-311-731A-79
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APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OP SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 122;
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.3%; Score 17; DB 4; Le 42.9%; Pred. No. 8.1e+02; iive 1; Mismatches 3;
                                           NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (701)893-5007
TELEPHONE: (701)893-507
INFORMATION FOR SEQ ID NO: 5330:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: misc_feature
; LOCATION: (B) LÖCATION 1...122
; SEQUENCE DESCRIPTION: SEQ ID NO: 5330:
US-09-107-532A-5330
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                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 49, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 ITDTÄËF 24
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                           ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Maseachusetts
COUNTRY: USA
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
                     NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/ACENT INFORMATION:
NAME: GATES, BDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                            CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 VRDAAEF 59
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US-09-107-532A-5330
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                                                                                                                                                          COUNTRY:
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12 VREAAEF 18
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                                                                                                                                                                                                                                                                                                                                                 Sequence 49, Application US/09022765
Patent No. 6375955
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Read, Steven G.
APPLICANT: Webb, John R.
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHWANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OF SEQUENCES:
ADDRESSEE: SEED and BERRY LLP
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                                                                                                                                             77.3%; Score 17; DB 3; Length 136; 57.1%; Pred. No. 9.1e+02; tive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATORING NOTION PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Washington
COUNTRY: USA
ZIP. USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPANE: (2006) 622-4900
TELEPANE: (2006) 682-6031
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                        , ORGANISM: Leishmania chagasi
US-09-183-861-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Leishmania chagasi
US-09-022-765-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                           Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
           STRANDEDNESS: single
TOPOLOGY: linear
                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE:
amino acid
                                                                                                                                                                                                                                                               12 VREAAEF 18
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RESULT 95

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0
Sequence 49, Application US/09551974A

Sequence 49, Application US/09551974A

Patent No. 6500437

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Rebb, John R.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: TILE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C5
CURRENT APPLICATION NUMBER: US/09/551,974A

CURRENT FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 101

SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Billion, Bavin C.
APPLICANT: Braix, Ajay
APPLICANT: Braix, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Coler, Rhea
APPLICANT: Peter Probet
ITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
ITLE OF INVENTION: LEISHMANIA ANTIGENS OF LEISHMANIASIS
ITLE REFERENCE: 210121.420C6
CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILLIG DATE: 2000-00-05
NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 136;
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-565-501A-49
; Sequence 49; Application US/09565501A
; Patent No. 6607311
; GENERAL INFORMATION:
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Best Local Similarity 57.1%;
Matches 4; Conservative (
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Best Local Similarity 57.1%;
Matches 4; Conservative
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: LENGTH: 136

; TYPE: PRT

; ORGANISM: Leishmania chagasi

US-09-551-974A-49
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LENGTH: 136
TYPE: PRT
CORGANISM: Leishmania chagasi
US-09-565-501A-49
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Patent No. 6617156
BERERAL INFORMATION:
APPLICANT: LyAN DOUCELTE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Willon, Davin C.
APPLICANT: Billon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bheatia, Ajay
APPLICANT: Brabatia, Ajay
APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
APPLICANT: Probst, Peter
APPLICANT: PLEISHWANIA ANTIGENS FOR USE IN THE
CURRENT APPLICATION NUMBER: US/09/874,923
CURRENT PILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 136
TYPE: PRT
CREATING ANTISM: Leishmania chagasi
US-09-874-923-49
            APPLICANT: Dillion, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Coler, Ralea
APPLICANT: Probst, Peter
ITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210.21.4207;
CURRENT APPLICATION NUMBER: US/09/639,206A
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 136
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.3%;
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Leishmania chagasi
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Best Local Similarity 57.1
These 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
Webb, John R.
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US-09-874-923-49
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Sequence 14343, Application US/09248796A

APPLICANT: Keith Weinstock et al
APPLICANT: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANIC
TITLE OF INVENTION: NUCLBIC AND THERAPEUTICS

FILE REFERENCE: 107196-113

PRIOR APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1998-02-13

PRIOR PELING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 14343

LENGTH: 143
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Pred. No. 9.6e+02;
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CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
LENGTH: 143
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                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4544
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Sequence 106, App Sequence 106, App Sequence 5641, A Sequence 302302, Sequence 72638, A Sequence 72638, A Sequence 128132, Sequence 51691, A Sequence 51691, A Sequence 7569, A Sequence 7569, A Sequence 6737, App Sequence 6737, App Sequence 49, Appl Sequence 49, Appl Sequence 212707, Sequence 212707, Sequence 158, Appl Sequence 158, Appl Sequence 158, Appl Sequence 158, Appl

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1 US-10-139-218-106
1 US-10-405-602-24
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7 US-10-425-115-29937
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       Sequence 200225,
Sequence 161742,
Sequence 361705,
Sequence 24, Appl
Sequence 106, App
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                                                                                                                 June 13, 2005, 14:00:08; Search time 109 Seconds (without alignments) 24.618 Million cell updates/sec
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Sequence 237245. Sequence 243983. Sequence 243983. Sequence 228254. Sequence 128254. Sequence 255955. Sequence 14633. Sequence 146433. Sequence 146433. Sequence 146433. Sequence 146433. Sequence 146433. Sequence 146433.

237245, 243983, 275053,

Sequence 7611, Ap Sequence 199, App Sequence 199164, Sequence 162790,

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Sequence 119 Sequence 33 Sequence 81 Sequence 8, Sequence 23 Sequence 23 Sequence 25	Sequence 70 Sequence 70 Sequence 2 Sequence 12	Sequence 3 Sequence 6 Sequence 6	Sequence 1 Sequence 1 Sequence 1	Sequence 1: Sequence 1:	Sequence 18	Sequence 1 Sequence 2	Sequence 3	Sequence 2: Sequence 5:	Sequence 2	Sequence 7.	Sequence 1	Sequence 5	Sequence 1	Sequence 1	Sequence 1	Sequence 1	Sequence 5	Sequence 7	Sequence 4	Sequence 5		equence 2	sequence 28 equence 28		Sequence					
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46, Appl 274705, 274705, 600, App 114362, A	App Appl Appl 81, A	27, A 888,	3, Ap 47, A 85, A	08, A 110, A	42, A 45, A	115, A 121, A Appl	4, Ap 107, A	6, A 14, A	App	12, A 20, A	, App 8, Ap	63, A 195, A	73, A 47, A 982	, Ap 114,	Appii 516,	06, A	48, A 8, Ap	09, A 4, Ap	0, Ap	4, Ap	App	5, Ap	Appli	26, A Appl	App1	, AP 88, A	0, Ap	162, A	App	82, A
Sequence 45. Sequence 274 Sequence 5807 Sequence 600 Sequence 610 Sequence 650	Sequence 170 Sequence 16, Sequence 721	Sequence 383 Sequence 265 Sequence 265	Sequence 525 Sequence 130	Sequence 694 Sequence 670	Sequence 617 Sequence 624	Sequence 639 Sequence 648 Sequence 73,	Sequence 848 Sequence 448	Sequence 1334 Sequence 739			Sequence 346 Sequence 214						Sequence 742 Sequence 469											Sequence 121		
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 161742
LENGTH: 130
                                                                                                                         APPLICANT: LA ROYALLOW:

APPLICANT: LA ROYALLOW:

APPLICANT: Exou, Yihua

APPLICANT: Show, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Browsharov, Andrey A.

APPLICANT: Browsharov, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5321)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER: OF 100 NOS: 204966

SEQ ID NO 200225

LENGTH: 78
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Pred. No. 1e+03;
0; Mismatches 3; Indels
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US-10-437-963-161742
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LOCATION: (1)..(130)
PERT INFORMATION: unsure at all Xaa locations
PEATURE:
                                     RESULT 1
US-10-437-963-200225
; Sequence 200225, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Sequence 161742, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity 57.1%;
Matches 4; Conservative (
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ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
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Sequence 46, Appl
Sequence 47, Appl
Sequence 51, Appl
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Sequence 63, Appl
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US-10-424-599-225697
US-10-394-575-47
US-10-394-575-47
US-10-424-599-264908
US-10-674-475-273
US-10-474-599-199286
US-10-425-115-308930
US-10-424-599-166382
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US-10-425-115-301629
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US-10-801-487-143

US-10-801-487-144

US-10-801-938-144

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US-10-801-938-144

US-10-801-486-144

US-10-801-486-144

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US-10-818-92-17
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US-10-281-092-50
US-10-776-013-477
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APPLICANT: Trang, Maria
APPLICANT: Trang, Maria
APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
APPLICANT: Geneson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUC
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CFI
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REPERENCE: 1010-12
CURRENT APPLICATION NUMBER: US/09/976,800
CURRENT FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 106
LENGTH: 267
                                       Sequence 24, Application US/09911781
Patent No. US20020034788A1
GENERAL INFORMATION:
APPLICANT: Craft, David L.
APPLICANT: Elrich, Dudley
APPLICANT: Application USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
FILE REPRENCE: U0012 OS/0AAP (1010-49)
CURRENT PILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 24
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
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US-09-976-800-106
Sequence 106, Application US/09976800
Publication No. US20030077795A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Eirich, Budley
APPLICANT: Eshoo, Mark
APPLICANT: ABROWN MARK
APPLICANT: ABROWN MARK
APPLICANT: ABROWN MARK
APPLICANT: Benoe, Mark
APPLICANT: Branner, Alfred A.
APPLICANT: Branner, Alfred A.
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US-10-138-838-106
S. Sequence 106, Application US/10138838
; Publication No. US20030049821A1
; GENERAL INFORMATION:
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Similarity 57.1%;
4; Conservative (
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Best Local Similarity 57.1%;
Matches 4; Conservative
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US-09-911-781-24
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; ORGANISM: CANDIDATROPICALIS
US-09-976-800-106
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                            Sequence 126883, Application US/10437963
; Sequence 126883, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Rice Nucleic Acid Molecules
TITLE OF INVENTION: Rice Nucleic Acid Molecules
CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 126883
LENGTH: 146
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Sequence 361705, Application US/10425115
Sequence 361705, Application US/10425115
FUBLication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.4%; Score 19; DB 16; Length 146; 57.1%; Pred. No. 1.1e+03; Live 0; Mismatches 3; Indels
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US-10-425-115-361705
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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
LENGTH: 241
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Matches 4; Conservative
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ORGANISM: Oryza sativa
                                            VSASAEF 42
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ORGANISM: Zea mays
1 VXXXAEF
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US-10-437-963-126883
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APPLICANT: Gleeson, Martin
TITLE OF INVENTION: TYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROPERINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
CURRENT APPLICATION NUMBER: US/10/138,905
CURRENT FILING DATE: 2002-05-03
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 09/976,800
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/302,602
PRIOR FILING DATE: 1999-04-30
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PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 106
LENTH: 267
                                                                                                           S-10-138-905-106
Sequence 106, Application US/10138905
Publication No. US20030068800A1
GENERAL INFORMATION:
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Publication No. US20030073220A1
GENERAL INFORMATION:
                                                                                                                                                                                                       APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Exich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
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APPLICANT: Craft, David L.
APPLICANT: Estich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Maddari, Krishna M.
APPLICANT: Corrett, Cathy A.
APPLICANT: Brenner, Alfred A.
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Best Local Similarity 57.1%;
Matches 4; Conservative (
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SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                           Loper, John C.
                                                                                                                                                                                                                                                                                                                                                                       Tang, Maria
                     39 VTTTAEF 45
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APPLICANT: Wilson, Ron C.
APPLICANT: Erich, David L.
APPLICANT: Erich, David L.
APPLICANT: Erich, David L.
APPLICANT: Erich, David L.
APPLICANT: Brenct, Cathy A.
APPLICANT: Cornett, Cathy A.
APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: GRNES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION: GRNES AND PROTEINS RELATING THERETO
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION: GRNES AND SECOLOS OF CURRENT PILING DATE: 2002-05-03
FILE REFERENCE: 1010-16
CURRENT FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 106
LENGTH: 267
                                                                               APPLICANT: Madduri, Krishna M.
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Cornett, Cathy A.
APPLICANT: Bremmer, Alfred A.
APPLICANT: Targ, Maria
APPLICANT: Toper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: CYTOCHROME PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
TITLE OF INVENTION: GROSS AND PROTEINS RELATING THERETO
TITLE OF INVENTION: UNMBER: US/10/138,838
CURRENT PILING DATE: 2002-05-03
PRIOR PRILING DATE: 2001-16-12
PRIOR FILING DATE: 2001-16-12
NUMBER OF SEQ ID NOS: 118
SSOFTWARE: PatentIn version 3.1
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
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57.1%;
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CS-10-139-031-106
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on, Ron C.
Et, David L.
Ich, Dudley
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Best Local Similarity 57.17
Terhes 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                     Mark
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Sequence 24, Application US/10400902
Sequence 24, Application US/10400902
Sequence 24, Application No. US20030175896A1
Seblication No. US20030175896A1
SEDERAL INFORMATION:
APPLICANT: Wilson, C. Ron
APPLICANT: Wilson, C. Ron
APPLICANT: Exitéch, Dudley
APPLICANT: Exitéch, Dudley
APPLICANT: Exitéch, Dudley
APPLICANT: Exitéch, Dudley
CURRENT PERERNCE: US2 OS/OAAP (1010-49)
CURRENT PELING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US/10/400,902
CURRENT PILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
LENGTH: 267
TYPE: PRI
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APPLICANT: CLOBER, John C.
TITLE OF INVENTION: CTYOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUC
TITLE OF INVENTION: CTRUES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CT
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
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Pred. No. 2.1e+03;
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  TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
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                 FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,218
CURRENT FILING DATE: 2002-05-03
FRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SENGTH: 267
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APPLICANT: Craft, David L.
APPLICANT: Errich, Dudley
APPLICANT: Bshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
                                                                                                                                                                                                                                                                                                                                    86.4%;
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US-10-400-902-24
                                                                                                                                                                                                                                                               ; ORGANISM: CANDIDATROPICALIS
US-10-139-218-106
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Best Local Similarity 57.11
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APPLICANT: Craft, David L.
APPLICANT: Elitch, Dudley
APPLICANT: Elboo, Mark
APPLICANT: Cornett, Cathy A.
APPLICANT: Cornett, Cathy A.
APPLICANT: Gleeson, Maria
APPLICANT: Idea A.
APPLICANT: Gleeson, Maria
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICANTON NUMBER: US/10/139,296
CURRENT APPLICANTON NUMBER: US/20/976,800
PRIOR APPLICANTON NUMBER: US/20/976,800
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APPLICANT: Madduri, Cathy A.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Tang, Maria
APPLICANT: Glesson, Martin
TITLE OF INVENTION: CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF (
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                                                                                                                  Score 19; DB 14;
Pred. No. 2.1e+03;
                                                                                                                                                                   0; Mismatches
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                                                                                                                     86.4%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 106
LENGTH: 267
; LENGTH: 267
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-10-138-916-106
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APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
                                                                                                                                                                   4; Conservative
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                                                                                                                Query Match
Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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US-10-139-296-106
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APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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         APPLICANT: Carr, Grant U.

APPLICANT: Vanamoto, Robert T.

APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Probaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: (0/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILICATION NUMBER: 60/206,848
PRIOR PILICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/205,65
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-21-67
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR PRIOR PRESENCE FOR WINDER: 60/269,308
PRIOR PRIOR PRESENCE FOR WINDER: 60/269,308
PRIOR PRIOR PRIOR DATE: 2001-02-16
PRIOR PRIOR PRESENCE FOR WINDER: 60/269,308
PRIOR PRIOR PRESENCE FOR WINDER: 60/269,308
PRIOR PRIOR PRIOR DATE: 2001-02-16
PRIOR PRIOR PRESENCE FOR WINDER: 60/269,308
PRIOR PR
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Pred. No. 2.3e+03;
0; Mismatches 3
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-66
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-66
PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 56631, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Samudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Escherichia coli
US-09-815-242-10242
Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 VSTTAEF 178
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APPLICANT:
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APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOCXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: GENES AND PROTBINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF (TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
TITLE OF INVENTION: 1100-16
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATCHIN Version 3.1
SEQ ID NO 106
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
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Pred. No. 2.1e+03;
0; Mismatches 3; Indels
                  CURRENT APPLICATION NUMBER: US/10/405,660
CURRENT FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.1
SEQ ID NO 106
LENGTH: 267
TYPE: PRT
ORGANISM: CANDIDATROPICALIS
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Patent No. US20020061569A1;
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 106, Application US/10138898
; Publication No. US20030212946A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.4%;
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57.1%;
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Best Local Similarity 57.1
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Best Local Similarity 57.1
Matches 4; Conservative
FILE REFERENCE: 1010-16
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US-09-815-242-10242
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US-10-138-898-106
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APPLICANT:
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APPLICANT:
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRIOR PELION DATE: 2000-03-21
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR PELION DATE: 2000-05-28
FRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-11-27
FRIOR PELION NUMBER: 60/253,625
FRIOR PELION NUMBER: 60/257,931
FRIOR PELION NUMBER: 60/257,931
FRIOR PELING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-24
FRIOR FILING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR FILING DATE: 2001-02-16
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR PELING DATE: 2001-02-16
FRIOR FILING DATE:
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Publication No. US20050106588A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: B568
CURRENT APPLICATION NUMBER: US/10/888,656
CURRENT FILING DATE: 2004-07-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 355
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Pred. No. 2.8e+03;
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US-10-425-114-57008
; Sequence 57008, Application US/10425114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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ORGANISM: Papaver somniferum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 VATAAEF 232
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US-10-888-656-2
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; Sequence 302302, Application US/10425115
; Publication No. US2004021427241
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Exovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; CURRENT FILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 302302
LENTH: 330
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 56531
LENGTH: 298
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US-10-425-115-302302
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Aselbeck, Robert
APPLICANT: Cyskind, Judith
APPLICANT: Tyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, Grant
APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
APPLICANT: Yamanoto, Robert
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ORGANISM: Escherichia coli
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Best Local Similarity 57.1°
The Conservative
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Matches 4; Conservative
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US-10-425-115-302302
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Gaps

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Page 9

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: NuCleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(53222)8
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 336689
LENGTH: 747
TYPE: ...
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: ABSOCIATED Windleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 51691
LENGTH: 751
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APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 5.8e+03;
0; Mismatches 3; Indels
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Local Similarity 57.1%; Pred. No. 5.9e+03;
Nes 4; Conservative 0; Mismatches 3;
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US-10-425-115-336689
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Publication No. US20040034888A1
GENERAL INFORMATION:
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Best Local Similarity 57.1%;
Matches 4; Conservative
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APPLICANT: Zhou, Yihua
APPLICANT: Scoralic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             577 VTAAAEF 583
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ORGANISM: Zea mays
FEATURE:
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APPLICANT: Boukharov, Andrey A.

APPLICANT: Baukharov, Andrey A.

APPLICANT: Baukharov, Andrey A.

APPLICANT: Baukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53221)B

CURRENT PILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 128132

LENOTH: 586

TYPP: TYPP: TENOTHER T
                                                                                                                                                                                                                                                                             APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Sorean, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Sor Yough Since A Soriated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: UNMBER: US/10/425,114
UNMBER OF SEQ ID NOS: 73128
SEQ ID NO 57008
LENGTH: 396
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US-10-425-114-57008
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 336689, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                       Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Oryza sativa
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ORGANISM: Zea mays
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US-10-437-963-128132
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; Sequence 48, Application US/10032818
; Publication No. US20030092629A1
; PUBLICATION INFORMATION;
; APPLICANT: Tang, Jordan J.N.
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Best Local Similarity 57.1%;
Matches 4; Conservative
            4; Conservative
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            Matches
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APPLICANT: Askind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamanco, Robert
APPLICANT: Robert 2000-05-26
APPLICANT: Robert 2000-05-36
APPLICANT: Robert 2000-05-36
APPLICANT: Robert 2000-11-27
APPLICANT: Robert 2000-11-27
APPLICANT: Robert 2000-12-22
APPLICANT: R
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                               Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
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US-10-425-114-62401
                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 15;
Pred. No. 5.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
FILE REFERENCE: 30-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 62401
LENGTH: 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 75669, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
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57.1%;
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Best Local Similarity 57.1
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Best Local Similarity
                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays
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LENGTH: 1266
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Sequence 6737, Application US/10369493
; Bedraction No. US2003023367541
; Bedraction No. US2003023367541
; Bedraction No. US2003023367541
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES
; FILE REFERENCE: 38-10(52052)8
; CURRENT APPLICATION WHORER: US 40/360,039
; PRIOR FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6737
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; Sequence 173, Application US/10489740
; Publication No. US20050112574A1
; GENERAL INFORMATION:
; APPLICAMT: Bionomics Limited
; TITLE OF INVENTION: P9
; FILE REPERENCE: Anglogenesis PCT
; CURRENT APPLICATION NUMBER: US/10/489,740
; CURRENT PILING DATE: 2004-03-15
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
LENGTH:: 1584
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Abou Yihua
APPLICANT: Abou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8 LOGA24, 599
CURRENT APPLICATION NUMBER: US/10/424, 599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 227707
LENGTH: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 158, Application US/09984429
Publication No. US20040010132A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFRENCE: P2018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT APPLICATION NUMBER: 60/244,591
PRIOR APPLICATION NUMBER: 09/288,143
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 14;
Pred. No. 1.8e+02;
0; Mismatches 3
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Pred. No. 7.3e+02;
0; Mismatches 3
             CURRENT APPLICATION NUMBER: US/10/032,818
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 60/275,756
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 83
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 212707, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic peptide US-10-032-818-54
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                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
FILE REFERENCE: 2932.1006-007
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               APPLICANT: Ghosh, Arun K.

7 ITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REFERENCE: 293-1006-007

CURRENT APPLICATION NUMBER: US/10/032,818

CURRENT APPLICATION NUMBER: US/10/032,818

FRIOR PRIOR APPLICATION NUMBER: US 60/275,756

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-12-28

NUMBER OF SEQ ID NOS: 83

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 48

LENGTH: 12
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APPLICANT: Koelsch, Gerald

APPLICANT: Ghosh, Arun K.

TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof

FILE REFERENCE: 2932.1006-007

CURRENT APPLICATION NUMBER: US/10/032,818

CURRENT PILING DATE: 2001-12-28

PRIOR FILING DATE: 2001-12-28

PRIOR FILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 83

SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Koelsch, Gerald
APPLICANT: Ghosh, Arun K.
IITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 18; DB 14; Length 12; 57.1%; Pred. No. 1.8e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 14; Length 12;
Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/10032818; Publication No. US20030092629A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%;
57.1%;
                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
Koelsch, Gerald
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Best Local Similarity 57.1
Matches 4; Conservative
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US-10-032-818-49
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LENGTH: 12
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Page 12

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Sequence 243983, Application US/10425115
| Sequence 243983, Application US/10425115
| Publication No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: APPLICANT: Zhou, Yihua |
| APPLICANT: Zhou, Yihua |
| APPLICANT: Zhou, Yihua |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Plants |
| TITLE OF INVENTION: Pla
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23745, Application US/10425115
Sequence 23745, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Enou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-64-28
CURRENT FILING DATE: 2003-64-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 237245
LENGTH: 60
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Pred. No. 9e+02;
0; Mismatches 3; Indels
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US-10-425-115-237245
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US-10-425-115-243983
            57.1%; Pred. No. 8.3e+02;
tive 0; Mismatches 3;
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Pred. No. 9.1e+02;
0; Mismatches 3
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57.1%;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
            Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Zea mays
FEATURE:
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US-10-425-115-237245
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US-10-425-115-243983
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-150-111-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , LOCATION: (55)
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-984-429-158
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81.8%; Score 18; DB 11; Length 56;
Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels
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| Publication No. US20030078386A1
| GENERAL INFORMATION:
| APPLICANT: Rubin et al.
| TITLE OF INVENTION: Secreted Protein HPEAD48
| FILE REFERENCE: PZ018101
| CURRENT APPLICATION NUMBER: US/10/150,111
| CURRENT FILING DATE: 2002-05-20
| PRIOR FILING DATE: 1999-04-08
| PRIOR FILING DATE: 1999-06-08
| PRIOR FILING DATE: 1999-10-09
| PRIOR APPLICATION NUMBER: 60/061,463
| PRIOR APPLICATION NUMBER: 60/061,463
| PRIOR PILING DATE: 1997-10-09
| PRIOR PILING DATE: 1997-10-09
| PRIOR PILING DATE: 1997-10-09
| PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR PILING DATE: 1997-10-09
PRIOR PLING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,527
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 727
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LENGTH: 56
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RESULT 37

Score 18; DB 14; Length 56;

81.8%;

Query Match

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and Other Molecules Associated With
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US-10-369-493-10066

US-10-369-493-10066

Application No. US2000233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52502)B

CURRENT APPLICATION NUMBER: US/10/369,493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Dlants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)B
CURRENT PLLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 49255
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ALTICANT: CAN YINUA
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ass;
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ass;
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement;
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 228254
LENGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_48141C.1.pep
US-10-44-599-228254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 15; L. Pred. No. 1.3e+03; 0; Mismatches 3;
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57.1%; Pred. No. 1.4e+03;
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US-10-425-114-49255
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 VTSOAEF 70
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                                                                                                                                                                                       APPLICANT: La Rosa, Thomas J.
APPLICANT: A Rosa, Thomas J.
APPLICANT: APPLICANT: Should K.
APPLICANT: Shoul Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 275053
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APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
TITLE OF INVENTION: NOVEL GENE EXPRESSED IN PROSTATE CANCER FILE REFERENCE: 511582003110
CURRENT APPLICATION NUMBER: US/10/334,561A
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: 09/410,132
PRIOR APPLICATION NUMBER: 60/146,584
PRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1999-09-32
PRIOR PILING DATE: 1999-09-32
PRIOR PILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFERMATION: Clone ID: MRT4577_182439C.1.pep
US-10-425-115-275053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                    ; Sequence 275053, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
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US-10-424-599-228254
US-10-424-599-228254, Application US/10424599; Publication No. US20040031072A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/10334561A; Publication No. US20030211520A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
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US-10-334-561A-4
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; OTHER INFORMATION: Clone ID: MRT4577_60920C.1.pep
US-10-425-115-326590
    81.8%;
57.1%;
  Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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Matches 4; Conservative
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ORGANISM: Zea mays
                                                                                                                      41 VSVSAEF
                                                                                                                                                                                RESULT 44
US-10-425-115-190652
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US-10-767-701-53633

is Sequence 53633, Application US/10767701

is Publication No. US20040172684A1

is GENERAL INFORMATION:

is APPLICANT: Shou, Yihua

is APPLICANT: Cao, Yongwei

is TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

if TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

if TITLE OF INVENTION: DIABLES 18-21 (53535) B

is CURRENT FILING DATE: 2004-01-29

is NUMBER OF SEQ ID NOS: 63128

is SEQ ID NO 53633

LENGTH: 95
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 255955
LENGTH: 100
TENGTH: 100
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                                                                                                                                                                                                 81.8%; Score 18; DB 15; Length 93; 57.1%; Pred. No. 1.4e+03; ive 0; Mismatches 3; Indels
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US-10-425-115-255955
                                                                                                                  ; TYPE: PRT
; ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-10066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: 13468723.pep
US-10-767-701-53633
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10066
LENGTH: 93
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Best Local Similarity 57.1°
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Matches 4; Conservative
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ORGANISM: Zea mays
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US-10-425-115-255955
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Sequence 326590, Application US/10425115
; Publication No. US20040214272A1
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REPERENCE: 38-21(5222)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 326590
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Score 18; DB 16; Length 100;
Pred. No. 1.5e+03;
0; Mismatches 3; Indels
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US-10-425-115-190652
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WS-10-424-599-156801

Sequence 156801, Application US/10424599

Sequence 156801, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 274994, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules Associated With
TITLE Acid Molecules Acid Molecules Associated With
TITLE Acid Molecules 
                                                                          APPLICANT: In CONTROL Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Avain, Yihua
APPLICANT: Cao, Yingwei
TITLE OF INVENTION: Dlants
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 271612
LENGTH: 122
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US-10-425-115-274994
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57.1%; Pred. No. 1.8e+03;
iive 0; Mismatches 3;
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Best Local Similarity 57.1%; Pred. No. 1.8e+03; Matches 4; Conservative 0; Mismatches 3.
Sequence 271612, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local Similarity 57.1.
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
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              Sequence 144633, Application US/10424599
Sequence 146634, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 144633
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Pred. No. 1.8e+03;
0; Mismatches 3; Indels
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Pred. No. 1.8e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_101616C.1.pep
US-10-424-599-144633
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US-10-437-963-184577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
LOCATION: (1)..(121)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 VLASAEF 38
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US-10-437-963-184577
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RESULT 48

Wed Jun 15 09:21:18 2005

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WS-10-425-115-297969

Sequence 297969, Application US/10425115

Sequence 297969, Application US/10425115

Sequence 297969, Application US/0040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 297969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 51
US-10-767-701-33440
; Sequence 33440, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, YNOGWei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa;
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REPERENCE: 38-21(5335) B
; CURRENT APPLICATION NUMBER: US/10/767,701
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 33440
; LENGTH: 124
    Plants and Uses Thereof for Plant Improvement
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57.1%; Pred. No. 1.9e+03;
cive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 81.8%; Score 18; DB 16; Length 124; Similarity 57.1%; Pred. No. 1.9e+03; 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C32083_1.pep
US-10-767-701-33440
                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_112613C.1.pep
US-10-424-599-156801
TITLE OF INVENTION: Plants and Uses There FILE REPERENCE: 38-21(5)213)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 124
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Best Local Similarity 57.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Sorghum bicolor
                                                                                                                                                                                     ORGANISM: Glycine max
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Best Local Similarity
Matches 4, Conserva
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ORGANISM: Zea mays
                                                                                                                                                                                                               FEATURE:
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exvalic David K
APPLICANT: And Vibua
APPLICANT: Abus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICANION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 129
                                                                                                                                                                                                                                                                                                                  Sequence 238741, Application US/10425115
Sequence 238741, Application No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Youla
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 238741
LENGTH: 125
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                                                                Query Match 81.8%; Score 18; DB 16; Length 124; Best Local Similarity 57.1%; Pred. No. 1.9e+03; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%; Score 18; DB 16; Length 125; 57.1%; Pred. No. 1.9e+03; ive 0; Mismatches 3; Indels
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US-10-424-599-228146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: MRT4577_14931C.1.pep
US-10-425-115-238741
OTHER INFORMATION: Clone ID: MRT4577_34819C.1.pep
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 57.1.
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ORGANISM: Glycine max
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ORGANISM: Zea mays
                      US-10-425-115-297969
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US-10-425-115-238741
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                     APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Succident Single
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 67704
LENGTH: 141
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Application Yibra
APPLICANT: Cao, Yibra
APPLICANT: Pance
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE BEFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 274236
LENGTH: 142
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US-10-425-114-61704
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US-10-425-115-274236
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57.1%; Pred. No. 2.1e+03;
iive 0; Mismatches 3
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 57.1
Matches 4; Conservative
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Matches 4, Conservative
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US-10-425-115-274236
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US-10-424-599-279916
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                                                                                    Sequence 274885

Sequence 274885

Sequence 274885, Application US/10424599

Sequence 274885, Application US/10424599

Publication No. US20040031072A1

SERBRAL INFORMATION

APPLICANT: La Rosa Thomas J

APPLICANT: Abou Yihua

APPLICANT: Cao Yongwai

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT PILING DATE: 2003-04-28

SEQ ID NO 274885

LENGTH: 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WU, THOMAS D. TITLE OF INVENTION: COMPOSITIONS and Methods for the Treatment of Immune TITLE OF INVENTION: Related Diseases FILE REFERENCE: P1948R1-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.1e+03;
0; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; Score 18; DB 15; Length 137; 57.1%; Pred. No. 2.1e+03; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_90241C.1.pep
US-10-424-599-274885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 390
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US-10-425-114-61704
; Sequence 61704, Application US/10425114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 390, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T: BRISDELL, HUNTE
JACKMAN, JANET
T: SCHOENFELD, JILL R.
WILLIAMS, P. MICKEY
T: WOOD, WILLIAM I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%;
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patin Docket Preview
APPLICANT: BODARY, SARAH C.
APPLICANT: CLARK, HILLARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 VAAEAEF 109
  33 VAVAAEF 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 VITAÄEF 13
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Sequence 16912, Application US/10369493

Sequence 16922, Application US/10369493

Sequence 16922, Application US/10369493

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: One INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
ITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITLE REFERENCE: 38-10(5205.)B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT PILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 16332

LENGTH: 159
                                                                                               APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 199547
LENGTH: 155
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Can Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_94196C.1.pep
US-10-437-963-198547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18; DB 16;
Pred. No. 2.3e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
81.8%; Score 18; DB 15;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 234753, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Caulobacter crescentus US-10-369-493-16932
                                                                             Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cao, Yongwei
Wu, Wei
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
     Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 VAAEAEF 148
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                                                                             APPLICANT:
                                                      APPLICANT
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zoo, Yongwei
APPLICANT: Go, Yongwei
APPLICANT: W. Wei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 169685
LENGTH: 149
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 144
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                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%; Score 18; DB 15; Length 144; 42.9%; Pred. No. 2.2e+03; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 81.8%; Score 18; DB 16; Length 149; Best Local Similarity 57.1%; Pred. No. 2.2e+03; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_94788C.1.pep
US-10-424-599-279916
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US-10-437-963-169685
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                           LOCATION: (1)..(144)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 169685, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: A ROSa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bradauk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 198547, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : |||
133 IATAAEF 139
                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 VGTAAEF 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VXXXAEF 7
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NAME/KEY: ungure
                                                                                                                                                                                                                        FEATURE:
NAME/KEY: unsure
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Gaps
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Fublication No. US20040009490A1
GENERAL INFORMATION:
APPLICANT: Glenn, Mathew
APPLICANT: Glenn, Mark William
APPLICANT: Lubbers, Mark William
APPLICANT: Dekker, James
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
FILE REPRENEUR: 11000.1043c3
CURRENT APPLICATION WHORER: US/10/264,213
CURRENT PILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 199
                                                                                                                                                                       Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 171;
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Pred. No. 2.6e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                          Indels
                                                                     ; OTHER INFORMATION: Clone ID: LIB3632-058-F7_FLI.pep
US-10-425-114-64341
                                                                                                                                                                       Score 18; DB 15; L
Pred. No. 2.5e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERRNCE: 249-226
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7611
LENGTH: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7611, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptomyces avermitilis US-10-156-761-7611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Lactobacillus rhamnosus
                                                                                                                                                                       Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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      ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-264-213-199
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Sequence 245373, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: About Yihua

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 18-21 (55223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 245373
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Sequence 6434.34

Publication No. US20040034888A1

Publication No. US2004003488BA1

Settle Cavity Sequence 6434.34

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: APPLICANT: Acvel E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Corrent, Serven E

APPLICANT: Tabaska, Jack E

APPLICANT: APPLICANT: Application of the correction of the corr
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 15; Length 161;
Pred. No. 2.4e+03;
0; Mismatches 3; Indels
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US-10-424-599-234753
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US-10-424-599-245373
FILE REFERENCE: 38-21 (53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 234753
LENGTH: 161
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81.8%;

Best Local Similarity 57.1%;

Matches 4; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
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Matches 4; Conserv
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LENGTH: 167
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Sequence 162790, Application US/10424599;
Sequence 162790, Application US/10424599;
Bublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cover Solve So
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Sovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Calo, Yongua
APPLICANT: Calo, Yongua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
KUMBER OF SEQ ID NOS: 369326
SEQ ID NO 241928
LENGTH: 188
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US-10-424-599-162790
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Pred. No. 2.8e+03;
0; Mismatches 3;
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US-10-425-115-241928
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Pred. No. 2.8e+03;
0; Mismatches 3;
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Publication No. US20040214272A1
GENERAL INFORMATION:
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US-10-156-761-9937
; Sequence 9937, Application US/10156761
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                              11 VSGAÁEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 VATGAEF 97
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                                1 VXXXAEF 7
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                                                                                                                                                                                                                         US-10-424-599-162790
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Sequence 40084, Application US/2040172684A1
Sequence 40084, Application No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yorigwei
TITLE OF INVENTION: Dlants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Dlants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Dlants and Uses Thereof For Plant Improvement
TITLE OF SEQUENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
SEQ ID NO 40084
LENGTH: 187
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81.8%; Score 18; DB 16; Length 187;
Best Local Similarity 57.1%; Pred. No. 2.8e+03;
Matches 4; Conservative 0; Mismatches 3; Indels
   57.1%; Pred. No. 2.7e+03;
tive 0; Mismatches 3; Indels
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US-10-767-701-40084
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US-10-425-115-199164
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OTHER INFORMATION: unsure at all Xaa locations
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OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 57.1:
....nes 4; Conservative
Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                        162 VSTIAEF 168
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                                                                                              1 VXXXAEF 7
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ORGANISM: Zea mays
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APPLICANT: LA ROALICANT
APPLICANT: LA SOLUTION:
APPLICANT: Exolution of the state o
                                                                                                                                 APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 165533
LENGTH: 201
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US-10-437-963-121186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_6432C.1.pep
US-10-437-963-165533
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Pred. No. 3.2e+03;
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LOCATION: (1)..(201)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 121186, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
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Best Local Similarity 57.1%
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Best Local Similarity 57.1%
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 VAAGAEF 184
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; Sequence 271613, Application US/2040214272A1
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NOS: 369326
; SEQ ID NO 271613
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Pred. No. 2.9e+03;
0; Mismatches 3; Indels
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57.1%; Pred. No. 3e+03;
tive 0; Mismatches 3; Indels
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                                                    APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: BHIRA, HIROSHI
APPLICANT: SHIRAM, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHARA, HAROSHI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Expense Thomas J.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9937
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57.1%;
Publication No. US20030119018A1 GENERAL INFORMATION:
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-437-963-165533
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US-10-425-115-199685
; Sequence 199685, Application US/10425115
; Sequence 199685, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: ADOU, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 199685
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US-10-389-566-1581

Sequence 1581, Application US/10389566

Publication No. US20040025202A1

GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C

TITLE OF INVERTION:
CURRENT APPLICATION NUMBER: US/10/389,566

CURRENT APPLICATION NUMBER: US/10/389,566

CURRENT PILING DATE: 2002-03-15

PRIOR FILING DATE: 2002-03-15

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR PILING DATE: 2002-06-25

PRIOR PILING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 2459

SOFTWARE: PatentIn version 3.2
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       TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 213;
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                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_105623C.1.pep
US-10-424-599-149059
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                                      FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 149059
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 VGAAAEF 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-425-115-199685
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Covalic David K
APPLICANTON NUMBER: US/10/424,599
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 149058
SEQ ID NO 149058
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323.3) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 230315
LENGTH: 212
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Sequence 149059, Application US/10424599

Sequence 149059, Application US/10424599

SEQUENCE OF USE OF USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 81.8%; Score 18; DB 15; Length 212; Best Local Similarity 57.1%; Pred. No. 3.2e+03; Matches 4; Conservative 0; Mismatches 3; Indels
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US-10-424-599-149058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_49999C.1.pep
US-10-424-599-230315
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Best Local Similarity 57.13
Local 4; Conservative
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APPLICANT: Lea Rose Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Wawii David K
APPLICANT: Cao Wawii David K
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
KUMBER OF SEQ ID NOS: 285684
SEQ ID NO 262409
LENGTH: 241
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                             Gaps
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| Publication No. US20050064527A1
| Publication No. US20050064527A1
| GENERAL INFORMATION:
| APPLICANT: Levy, Stuart, et. al.
| TITLE OF INVENTION: NIME COMPOSITIONS AND THEIR METHODS OF USE
| FILE REFERENCE: PKZ-043
| CURRENT APPLICATION NUMBER: US/09/801,563
| PRIOR PILING DATE: 2001-03-08
| PRIOR PILING DATE: 2001-03-08
| PRIOR PILING DATE: 2000-03-10
| NUMBER OF SEQ ID NOS: 98
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 98
| LEVYTH: 240
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Pred. No. 3.6e+03;
0; Mismatches 3; Indels
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81.8%; Score 18; DB 15; Length 241;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels
                             Indels
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US-10-424-599-262409
    Pred. No. 3.5e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-262409
; Sequence 262409, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 81.8%;
Best Local Similarity 57.1%;
Matches 4; Conservative 0
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Escherichia coli
US-10-893-671-98
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                      151 VSSLAEF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
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                                                                       1 VXXXAEF 7
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US-10-437-963-115265
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| Publication No. US20040031072A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: AROUST Thus
| APPLICANT: AROUST Thus
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| CURRENT APPLICATION NUMBER: US/10/424,599
| CURRENT APPLICATION NUMBER: US/10/424,599
| NUMBER OF SEQ ID NOS: 285684
| SEQ ID NO 247828
                                                                                                                                                                                                                                                                                                                                                                                     costology, Application US/10389566

publication No. US20040025202A1

GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFREENCE: 38-77 52900 UD
CURRENT PILLING DATE: 2003-03-31
PRIOR PILLING DATE: 2003-03-31
PRIOR PILLING DATE: 2002-04-15
PRIOR PILLING DATE: 2002-06-25
PRIOR FILLING DATE: 2002-06-25
PRIOR FILLING DATE: 2002-06-25
PRIOR FILLING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459

NUMBER OF SEQ ID NOS: 2459
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                                                                                                                                       Score 18; DB 15; Length 228;
Pred. No. 3.4e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%; Score 18; DB 15; Length 228; 57.1%; Pred. No. 3.4e+03; Live 0; Mismatches 3; Indels
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                                                                                                                                            81.8%;
                                                                                                                                       Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pisum sativum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                              ; TYPE: PRT
; ORGANISM: Vicia faba
US-10-389-566-1581
                                                                                                                                                                                                                                                                                41 VEAAAEF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 VEAAAEF 47
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US-10-424-599-247828
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US-10-389-566-1597
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SEQ ID NO 1581
LENGTH: 228
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LENGTH: 228
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8

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RESULT 87

US-10-424-599-274705

Sequence 274705, Application US/10424599

Sequence 274705, Application No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

IENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT3847_9007C.1.pep
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81.8%; Score 18; DB 15;
Best Local Similarity 57.1%; Pred. No. 3.9e+03;
Matches 4; Conservative 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUGHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: O'CHIAI, MEIKO
APPLICANT: TAYENI, NAOKO
APPLICANT: TAYENIH, NAOKO
APPLICANT: TEEDA, MASATO
APPLICANT: TEEDA, MASATO
APPLICANT: OZAKI, AKID
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
SOFTWARE OF SEQ ID NOS: 7059
SEQ ID NO 5807
LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5807, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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US-09-738-626-5807
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 VATGAEF 52
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Best Local Similarity
Matches 4; Conserv
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US-09-738-626-5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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APPLICANT: ECOFIA BIOSCIENCES INC.
APPLICANT: EATHER, Chris
APPLICANT: MCALDine, James
APPLICANT: AZAZOPOULOS, Emmanuel
APPLICANT: Bachmann, Brian
APPLICANT: Brownion: A PHARMACEUTICAL
TITLE OF INVENTION: A PHARMACEUTICAL
FILE REFERENCE: 3005-505
CURRENT APPLICATION NUMBER: USSN 60/441,126
PRIOR APPLICATION NUMBER: USSN 60/442,997
PRIOR APPLICATION NUMBER: USSN 60/492,997
PRIOR APPLICATION NUMBER: USSN 60/492,997
PRIOR FILING DATE: 2003-01-10
NUMBER: PROBLICATION NUMBER: USSN 60/518,286
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Version 3.0
SEQ ID NO 46
                                                                                                                                                                                                       APPLICANT: Li Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 115265
LENGTH: 252
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81.8%; Score 18; DB 16; Length 252;
Best Local Similarity 57.1%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_1887C.1.pep
US-10-437-963-115265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Micromonospora sp. strain 046-ECO11
US-10-762-107-46
Sequence 115265, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: APPLICANT: Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-762-107-46
; Sequence 46, Application US/10762107
; Publication No. US20050043297A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 VAVAAEF 129
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## APPLICANT: Xu, H.

## APPLICANT: Xu, H.

## TITLE OF INVERTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

## CURRENT APPLICATION WUMBER: 60/192,078

## PRIOR APPLICATION WUMBER: 60/192,078

## PRIOR FILING DATE: 2000-05-23

## PRIOR FILING DATE: 2000-05-23

## PRIOR FILING DATE: 2000-05-23

## PRIOR FILING DATE: 2000-05-26

## PRIOR FILING DATE: 2000-05-26

## PRIOR FILING DATE: 2000-05-26

## PRIOR FILING DATE: 2000-09-06

## PRIOR FILING DATE: 2000-09-09

## PRIOR FILING DATE: 2000-10-23

## PRIOR FILING DATE: 2000-11-27

## PRIOR FILING DATE: 2000-11-27

## PRIOR FILING DATE: 2000-12-22

## PRIOR FILING DATE: 2001-12-22

## PRIOR FILING DATE: 2001-02-06

## PRIOR FIL
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                                                                                                                                                                                                                                                                                            Length 259;
                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_18060C.1.pep
US-10-437-963-114362
                                                                                                                                                                                                                                                                                        81.8%; Score 18; DB 16;
57.1%; Pred. No. 3.9e+03;
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 57.1%;
4; Conservative
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                               Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                       ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 VSVSAEF 214
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Best Local Similarity
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US-10-282-122A-65087
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SEQ ID NO 114362
                                                                         TYPE: PRT
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Goo, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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Pred. No. 3.9e+03;
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CURRENT APPLICATION UMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 784
SEQ ID NO 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 90
US-10-437-963-114362
; Sequence 114362, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.8%;
57.1%;
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Best Local Similarity 57.1
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                                                             US-10-781-014-600
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GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
   PRIOR FILING DATE: 2001-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 VGSSAEF 112
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                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 4; Conserv
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US-10-282-122A-72181
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                                                                                                                                                                                                                                 TYPE: PRT
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/202,848
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-66
PRIOR PLILING DATE: 2000-05-69
PRIOR PLILING DATE: 2000-01-03
PRIOR PLILING DATE: 2000-01-23
PRIOR PLILING DATE: 2000-01-23
PRIOR PLILING DATE: 2000-01-23
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2001-10-20
PRIOR PLILING DATE: 2001-10-20
PRIOR PLILING DATE: 2001-10-20
PRIOR PLILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-03-03
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Publication No. US2004008770A1
GENERAL INFORMATION:
APPLICANT: Tang, Ciristoph
TITLE OF INVENTION: Virulence Genes, Proteins, and Their Use
FILE REFERENCE: GJE-6436
CURRENT APPLICATION UNDSER: US/10/275,026A
CURRENT FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: PCT/GB01/02003
                                                                                                                                                        Sequence 66020, Application US/10282122A Publication No. US20040029129A1
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ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Wall, Daniel
41 VASNAEF 47
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Matches 4; Conserv
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APPLICANT:
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PRIOR APPLICATION WORSE: G8 0011108.8

PRIOR EDITORING DATE: 2000-05-08

1 SOUTHARE: Patentin version 3.2

1 OBBANIENT Noiseeria meningitidis

1 OPPLICATION VERSIONALIA

1 VAXABP 7

DD 41 VASNABP 47

DD 41 VASNABP 47

DD 41 VASNABP 47

DD 41 VASNABP 47

APPLICANT: OBBANIENT NOISE (1970/AN)

1 OPPLICANT: OBBANIENT NOISE (1970/AN)

1 OPPLICANT: OBBANIENT NOISE (1970/AN)

1 TITLE OF INVERTION: DAGE (1970/AN)

1 OPPLICANT: OBBANIENT NOISE (1970/AN)

1 OPPLICANT: OBBANIENT NOISE (1970/AN)

1 OPPLICANT: OBBANIENT NOISE (1970/AN)

1 OPPLICANT: ABBANIENT NOISE (1970/AN)

1 OPPLICANT: A
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CURRENT APPLICATION NUMBER: US/10/282,122A

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; Sequence 9623, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine max
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US-10-767-701-34443

// Sequence 34443, Application US/10767701

// Sequence 34443, Application US/10767701

// Sequence 34443, Application No. US20040172684A1

// GENERAL INFORMATION:

// APPLICANT: Zhou, Yihua

// APPLICANT: Zhou, Yihua

// APPLICANT: Cao, Yongwei

// TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

// TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

// TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

// TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

// TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

// TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

// CURRENT APPLICATION NUMBER: US/10/767,701

// CURRENT FILING DATE: 2004-01-29

// NUMBER OF SEQ ID NOS: 63128

// SEQ ID NO 34443

// LENGTH: 293

LENGTH: 293
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CURRENT FILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/191,078
FRIOR APPLICATION NUMBER: 60/22-20
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR PILING DATE: 2000-05-23
FRIOR PELING DATE: 2000-05-66
FRIOR APPLICATION NUMBER: 60/230,335
FRIOR APPLICATION NUMBER: 60/230,347
FRIOR APPLICATION NUMBER: 60/230,347
FRIOR APPLICATION NUMBER: 60/230,347
FRIOR PILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-11-27
FRIOR PILING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR PILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/257,931
FRIOR FILING DATE: 2001-02-29
FRIOR FILING DATE: 2001-02-20
FRIOR FILING DATE: 2001-02-20
FRIOR FILING DATE: 2001-02-06
FRIOR FILING DATE: 2001-02
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US-10-767-701-34443
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Pred. No. 4.4e+03;
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LOCATION: (1)..(293)
OTHER INFORMATION: unsure at all Xaa locations
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US-10-282-122A-72181
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Best Local Similarity 57.19
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Best Local Similarity 57.1
Matches 4; Conservative
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LENGTH: 288
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Sequence 38327, Application US/10425114

Sequence 38327, Application No. US20040034888A1

Sequence 38327, Application No. US20040034888A1

Sequence 38327, Application No. US20040034888A1

Sequence 38327, Application No. US2004003488BA1

Sequence 3820, APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

WUMBER OF SEQ ID NOS: 73128

SEQ ID NO 38327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 255888, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILLE REPERENCE: 39-21(53223)
CURRENT APPLICANT: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 301
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Pred. No. 4.5e+03;
0; Mismatches 3; Indels
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US-10-424-599-265888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3242-388-G1_FLI.pep
US-10-425-114-38327
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Best Local Similarity 57.1%;
Matches 4; Conservative
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9623
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US-10-282-22647 APDICation US/10282122A

| Sequence 52247 APDICation US/10282122A
| Publication No. US20040029129A1
| Sequence 52247 APDICation US/10282122A
| Publication No. US20040029129A1
| SEPEZANT: Name of the property of the property of the publication No. US20040029129A1
| APPLICANT: Malone, Cheryl
| APPLICANT: Malone, Cheryl
| APPLICANT: Malone, Cheryl
| APPLICANT: Transity of the property of the publicant of
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Pred. No. 4.7e+03;
0; Mismatches 3; Indels
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; ORGANISM: Desulfitobacterium hafniense
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; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-10-282-122A-52547

Query Match
Best Local Similarity 57.1%; Pred. No. 4.8e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VXXXAEF 7

Db 115 VATLAEF 121

Search completed: June 13, 2005, 14:18:24
Job time: 112 secs
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A;Cross-references: UNIPROT:Q9KU15; GB:AE004158; GB:AE003852; NID:g9655156; PIDN:AAF93886 A;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics: A;Gene: VCO715 A;Gene: VCO715 A;Map position: 1 C;Superfamily: NADPH-flavin oxidoreductase homolog
                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; WUID:21074935; PMID:11206551
A;Reference number: A85480; WUID:21074935; PMID:11206551
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <STO>
A;Cross-references: GB:AB005174; NID:g12516806; PIDN:AAG57546.1; GSPDB:GN00145; UWGP:236
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Cispecies: Coli

Ribattenaria (Coli)

Ribattenaria (Coli)
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                                                                                                                                              Similarity 57.1%; Pred. No. 2.4e+02;
4; Conservative 0; Mismatches 3; Indels
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C;Superfamily: conserved hypothetical protein b2428
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82288
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUD:20406833; PMID:10952301
A;Accession: D82288
A;Accession: D82288
A;Kestius: preliminary
A;Molecule type: DNA
A;Residues: 1-240 <HEI>
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B85958
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R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; Ge submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromatic
A;Reference number: Z20992
                                                                                                                                                   A,Accession: T31224
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-484 <ROM>
A,Cross-references: UNIPROT:085932; EMBL:AF079317; NID:g3378261; PID:g3378365; PIDN:AADOCC,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: AF0911
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, t., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Aitle: Complete genome sequence of a multiple drug reeistant Salmonella enterica serove, A;Reference number: Ab0502; MUID:21534947; PMID:11677608
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C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00095; T47155
R;Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
A;Title: Characterization of CDNA clones in size-fractionated cDNA libraries from human h
A;Reference number: 214085; MUID:98116662; PMID:9455484
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A;Residues: 1-1460 <SEK>
A;Cross-references: UNIPROT:075058; EMBL:AB007939; NID:g3413901; PIDN:BAA32315.1; PID:g34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable exported protein [imported] - Salmonella enterica subsp. enterica serovar Typhi
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A,Status: preliminary
A,Rolecule type: DNA
A,Residues: 1-1266 <PAR>
A,Coss.references: GB:AL513382; PIDN:CAD07884.1; PID:g16504431; GSPDB:GN00176
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A,Note: this species has also been called Salmonella typhi
C,Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann,
submitted to the Protein Sequence Database, March 2000
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Pred. No. 1.3e+03;
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C;Superfamily: Escherichia coli hypothetical protein yhdP
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Pred. No. 4.8e+02;
0; Mismatches 3,
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Best Local Similarity 57.1
Matches 4; Conservative
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A,Note: traH
C,Superfamily: traH protein
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A;Gene:EG83299
C;Superfamily: conserved hypothetical protein b2428
                                                                                                    protein F15K9.6 [imported] - Arabidopsis thaliana protein F15K9.6 [imported] - Arabidopsis thaliana (mouse-ear cress) ("Species: Arabidopsis thaliana (mouse-ear cress) ("Species: Oz-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 ("Stacession: A86165 ("Stacession: A.F. Hughes, B.; Muzar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huzar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ayuthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.; Sakano,
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A;Cross-references: UNIPROT:Q9ZVT5; GB:AE005172; NID:g3850570; PIDN:AAC72110.1; GSPDB:GN
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C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T31224
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C;Superfamily: Arabidopsis thaliana hypothetical protein T419.20
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Pred. No. 3e+02;
0; Mismatches 3; Indels
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57.1%;
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-298 < HAY>
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C;Accession: A54252
R;Extel, E.A.; Warren, V.A.; Adams, M.B.; Griffin, P.R.; Cohen, C.J.; Smith, M.M.
Biochemistry 33, 5098-5108, 1999
A;Title: Type III omega-agatoxins: a family of probes for similar binding sites on L- analyReference number: A54252; MUID:94227039; PMID:8172884
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R;Ettel, B.A.; Warren, V.A.; Adams, M.E.; Griffin, P.R.; Cohen, C.J.; Smith, M.M.
Biochemistry 33, 5098-5108
A;Title: Type III omega-agatoxins: a family of probes for similar binding sites on L- and A;Reference number: A54252; WUID:94227039; PMID:8172884
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C;Species: Agelenopsis aperta
C;Accession: 1994 #sequence_revision 18-Nov-1994 #text_change 19-Jan-1996
C;Accession: 1854252
R;Extel, B.A.; Warren, V.A.; Adams, M.E.; Griffin, P.R.; Cohen, C.J.; Smith, M.M.
Biochemistry 33, 5098-5108, 1994
Biochemistry 33, 5098-5108, 1994
A;Title: "Type III omega-egatoxins: a family of probes for similar binding sites on L- an A;Reference number: A54252; MUID:94227039; PMID:8172884
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C;Species: Agelenopsis aperta
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Jan-1996
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C.Species: Agelenopsis aperta
C.Date: 06-0ct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Jan-1996
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    Indels
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A,Residues: 1-76 «ERI»
A,Experimental source: venom
A,Note: sequence extracted from NCBI backbone (NCBIP:148242)
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Pred. No. 1.5e+02;
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Best Local Similarity 57.1%;
Matches 4; Conservative
4; Conservative
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A,Residues: 1-76 <ERT>
A,Experimental source: venom
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AE3401

AE3401

AE3401

AE3401

C; Species: Disteria innocua

C; Species: Listeria innocua

C; Species: Listeria innocua

C; Date: 27-Nov-2001 #text_change 09-Jul-2004

C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C; Accession: AE1449

R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.

C; Dominguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D; Jonnes, L.M.; Karst, U.

Science 294, 849-852, 2001

A; Authors: Kreft, J; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

Ok, C.; Schlueter, T.; Simoes, N.; Tierrerz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Accession: AE1449

A; Molecule type: DNA

A; Datus DNA

A; D
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A,Residues: 1-1946 <GLA>
A;Cross-references: UNIPROT:Q92FH4; GB:AL592022; PIDN:CAC95365.1; PID:g16412551; GSPDB:G
A;Experimental source: strain Clip11262
C;Genetics:
A,Gene: lino132
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C;Species: Caenorhabditis
R;Wilson, R:
R;Wilson, Tid Solata Library, November 1995
A;Reference number: Z18493
A;Reference number: Z18493
A;Recession: Tid Solata Library translated from GB/EMBL/DDBJ
A;Recession: Tid Solata Library translated from GB/EMBL/DDBJ
A;Residues: 1-2214 *WIL>
A;Residues: 1-2214 *WIL>
A;Residues: 1-2214 *WIL>
A;Residues: Lost References: UNIPROT: Q20219; EMBL: U40420; NID: g1065513; PID: g1065514; PIDN: AAAB14
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A;Introns: 57/3; 95/1; 302/3; 323/1; 380/1; 404/1; 468/1; 507/2; 547/3; 595/3; 1532/1;
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                                  A;Accession: T47155
A;Status: preliminary
A;Molecule type: mRNA
A;Mesidues: 1288-1460 «AAA»
A;Cross-references: EMBL:AL161964
A;Experimental source: fetal brain; clone DKFZp564B0982
                                                                                                                                                                                                                                                                                                                    A; Map position: 1
A; Note: KIAA0470; DKFZp564B0982.1
A; Reference number: Z24374
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C;Genetics:

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Rismith, V.

submitted to the EMBL Data Library, September 1994

A;Refecence number: S48407

A;Accession: S48420

A;Molecule type: DNA

A;Residues: 1-121 <SIA.

A;Residues: 1-121 <SIA.

A;Cross_references: UNIPROT:P40520; GB:Z47047; EMBL:Z38060; NID:g603997; PID:g763287; GSi.
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06471
R;Pohlmeyer: K.; Soll, J.; Steinkamp, T.; Wagner, R.
R;Dohlmeyer, K.; Soll, J.; Steinkamp, T.; Wagner, R.
R;Dohlmeyer: Isolation and characterisation of a new type of pore protein present in the A;Reference number: 215701
Proc. Natl. Acad. Sci. U.S.A. 86, 10139-10143, 1989
Affile: Isolation, partial amino acid sequence, and immunohistochemical localization of
A;Reference number: A34520; MUID:90099311; PMID:2602362
A;Accession: A34520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YIL059c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48420
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                                                                                                            A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-92 -WIN>
A;Cross-references: UNIPROT:P20658
C;Superfamily: calretinin; calmodulin repeat homology
C;Keywords: brain; calcium binding; duplication; BF hand; vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-146 < POH>
A;Cross-references: UNIPROT: 041050; EMBL: Z73553; PIDN: CAA97910.1
A;Experimental source: cv. Golf
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                                                                                                                                                                                                                                                                                                           / Match 81.8%; Score 18; DB 2; Length 92; Local Similarity 57.1%; Pred. No. 1.9e+02; Pred. No. 4; Conservative 0; Mismatches 3; Indels
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C;Superfamily: Saccharomyces probable membrane protein YIL059c
C;Keywords: transmembrane protein
F;6-22/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: MIPS:YIL059c
A;Cross-references: SGD:S0001321
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Best Local Similarity 57.1
Matches 4; Conservative
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C54252
Omega-agatoxin III, 8.607K - funnel-weaving spider (Agelenopsis aperta)
C;Species: Agelenopsis aperta
C;Species: Agelenopsis aperta
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: C54252
E;Ertel, E.A.; Warren, V.A.; Adams, M.E.; Griffin, P.R.; Cohen, C.J.; Smith, M.M.
Biochemistry 33, 5098-5108, 1994
A;Title: Type III omega-agatoxins: a family of probes for similar binding sites on L-A;Reference number: A54252; MUID:94227039; PMID:8172884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omega-agatoxin IIIA - funnel-weaving spider (Agelenopsis aperta)
C;Species: Agelenopsis aperta
C;Species: Agelenopsis aperta
C;Dacession: Ad3335
R;Venema, V.J.; Swiderek, K.M.; Lee, T.D.; Hathaway, G.M.; Adams, M.E.
J. Blol. Chem. 267, 2610-2615, 192
J. Blol. Chem. 267, 2610-2615, 192
J. Briol. Chem. 267, 2610-2615, 192
J. Richtle: Antagonism of synaptosomal calcium channels by subtypes of omega-agatoxins.
A;Reference number: A42335; MUID:92129351; PMID:1310319
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81.8%; Score 18; DB 2; Length 76;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                     Query Match 81.8%; Score 18; DB 2; Length 76; Best Local Similarity 57.1%; Pred. No. 1.5e+02; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 81.8%; Score 18; DB 2; Length 76; Similarity 57.1%; Pred. No. 1.5e+02; 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: C54252
A;Status: preliminary
A;Molecule: type: protein
A;Residues: 1-76 - RER3-
A;Cross-references: UNIPROT:P81744
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:148241)
                                A; Note: sequence extracted from NCBI backbone (NCBIP:148240)
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A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:78693)
     A; Experimental source: venom
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Best Local Similarity
Matches 4; Conserva
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-76 <VEN>
                                                                                                                                                                                                                                                         42 VGTSAEF 48
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A;Cross-references: UNIPROT:Q9A714; GB:AE005673; NID:g13423365; PIDN:AAK23887.1; GSPDB:GN C;Genetics: A;Gene: CC1912 C;Superfamily: (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-190 < ELL>
A; Cross-references: UNIPROT: Q08331; EMBL: X73985; NID: G393386; PIDN: CAA52163.1; PID: G393386
A; Cross-references: UNIPROT: Q08331; EMBL: X73985; NID: G393386; PIDN: CAA52163.1; PID: G393386
C; Superfamily: calretinin; calmodulin repeat homology
C; Keywords: brain; calmodulin repeat homology < EF3>
F; 70-102, Domain: calmodulin repeat homology < EF4>
F; 114-146/ Domain: calmodulin repeat homology < EF5>
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R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z21558
A;Accession: T34819
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-194 <OLI>A;Residues: 1-194 <OLI>A;Residues: 1-194 <OLI>A;Residues: Submitted By Colidentics: Strain A3(2)
A;Coss-references: UNIPROT:O54133; EMBL:AL021530; PIDN:CAA16476.1; GSPDB:GN00070; SCOEDF
A;Experimental source: strain A3(2)
A;Gene: SCOEDB:SC2E9.08
C;Guperfamily: Streptomyces coelicolor hypothetical protein SC2E9.08
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
Afritia: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87486
A;Accession: preliminary
A;Statuus: preliminary
A;Residues: 1-159 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             calretinin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: 841476; 834391
R;Ellis, J.; Rogers, J.
Nucleic Acids Res. 21, 5171-5178, 1993
A;Title: Design and specificity of hammerhead ribozymes against calretinin mRNA. A;Reference number: 841476; MuID:94077721; PMID:8255773
A;Accession: S41476.
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C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 2; Length 155
Pred. No. 3.3e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 81.8%; Score 18; DB 2; Le:
Similarity 57.1%; Pred. No. 3.9e+02;
4; Conservative 0; Mismatches 3;
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81.8%; Score 18; DB 2;
Best Local Similarity 57.1%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Matches 4; Conserv
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                                                                                                                                                                                                                                                           hypothetical protein Vng1907h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H8441
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
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CiDate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
CiAcces: 189.486
Rivierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-147 <STO>
A;Cross-references: UNIPROT:Q9HNXO; GB:AE004437; NID:g10581349; PIDN:AAG20100.1; GSPDB:G
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-148 <STO>
A;Experimental source: strain IL1403
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C87486
hypothetical protein CC1912 [imported] - Caulobacter crescentus
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Pred. No. 3e+02;
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A,Gene: dpsA
C,Superfamily: hypothetical protein HI1349
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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Matches 4; Conser
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A,Status: preliminary
A,Molecule type: DNA
                                                  VXXXAEF
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C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell. Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyperaR;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Clostridium acetobutýlicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 16-Aug-2004
C;Accession: E97174
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Baly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A;Reference number: A96900; MUID:21359325; PMID:21359325
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C;Superfamily: Conserved hypothetical protein with haloacid dehalogenase-like hydrolase <
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C;Species: Pisum sativum (garden pea)
C;Species: Disum sativum (garden pea)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 12-Jul-2004
C;Accession: S65425
C;Accession: S65425
A;Ritle: Pyruvate decarboxylase from Pisum sativum. Properties, nucleotide and amino acic A;Reserner S65423; MUID:96215432; PMID:8647075
A;Retus: preliminary
                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q9PPH4; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73007 A;Experimental source: serotype O2, strain NCTC 11168 C;Genetics:
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A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphoserine phosphatase family enzyme [imported] - Clostridium acetobutylicum
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Pred. No. 4.3e+02;
1; Mismatches 3; Indels
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Best Local Similarity 42.9%; Pred. No. 4.4e+02;
Matches 3; Conservative 1; Mismatches 3; Indels
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C;Superfamily: thiamin pyrophosphate-binding domain homology
C;Keywords: carbon-carbon lyase; carboxy-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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Best Local Similarity 42.9
Matches 3; Conservative
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                                                                                                                             A, Accession: H81344
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-212 < PAR>
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-213 < KUR>
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A;Residues: 1-228 <MUE>
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C;Species: Campylobacter jejuni
C;Species: Janar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81344
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aryl hydrocarbon receptor - mummichog (fragment)
C;Species: Fundulus heteroclitus (mummichog)
C;Species: Fundulus heteroclitus (mummichog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150543
B;Hahn, M.E.; Karchner, S.I.
Biochem. J. 310, 383-387, 1995
A;Fitle: Evolutionary conservation of the vertebrate Ah (dioxin) receptor: amplification A;Accession: 150543; MUD:95382748; PMID:7654172
                                                                                                                                                                                                            ribosomal protein S6, cytosolic - common tobacco (fragment)
C;Species: Nicoriana tabacum (common tobacco)
C;Species: Nicoriana tabacum (common tobacco)
C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 15-Sep-2003
C;Accession: S26078; S2550
R;Hansen, G.; Estruch, J.J.; Spena, A.
Nucleic Acids Res. 20, 5230, 1992
A;Title: Tobacco cDNA encoding the ribosomal protein S6.
A;Reference number: S26078; MUID: 93027271; PMID: 1408841
A;Accession: S26078
A;Molecule type: mRNA
A;Residues: 1-211 < HAN>
A;Cross-references: EMBL: X68050
R;Hansen, G.; Estruch, J.J.; Pisabarro, G.; Sommer, H.; Spena, A.
submitted to the EMBL Data Library, August 1992
A;Reference number: S2550
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A;Molecule type: mRNA
A;Residues: 1-212 <HAH>
A;Cross-references: UNIPROT:Q90505; EMBL:U29679; NID:g976397; PID:g976398
C;Genetics:
A;Gene: AHR2
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A;Residues: 20-211 <HAW>
A;Cross-references: EMBLX68050; NID:g20021; PIDN:CAA48187.1; PID:g20022
C;Superfamily: ribosomal protein S6, eukaryotic type
C;Keywords: phosphoprotein; protein biosynthesis; ribosome
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57.1%; Pred. No. 4.3e+02;
iive 0; Mismatches 3; Indels
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4; Conservative
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4, Conservative
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Matches 4; Conserv
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                                                                                              58 VSITAEF
                                     VXXXAEF
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n; Unatterjee, P.K.; Sternberg, N.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 8950-8954, 1995
A; Title: A general genetic approach in Escherichia coli for determining the mechanism(s)
A; Reference number: IS9418; MUID: 96004656; PMID: 7568050
A; Accession: I80318
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residence type: DNA
                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:P17117; EMBL:U18655; NID:g609323; PIDN:AAC43450.1; PID:g6093; R. S. Blattner, F. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 134-154,'CA',157,'AGH',161-186,'RHWRSMTSNWRNITSPVAAIIAGIPGAIISAEQSLKKAAHLFWI]
A;Cross-references: GB:X15859; NID:g42745; PIDN:CAA33867.1; PID:g42746
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A,Experimental source: strain O157:H7, substrain RIMD 0509952
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R;Kang, W.K.; Icho, T.; Isono, S.; Kitakawa, M.; Isono, K.
Mol. Gen. Genet. 217, 281-288, 1989
A;Title: Characterization of the gene rimK responsible for the addition of glutamic acid A;Reference number: S04774; MUID:89364710; PMID:2570347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-240 <BLAT>
A;Cross.references: GB:AE000187; GB:U00096; NID:g1787070; PIDN:AAC73938.1; PID:g1787075;
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H.
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: C90745
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNR Res B., 11-22, 2001
A;Tille: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gasence number: A99629; MUID:21156231; PMID:11258796
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Pred. No. 4.9e+02;
0; Mismatches 3;
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57.1%; Pred. No. 4.9e+02;
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C;Superfamily: NADPH-flavin oxidoreductase homolog
C;Keywords: flavoprotein; FMN; oxidoreductase
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Similarity 57.1%;
4; Conservative
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Best Local Similarity
Matches 4; Conserv
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-240 <HAY>
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Oxygen-insensitive NADPH nitroreductase (EC 1.-..-) [imported] - Salmonella enterica subsouring the subsouring subspace oxygen-insensitive NADPH nitroreductase (EC 1.-..-) [imported] - Salmonella enterica subspace enterica serovar Typhi
A,Note: this species has also been called Salmonella typhi
A,Note: this species has also been called Salmonella typhi
C,Date: 09-Nov-2001 #text_change 18-Nov-2002
C,Accession: AGOGOS
R,Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A,Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A,Reference number: ABOSO2; MUID:21534947; PMID:11677608
A,Sccession: AGOGOS
A,Status: preliminary
A,Nolecule type: DNA
A,Residues: 1-240 < PAR>
A,Cross-references: GB:AL513382; PIDN:CADO5313.1; PID:g16502077; GSPDB:GN00176
C;Gene: nfsA
C;Gene: nfsA
C;Gene: nfsA
C;Gene: nfsA
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                           Pyruvate decarboxylase (EC 4.1.1.1) - fava bean (fragment)
C.Species: Vicia faba (fava bean)
C.Species: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 12-Jul-2004
C.Accession: 865426
B.;Muecke, U.; Wohlfarth, T.; Fiedler, U.; Baeumlein, H.; Ruecknagel, K.P.; Koenig, S.
Bur. J. Biochem. 237, 313-382, 1996
A.Title: Pyruvate decarboxylase from Pisum sativum. Properties, nucleotide and amino aci
A,Reference number: 865426
A,Accession: 865426
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-28 «MUE»
A,Residues: 1-28 «MUE»
A,Cross-references: UNIPROY: Q7M228
C,Superfamily: thiamin pyrophosphate-binding domain homology
C,Keywords: carbon-carbon lyase; carboxy-lyase
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N;Contains: aromatic nitrate reductase (NADPH) (EC 1.6.6.-) oxygen-insensitive
C;Specias: Escherichia coli
C;Date: 07-Jun-1996 #sequence revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 180318; C64823; S04774
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Pred. No. 4.7e+02;
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57.1%;
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Matches 4; Conservative
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Best Local Similarity 57.1
Matches 4; Conservative
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Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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A; Residues: 1-247 <NAK>
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A;Residues: 1-240 <STO>
A;Coss-references: UNIPROT:Q8X681; GB:AE005174; NID:g12513866; PIDN:AAG55227.1; GSPDB:G
A;Exomental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: mdaA
C;Superfamily: NADPH-flavin oxidoreductase homolog
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A;Residues: 1-247 <NAK>
A;Crose-references: GB:D14621; NID:g287424; PIDN:BAA03472.1; PID:g287425
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemag
C;Genetics:
                                                                                                    C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G8595
R;Perrana N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Status: preliminary
                                                                              modulator of drug activity A [imported] - Escherichia coli (etrain 0157:H7, substrain Ed
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PQ0662
outer capsid spike protein VP4 - feline rotavirus A (strain Cat2) (fragment)
N;Alternate names: VP8* protein
C;Species: feline rotavirus A
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: PQ0662
R;Nakagomi, O:, Isegawa, Y:, Ueda, S:, Gerna, G:; Sarasini, A.; Kaga, E.; Nakagomi, T.;
J, Gen. Virol. 74, 1709-1713, 1993
A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A
A;Reference number: PQ0651; MUID:93346985; PMID:8393919
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A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A;Reference number: PQ0651; MUID:93346985; PMID:8393919
A;Accession: PQ0652
A;Molecule type: mRNA
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57.1%; Pred. No. 4.9e+02;
tive 0; Mismatches 3; Indels
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C;Superfamily: rotavirus outer layer protein VP3
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Best Local Similarity 57.1
Matches 4; Conservative
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A.Cross-references: GB:D14615; NID:g287412; PIDN:BAA03466.1; PID:g287413
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemage C;Comment: This protein plays a role in viral neutralization, viral virulence and haemage c;Comment: This protein plays a role in VP3
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
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R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.; I.
J. Gen. virol. 74, 1709-1713, 1993
A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the All A;Reference number: PQ0651; MUID:93346985; PMID:833919
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A;Molecule type: mRNA
A;Residues: 1-247 <NAK.
A;Cross-references: GB:D14622; NID:g287426; PIDN:BAA03473.1; PID:g287427
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemage
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R; Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.; El
J. Gen. Virol. 74, 1709-1713, 1993
A; Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the ACI
A; Reference number: PQ0651; MUID:93346985; PMID:8393919
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A;Molecule type: mRNA
A;Residues: 1-247 *CNAK>
A;Residues: 1-247 *CNAK>
C;Cross-references: GB-D14616; NID:g287414; PIDN:BAA03467.1; PID:g287415
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemage
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C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
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C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: PQ0655
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N;Alternate names: VP8* protein
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C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
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C, Keywords: hemagglutinin; outer capsid protein
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A,Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the Al
A,Reference number: PQ0651, MUID:93346985, PMID:8393919
                                                         A;Accession: P00660
A;Molecule type: mRNA
A;Residues: 1-247 - ANAX-
A;Cross-references: GB:D14624; NID:9287430; PIDN:BAA03475.1; PID:9287431
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemage
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N;Alternate names: VP8* protein
C;Species: human rotavirus
C;Date: human rotavirus
C;Date: human rotavirus
C;Accession: PQ0659
R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.; F J Gen. Virol. 74, 1709-1713, 1993
A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the Al A;Reference number: PQ0651; MUID:93346985; PMID:839919
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A;Residues: 1-247 <NAK>
A;Cross-references: GB:D14623; NID:9287428; PIDN:BAA03474.1; PID:9287429
C;Comment: This protein plays a role in viral neutralization, viral virulence and haemagg
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N;Alternate names: VP8* protein
C;Species: human rotavirus
C;Species: human rotavirus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: PQ0658
R;Nakagomi. O: Isegawa, Y: Ueda S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.; i
J;Gen. virol. 74, 1709-1713, 1993
A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the All A; Reference number: PQ0651; MUID:93346985; PMID:8393919
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C;Comment: This protein plays a role in viral neutralization, viral virulence and haemage
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
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C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
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Best Local Similarity 57.1%;
Matches 4; Conservative
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A;Molecule type: mRNA
A;Residues: 1-247 <NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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PQ0656
outer capsid spike protein VP4 - human rotavirus (strain AU387) (fragment)
NyAlternate names: VP8* protein
NyAlternate names: VP8* protein
C;Species: human rotavirus
C;Species: human rotavirus
C;Species: human rotavirus
C;Bote: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: PQ0656
R;Makagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
J. Gen. Virol. 74, 1709-1713, 1993
A;Reference number: PQ0651; MUID:93346985; PMID:833919
A;Recession: PQ0656
A;Molecule type: mRNA
A;Residues: 1-247 cNRNA
A;Comment: This protein plays a role in viral neutralization, viral virulence and haemag
                                                                                                                   Outer capsid spike protein VP4 - human rotavirus (strain AU115) (fragment)
Nyternate names: VP8* protein
Nyternate names: VP8* protein
C;Species: human rotavirus
C;Species: human rotavirus
C;Date: 14-Unl-1994 #sequence_revision 14-Unl-1994 #text_change 20-Unn-2000
C;Date: 14-Unl-1994 #sequence_revision 14-Unl-1994 #text_change 20-Unn-2000
C;Date: 14-Unl-1994 #sequence_revision 14-Unl-1994 #text_change 20-Unn-2000
C;Date: 14-Unl-1994 #sequence_comparison of the VP8* gene of rotaviruses possessing T:;
J. Gen. Virol. 74, 1709-1713, 1993
J. Gen. Virol. 74, 1709-1713, 1993
J. Gen. Virol. 74, 1709-1713, NID:9287408; PIDN:BAA03464.1; PID:9287409
A;Residues: 1-247 <ANAX>
A;Residues: 1-247 <ANAX>
A;Coss-references: GB:D14613; NID:9287408; PIDN:BAA03464.1; PID:9287409
C;Genetics: the authors translated the codon ATG for residue C;Genetics:
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N;Alternate names: VP8* protein
C;Species: human rotavirus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: PQ0666
R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.; J. Gen. Virol. 74, 1709-1713, 1993
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57.1%; Pred. No. 5.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: VP4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
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C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: hemagglutinin; outer capsid protein
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Best Local Similarity 57.1"
"-"-a 4; Conservative
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PQ0660
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C;Species: human rotavirus A
A;Variaty: isolate 5193
A;Variaty: isolate 5193
C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 09-Jul-2004
C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 09-Jul-2004
C;Accession: S61221
R;Gollop, R.; Kaga, E.; Silberstein, I.; Shulman, L.; Nakagomi, O.; Mendelson, E.; Shif, submitted to the EMBL Data Library, August 1995
A;Description: Three forms of AU-1 like viruses differentiated by their overall genomic of Appendix to the content of AU-1 like viruses differentiated by their overall genomic of the content of the content
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A;Experimental source: strain AU-1; isolate 5193
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                                                                                                           outer capsid spike protein VP-8 - human rotavirus A (isolate 5193) (fragment)
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A;Experimental source: strain AU-1; isolate 6584
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A;Experimental source: strain AU-1; isolate 7044
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: outer capsid protein
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C, Keywords: outer capsid protein
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                         N;Alternate names: VP-8 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: S61221
A;Accession: S61221
A;Molecule type: genomic RNA
A;Residues: 1-247 <GOL>
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A; Residues: 1-247 <GOA>
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Nylternate names: VP8* protein
C;Species: human rotavirus
C;Species: human rotavirus
C;Species: human rotavirus
C;Date: 14-7u1-1994 #text_change 20-Jun-2000
C;Accession: PQ0653
R;Nakagomi, O.; Isegawa, Y.; Ueda, S.; Gerna, G.; Sarasini, A.; Kaga, E.; Nakagomi, T.;
J. Gen. Virol. 74, 1709-1713, 1993
A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A;Molecule type: mRNA
A;Reference number: PQ0653
A;Molecule type: mRNA
A;Residues: 1-247 cNAK>
A;Residues: 1-247 cNAK>
A;Consos-references: GB:D14614; NID:g287410; PIDN:BAA03465.1; PID:g287411
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A,Molecule type: mRNA

A;Residues: 1-247 «NMKZ»

A;Cross-references: GB:D14618; NID:g287418; PIDN:BAA03469.1; PID:g287419

A;Experimental source: strain AU720

C;Goment: This protein plays a role in viral neutralization, viral virulence and haemag

C;Goment: This protein plays a role in viral neutralization, viral virulence and haemag
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NyAlternate names: VP9* protein
C;Species: human rotavirus A
C;Species: human rotavirus A
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: PQ0657; PQ0654
R;Nakagomi, O:; Isegawa, Y:; Ueda, S:; Gerna, G:; Sarasini, A.; Kaga, E.; Nakagomi, T.;
J;Gen. Virol. 74, 1709-1713, 1993
A;Title: Nucleotide sequence comparison of the VP8* gene of rotaviruses possessing the A
R;Reference number: PQ0651; MUID:93346985; PMID:8393919
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A;Experimental source: strain AU785
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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   Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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Pred. No. 5.1e+02;
0; Mismatches 3; Indels
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C,Superfamily: rotavirus outer layer protein VP3
C,Keywords: hemagglutinin; outer capsid protein
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A,Gene: VP4
C,Superfamily: rotavirus outer layer protein VP3
C,Keywords: hemagglutinin; outer capsid protein
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57.1%;
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Similarity 57.1%;
4; Conservative (
57.1%;
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Best Local Similarity 57.17
Best Local Similarity 4; Conservative
                                      4; Conservative
                                                                                                                                                                                        199 VSSDAEF 205
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   Best Local Similarity
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A; Residues: 1-247 <NAK1>
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Best Local Similarity
Matches 4; Conserv
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                                      Matches
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C.Species: Serratia marcescens
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C.Accession: S34724
Submitted to the EMBL Data Library, July 1993
A.Reference number: S34724
A.Reference number: S34724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 27-Oct-2003
C,Accession: 140886
K;Chlumsky, L.J.; Zhang, L.; Jorns, M.S.
J. Biol. Chem. 270, 1825-18259, 1995
A;Title: Sequence analysis of sarcosine oxidase and nearby genes reveals homologies with A,Reference number: A57385, MUID:95355441; PMID:7543100
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Date: 05-Dec-1997 #sequence 0.7 White, 0.; Nelson, K.B.; Ketchum, K.A.; Dodson
C; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.P.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycine hydroxymethyltransferase (EC 2.1.2.1) - Corynebacterium sp. (fragment) N;Alternate names: serine aldolase; serine hydroxymethylase; threonine aldolase C;Species: Corynebacterium sp.
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A;Cross-references: EMBL:U23955; NID:g927587; PIDN:AAC43458.1; PID:g927588
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C;Keywords: phosphoprotein; pyridoxal phosphate; transferase
F;60/Binding site: pyridoxal phosphate (Lys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 2; Length 254;
Pred. No. 5.2e+02;
0; Mismatches 3; Indels
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                                                                                                                        robable oxidoreductase (EC 1.1.1.-) - Serratia marcescens
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-254 <VIE>
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                                               RESULT 49
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5374373
heat shock protein grpE - Synechocystis sp. (strain PCC 6803)
N/Alternate names: hypothetical protein sll0057
C;Species: Synechocystis sp.
G;Avariety: PCC 6803
C;Accession: S74373
Rsquence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74373
G;Strancko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                           Outer capsid spike protein VP-8 - human rotavirus A (isolate 5829 and isolate 5960) (fra N;Alternate names: VP-8 protein C;Species human rotavirus A A;Variety: isolate 5829; isolate 5960 C;Date: 18-Sep-1997 #sequence revision 18-Sep-1997 #text_change 09-Jul-2004 C;Accession: S61222; S61223 Et 23 Est 25 Est 25
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A, Molecule type: genomic RNA
A, Residues: 1-247 <GQL>
A, Cross-references: UNIPROT: Q86510; EMBL: X90734; NID: g967072; PIDN: CAA62268.1; PID: g9670
A, Experimental source: strain AU-1; isolate 5829
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A;Molecule type: genomic RNA
A;Roseidues: 1-247 - GGON-
A;Roseidues: 1-247 - GGON-
A;Cross-references: EMBL:X90735; NID:g967074; PIDN:CAA62269.1; PID:g967075
A;Experimental source: strain AU-1; isolate 5960
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-249 <KAN>
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A;Gene: VP-8
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: outer capsid protein
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A;Gene: grpE
C;Superfamily: heat shock protein grpE
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Matches 4; Conservative
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VXXXAEF 7
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Histidine-binding periplasmic protein NMA1811 [imported] - Neisseria meningitidis (strair c) Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Accession: H81806
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell)
HAITOYA, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Attle: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUD:20222556; PMID:10761919
A;Accession: H81806
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-268 < PAR>
A;Cross-references: UNIPROT:Q9JTE4; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB850381
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid ABC transporter, periplasmic amino acid-binding protein NMB1612 [imported] - N
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A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Verl A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Reference number: A81000; MUID:20175755; PMID:10710307
A; Scauss: preliminary A; Molecule type: DNA.
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A;Cross-references: UNIPROT:Q9JYF0; GB:AE002511; GB:AE002098; NID:g7226857; PIDN:AAF4196</br>
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WiAlternate names: calbindin 29
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens
CiAccession: S14109; A60253
RiParmentier, M.; Lefort, A.
Bur. J. Blochen. 196, 79-88; 1991
A;Title: Structure of the human brain calcium-binding protein calretinin and its express; A;Feterence number: S14109; MUID:91160569; PMID:2001709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; DB 2; Length 268; Pred. No. 5.5e+02; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: hisJ; NMA1811
C;Superfamily: lysine-arginine-ornithine-binding protein
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Best Local Similarity 57.1%;
Matches 4; Conservative
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55.059

orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - yeast (Pichia ohmeri)

C;Species: Pichia ohmeri

C;Species: Pichia ohmeri

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: 550699

R;Piredda, S.; Gaillardin, C.

Yeast 10, 1601-1612, 1994

A;Title: Development of a transformation system for the yeast Yamadazyma (Pichia) ohmeri

A;Reference number: 550699; MUID:95242835; PMID:7725795
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A;Molecule type: DNA
A;Residues: 1-268 <LAV>
A;Cross-references: UNIPROT;Q06758; EMBL:X64421; NID:g49067; PIDN:CAA45768.1; PID:g49068
C;Superfamily: lysine-arginine-ornithine-binding protein
                                                                                                                      A;Reaidues: Î-260 <KLE>
A;Cross-references: UNIPROT:029556; GB:AE001056; GB:AE000782; NID:g2689379; PIDN:AAB9053
C;Superfamily: thiamin biosynthesis protein thil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-261 <PTR>
A;Cross-references: UNIPROT:P48844; EMBL:235100; NID:9510926; PIDN:CAA84483.1; PID:95109
A;Nots-the source was formerly designated as Pichia ohmeri
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate decarboxylas
C;Keywords: carbon-carbon lyase; carboxy-lyase; pyrimidine nucleotide biosynthesis
F;1-261/Domain: orotidine-5'-phosphate decarboxylase homology <0PD>
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C;Species: Neisseria gonorrhoeae
C;Species: Neisseria gonorrhoeae
C;Accession: 319184
R;Lavitola, A:Y Vanni, M:Y Martin, M:V.; Bruni, C.B.
submitted to the EMBL Data Library, January 1992
A;Description: Cloning and characterization of a Neisseria gene homologous to hisJ and
A;Reference number: 319184
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                              A;Accession: F69337
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A; Reference number: A69250; MUID:98049343; PMID:9389475
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Matches 4; Conserv
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chloramphenicol resistance protein BH2116 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                             R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and s. A; Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:09KB19; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB058C
A;Experimental source: strain C-125
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K.; Lim,
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A;Reference number: A82950; MUID:20437337; PMID:10984043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H8449
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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Pred. No. 5.9e+02;
0; Mismatches 3,
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C;Superfamily: probable transcription regulator lsyR
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57.1%;
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Matches 4; Conservative
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                                                   106 VGSSAEF 112
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A;Molecule type: DNA
A;Residues: 1-293 <STO>
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1 VXXXAEF
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A;Molecule type: DNA
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A; Residues: 'E',3,'X',5-6,'X',8-10,'X',12,'X',14-15,'X',17-21,'X',23,'X',42-47,'X',49-50
B; XX',161;164,'XD',167-170,'X',772,'X',174-178,'XX',181-186,'XX',189;'XN','XSVAYK';'W',
C; Superfamily: calretinin; calmodulin repeat homology
C; Reywords: brain; calcium binding; duplication; EF hand
F;16-48/Domain: calmodulin repeat homology <EF1>
F;63-95/Domain: calmodulin repeat homology <EF2>
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A; Residues: 1-271 <STR>
A; Residues: 1-271 <STR>
A; Residues: 1-271 <STR>
A; Cross-references: UNIFROT: P47728; EMBL: X66974; NID: 955852; PIDN: CAA47385.1; PID: 955853
R; Gabrielides, C.; McCormack, A.L.; Hunt, D.F.; Christakos, S.
Biochemistry 30, 656-662, 1991
A; Title: Brain calbindin-D-28k and an M-r 29 000 calcium binding protein in cerebellum a
A; Reference number: A38396; MUID: 91105154; PMID: 1988053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glu) #status predicted
Glu) #status predicted
Glu) #status predicted
                                                                                                          A; Cross-references: UNIPROT: P22676; GB: X56667; NID: 929635; PIDN: CAA39991.1; PID: 929636 R; Parmentier, M. Adv. Exp. Med. Biol. 255, 233-240, 1989 A; Title: The human calbidins: CDNA and gene cloning. A; Reference number: A60253; MUID: 90144185; PMID: 2618861
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(Asp, Asn, Asp, Lys,
(Asp, Asp, Ser, Tyr,
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                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
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F;151-183/Domain: calmodulin repeat homology <EF4>
F;151-227/Domain: calmodulin repeat homology <EF5>
F;29,31,33,35,40/Binding site: calcium (ABP, ABN, F;164,126,131/Binding site: calcium (ABP, ABP, F;164,166,170,175/Binding site: calcium (ASP, ASP, F;208,210,212,214,219/Binding site: calcium (ASP, ASP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 16q22.2-16q22.2
C;Superfamily: calretinin; calmodulin repeat homology
C;Keywords: brain; calcium binding; duplication; EF hr
F;16-48/Domain: calmodulin repeat homology <EF1>
F;63-95/Domain: calmodulin repeat homology <EF2>
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57.1%; Pred. No. 5.6e+02
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F;151-183/Domain: calmodulin repeat homology <EF4>
F;195-227/Domain: calmodulin repeat homology <EF5>
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4; Conservative
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                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-271 <PAR>
                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-271 <PA2>
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A;Cross-references: GDB
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Length 316;
   Score 18; DB 2; Le
Pred. No. 6.5e+02;
0; Mismatches 3;
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Pred. No. 6.5e+
0; Mismatches
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57.1%;
       Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                                                                                                                                                                   VITRAEF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 VEAAAEF 101
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                               1 VXXXAEF 7
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Matches 4; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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                                                                                                                                                                                                                   268
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H69312
conserved hypothetical protein AP0504 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10.5ep-1999 #sequence_revision 10.5ep-1999 #text_change 09-Jul-2004
C;Accession: H69312
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, E.
Natures 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woses, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Reterence number: Dray
A;Reterence number: Dr
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A;Cross-references: UNIPROT:029746; GB:AE001069; GB:AE000782; NID:g2689392; PIDN:AAB9073
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1629
                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q9ZUH5; GB:AE002093; NID:g4115379; PIDN:AAD03380.1; GSPDB:GN
Cydenteics:
A;Gene: Ac2g-190
A;Map position: 2
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NiAlternate names: protein T31P16.220
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cibate: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
CiAccession: T50027
RiBevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Kalicki, J.; Wohldmann, P.; submitted to the Protein Sequence Database, May 2000
A;Reference number: 225027
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A;Experimental source: cultivar Columbia; BAC clone T31P16
Nature 402, 761-768, 1999
Aritle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84633
A;Accession: preliminary
A;Accule type: DNA
A;Residues: 1-296 <STO>
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81.8%; Score 18; DB 1; Length 301;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 2; Length 296;
Pred. No. 6.1e+02;
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A;Gene: ATSP:T31P16.220
A;Gene: ATSP:T31P16.220
A;Map position: 5
A;Introns: 26/1; 74/3; 147/3
C;Superfamily: annexin I; annexin repeat homology
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A, Cross-references: UNIPROT: Q9LX07;
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Best Local Similarity 57.1.
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A; Status: preliminary
A; Molecule type: DNA
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C.)Accession: A84304

R.Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. F.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablorloud, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A.)Authors: Hou, S.; Daniells, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lite A; Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9HPSO; GB:AE004437; NID:g10580993; PIDN:AAG19797.1; GSPDB:GN
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A;Fille: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A;Reference number: A72450; MUID:99310339; PMID:10382966
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A;Residues: 1-120 <KAW>
A;Cross-references: UNIRKOT:Q9YE96; DDEJ:AP000060; NID:g5104188; PIDN:BAA79650.1; PID:dl(.
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0677
                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Vng1497c [imported] - Halobacterium sp. NRC-1
C, Species: Halobacterium sp. NRC-1
C, Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Feb-2003
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: B72656
Gaps
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A;Molecule type: DNA
A;Residues: 1-333 <GUS>
A;Cross-references: UNIPROT:Q59500; GB:L49392; NID:g1196506; PIDN:AAB38428.1; PID:g11965(
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C;Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hon
C;Keywords: isoleucine-valine biosyntheeis; isomerase; oxidoreductase
F;18-200/Domain: ketol-acid reductoisomerase homology <KAR>
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C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Os.Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: A69059
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
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A;Cross-references: UNIPROT:027491; GB:AE000905; GB:AE000666; NID:g2622541; PIDN:AAB8591:
A;Experimental source: strain Delta H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CjAccession: UC5166
R;Gusberti, L.; Cantoni, R.; De Rossi, E.; Branzoni, M.; Riccardi, G.
Gene 177, 83-85, 1996
A;Title: Cloning and sequencing of the ilvBNC gene cluster from Mycobacterium avium. A;Reference number: JC5164; MUID:97080504; PMID:8921849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ketol-acid reductoisomerase (EC 1.1.1.86) - Mycobacterium avium
NiAlternate names: acetoNydroxy acid isomeroreductase
CiSpecies: Mycobacterium avium
CiSpecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                           Length 327;
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            A, Experimental source: strain A3(2)
C, Genetics:
A, Gene: SCOEDB.SC5H1.06c
C, Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                   Score 18; DB 2; Les
Pred. No. 6.7e+02;
0; Mismatches 3;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 17-Feb-2003
C;Accession: F86918
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HC
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
C;Accession: C70653

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devilin, K.; Peltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature, 33, 537-544, 1998

Mature, 393, 537-544, 1998

Mythics: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

Mythile: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:9829597; PMID:9634230

Mycoession: C70653

A; Residuas: preliminary; nucleic acid sequence not shown; translation not shown

M; Residuas: 1-31 < COL.

A; Residuas: 1-31 < COL.

A; Cross-references: GB:283864; GB:AL123456; NID:93261687; PIDN:CAB06203.1; PID:91781119
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C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35322
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R;Oliver, R.; Harris, D.; James, M.A.
A;Reference number: Z21575
A;Accession: T3532
A;Accession: T3532
A;Accession: T3532
A;Accession: T3532
A;Reference number: DA
A;Residues: 1.327 < OLI>
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C;Superfamily: prephenate dehydratase; prephenate dehydratase homology
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F;2-284/Domain: prephenate dehydratase homology <PPW>
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Query Match 81.8%; Score 18; DB 2; Length 321; Best Local Similarity 57.1%; Pred. No. 6.6e+02; Matches 4; Conservative 0; Mismatches 3; Indels

A;Gene: pheA C, Genetics:

216 VAALAEF 222

1 VXXXAEF 7

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A,Cross-references: UNIPROT:Q9X7R4; EMBL:AL049863; PIDN:CAB42931.1; GSPDB:GN00070; SCOED
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81.8%; Score 18; DB 2; Length 322; 57.1%; Pred. No. 6.6e+02; tive 0; Mismatches 3; Indels

Best Local Similarity 57.1 Matches 4; Conservative

Query Match

A, Accession: F86918
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-322 <STO>

C, Genetics

218 VAALAEF 224

RESULT 67

1 VXXXAEF 7

09730329-59ed.rpr

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C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: F95103
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Bisen, J.A.; Read, T.D.; Peterson, S.; Heide On, J.D.; Umayam, D.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q97RC6; GB:AE005672; PIDN:AAK75023.1; PID:g14972371; GSPDB:GNA;Experimental source: strain TIGR4
C;Genetics:
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Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Cipate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Riboskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Estern R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mci
Y, B.; Sun, P.M.; Winkler, M.E.
A. Bacteriol. 183, 5709-5717, 2001
A. Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A.Reference number: A97872; MulD:21429245; PMID:11544234
A.Reference number: A97872; MulD:21429245; PMID:11544234
A.Reference number: A97872; MulD:21429245; PMID:11544234
A.Residues: 1-335 < KURS.
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C;Superfamily: ATP-dependent phosphofructokinase, prokaryotic type; 6-phosphofructokinase
C;Keywords: phosphotransferase
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R,Keilhauer, C.; Eggeling, L.; Sahm, H.
J. Bacteriol. 175, 5595-5603, 193
A,Title: Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ill A,Teference number: A48648; MUID:93374855; PMID:8366043
A,Accession: C48648
A,Status: preliminary
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C;Genetics:
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C,Species: Corynebacterium glutamicum
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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Pred. No. 6.9e+02;
0; Mismatches 3; Indels
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable ilvC protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70855
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.a.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Davies, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Davies, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Accession: D70855
A;Status: proliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-333 <COL>
A;Cross-references: UNIPROT:053248; GB:AL021287; GB:AL123456; NID:93261508; PIDN:CAA1608
A;Experimental source: strain H37RV
                                                                                                                                                                                                                                Ketol-acid reductoisomerase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Spacession: H87120
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R;Cole, S.T.; Eiglmeier, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Accession: H87120
A;Accession: H87120
A;Accession: H87120
A;Accession: H87120
A;Accession: H87120
A;Retius: preliminary
A;Residues: 1-333 <STO>
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A;Gene: ilvC
C;Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase ho
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C;Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hd
F;18-200/Domain: ketol-acid reductoisomerase homology <KAR>
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C;Species: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
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Pred. No. 6.9e+02;
0; Mismatches 3;
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57.1%;
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                                                              255 VSNTAÈF 261
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VXXXAEF
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09730329-59ed.rpr

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Lypothetical protein CC1726 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: B87463
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DesBoy, K.T.; Doagon, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
In J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; WUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT: Q9A7J7, GB:AE005673; NID:g13423142; PIDN:AAK23702.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein VC1791 [imported] - Vibrio cholerae (strain N16961 serogr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-346 <HEI>
A;Cross-references: UNIPROT:Q9KR55; GB:AE004256; GB:AE003852; NID:g9656310; PIDN:AAF9494
A;Experimental source: serogroup O1; strain NI6961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical 39.3 kD protein in cysG-trpS intergenic region - Escherichia coli (strain K C;Species: Escherichia coli (chia coli C;Species: Escherichia coli C;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002 C;Accession: F65131  
C;Accession: F65131  
A;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002 C;Accession: F65131  
A;Secience D: J; Mau, B.; Shao, Y. Science D: J; Burland, V.; Riley, M.; Co Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: C82156
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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A, Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conserved hypothetical protein AF0507 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69313
R;Klank, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.
F; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Utterback archaece of the hyperthermophilic, sulfate-reducing archaece
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69313
A;Accession: C69313
A;Accession: C69313
A;Accession: C69313
A;Accession: C69313
A;Accession: C69313
A;Residues: 1-342 <KLE>
A;Cross-references: UNIPROT:029743; GB:AE001069; GB:AE00782; NID:g2689392; PIDN:AAB9073
                             A, Cross-references: UNIPROT: 057179; GB:L092312; NID:g551777; PIDN:AAA62431.1; PID:g400336 (S. Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hd C; Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase F:22-204/bomain: ketol-acid reductoisomerase homology < KAR>
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C;Superfamily: Methanococcus ketol-acid reductoisomerase; ketol-acid reductoisomerase hd
F;28-210/Domain: ketol-acid reductoisomerase homology <KAR>
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Cipate: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jun-2000

CiAccession: T45415

Submitted to the EMBL Data Library, September 1997

Air Reference number: 216918

Air Accession: T45415

Air Residues: preliminary; translated from GB/EMBL/DDBJ

Air Residues: 1-343 - PAR>

Air Residues: 1-343 - PAR>
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4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                Score 18; DB 1; Length 338;
Pred. No. 76+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 81.8%; Score 18; DB 2; Length 342;
Similarity 57.1%; Pred. No. 7e+02;
4; Conservative 0; Mismatches 3; Indels
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T45415
ketol-acid reductoisomerase (imported) - Mycobacterium leprae
                                                                                                                                                                                                            Query Match 81.8%;
Best Local Similarity 57.1%;
Matches 4; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                         252 VSDTAEF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VATEAEF 159
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Matches 4; Conserv
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A;Residues: 1-338 <KEI>
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phosphoserine aminotransferase homolog serC [imported] - Listeria monocytogenes (strain L
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A;Molecule type: DWA
A;Residues: 1-363 <GLA>
A;Cross-references: UNIRROT:08Y3L0; GB:NC_003210; PIDN:CAD01038.1; PID:g16412325; GSPDB:C
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matlok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Tile: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-363 <GLA>
A;Crose-references: UNPROT: Q926T3; GB:AL592022; PIDN:CAC98182.1; PID:g16415498; GSPDB:GNA;Experimental source: strain Clip11262
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF1801
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C;Superfamily: phosphoserine aminotransferase
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C;Superfamily: phosphoserine aminotransferase
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC84222
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-347 < shirt>
A;Cross-references: GB:AE000413; GB:U00096; NID:g2367215; PIDN:AAC76396.1; PID:g1789772;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yhfN
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Matches 3; Conservative
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Best Local Similarity 57.1%;
Matches 4; Conservative
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A;Molecule type: DNA
A;Residues: 1-392 <KUR>
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                           Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A62950; MUD:20437337; PMID:10984043
A;Accession: H83369
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 85
D84140
citrate synthase III mmgD [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
C;Accession: D84140
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:09K611; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB076
A,Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT;Q911Q8; GB:AE004647; GB:AE004091; NID:g9948226; PIDN:AAG0559
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2209
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A;Cross-references: UNIPROT:P91984; EMBL:Z81050; PIDN:CAB02859.1; GSPDB:GN00023; CESP:C5
A;Experimental source: clone C50B6
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T20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 365;
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A;Gene. CESP.C5OB6.10
A;Map postLion: 5
A;Introns: 66/3; 96/1; 122/2; 167/2; 189/3; 210/3; 313/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 2; 1
Pred. No. 7.5e+02;
0; Mismatches 3;
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Pred. No. 7.6e+02;
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A;Reference number: 21922
A;Accession: T20093
A;Accession: T20093
A;Action: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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57.1%;
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C,Superfamily: Citrate synthase
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Best Local Similarity 57.1
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 VSQTÁEF 323
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-368 <STO>
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maltose ABC transporter, periplasmic maltose-binding protein - Thermotoga marítima (stran C; Species: Thermotoga marítima C; Species: Thermotoga marítima C; Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C; Accession: B72283 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C; Accession: B72283 #sequence_revision B7283 #sequence R; B7818 #sequence R; B781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequestence number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: UNIPROT: 09X0T1; GB: AE001777; GB: AE000512; NID: 94981751; PIDN: AAD36279
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A,Experimental source: Clostridium acetobutylicum ATCC824
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Pred. No. 8.1e+02;
1; Mismatches 3; Indels
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Pred. No. 8.1e+02;
1; Mismatches 3; Indels
Score 18; DB 2; I
Pred. No. 7.6e+02;
0; Mismatches 3;
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A;Accession: B98127
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-397 <KUR>
A;Residues: 1-397 <KUR>
A;Cross-references: UNIPROT:O06670; UNIPROT:Q8DMW2; GB:AE007317; PIDN:AAL00847.1; PID:g1:C;Genetics: sphera
C;Genetics: cpherical coli trypsin-like proteinase degS; GLGF domain homology; trypsin-lik
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Cybecides: G84200
Nucy, Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lië
A;Actesion: G84200
A;Accession: G84200
A;Accession: G84200
A;Accession: Chalobacterium species NRC-1
A;Melecule type: DNA
A;Residues: 1-405 < STO>
A;Genetics:
C;Genetics:
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C;Species: Pisum sativum (garden pea)
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 12-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 12-Jul-2004
C;Accession: S65471; S65424
R;Muecke, U; Wohlfarth, T.; Fiedler, U; Baeumlein, H.; Ruecknagel, K.P.; Koenig, S. Bur. J Biochem. 237, 373-382, 1996
A;Title: Pyruvate decarboxylase from Pisum sativum. Properties, nucleotide and amino acic
A;Reference number: S65423; MUID:96215432; PMID:8647075
A;Accession: S65471
A;Status: mucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-405 «MUE»
A;Cross-references: UNIPROT:P51851; EMBL:Z66544; NID:g1177604; PIDN:CAA91445.1; PID:g1177
A;Residues: 1-8;146-153;209-218;350-362;386-393 «MUW»
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: cyc
C;Superfamily: Bacillus halodurans cytochrome P450 BH0579; cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: heme; iron; metalloprotein
F;353/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 2; Length 397;
Pred. No. 8.2e+02;
0; Mismatches 3; Indels
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Best Local Similarity 57.1%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels
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C;Superfamily: thiamin pyrophosphate-binding domain homology
              A;Reference number: A97872; MUID:21429245; PMID:11544234
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Similarity 57.1%;
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
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G84200
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serine proteinase [imported] - Streptococcus pneumoniae (strain TIGR4)

(;Species: Streptococcus pneumoniae

C;Date: 03-wug-2001 #sequenc_revision 03-wug-2001 #text_change 09-Jul-2004

C;Accession: E95261

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt. I.E.

Science 293 498-506, 2001

A;Authors: Loftud, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916
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C;Species: Halobacterium sp. NRC-1
C;Dates: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C;Accession: C84394
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Prettas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S., Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Title: Genome sequence of Halobacterium species NRC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Generics:
A,Gene: SP2239
C,Superfamily: Escherichia coli trypsin-like proteinase degS; GLGF domain homology; tryp
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C;Genetics:
A;Gene: argG
C;Superfamily: argininosuccinate synthase
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C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: 22-06t-2001 #sequence_revision 22-06t-2001 #text_change 09-Jul-2004
C;Accession: B98127
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Ie, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; I., P.; J.; V.; W.; W.; W.; W.; Leftowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; I., P.; P.; Sion, P.M.; Winher, M.S.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R. A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Accession: E95261
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-393 «KUR»
A, Cross-references: UNIPROT: Q97N37; GB: AE005672; PIDN: AAK76286.1; PID: g14973750; GSPDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%; Score 18; DB 2; Length 393;
57.1%; Pred. No. 8.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: strain TIGR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 VTTVAÈF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDATAEF 69
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A;Molecule type: DNA
A;Residues: 1-396 <STO>
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P450 homology

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A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endor A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95972
                                                                                                                                                                                                          A; Cross-references: UNIPROT: 0926G0; GB: AL5919B5; PIDN: CAC49444.1; PID: GI5140930; GSPDB: GRA; Experimental source: strain 1021, megaplasmid pSymB (FGalibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A; Author S. Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholeer, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.(A.); Marfile: The composite genome of the legume symbiont Sinorhizobium meliloti.
C; Genetics: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1.438 <TEL>
A;Cross-references: UNIPROT:Q66640; GB:U20824; NID:g695172; PIDN:AAC13824.1; PID:g695209
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
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C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S6588
A;Akiyama, N.; Shima, H.; Hatano, Y.; Osawa, Y.; Sugimura, T.; Nagao, M.
Eur. J. Biochem. 230, 766-772, 1995
A;Title: cDNA cloning of BR-gamma, a novel brain-specific isoform of the B regulatory sul A;Reference number: S65685; MUID:95331316; PMID:7607250
A;Reference number: S65685
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-443 <a href="https://doi.org/10.1007991">doi:0.07991</a>; PID:g17773
A;Cross-references: EMBL:D38260; NID:g1065605; PIDN:BAA07412.1; PID:d1007991; PID:g17773
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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C;Species: equine herpesvirus 2
C;Date: 27-CCT-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S55631
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J, Mol. Biol. 249, S20-528, 1995
A;Title: The DNA sequence of equine herpesvirus 2.
A;Reference number: S55594; MUID:95302501; PMID:7783207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 420;
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57.1%; Pred. No. 8.7e+02;
      Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
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C;Species: Rattus sp. (rat)
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                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-420 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: SMb21604
A;Genome: plasmid
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Matches
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C18351
phosphorotein phosphatase (EC 3.1.3.16) 2A-beta 55K regulatory chain - rabbit (fragment phosphorotein phosphorotein domestic rabbit)
C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Accession: C38351
R;Mayer, R.E.; Hendrix, P.; Cron, P.; Matthies, R.; Stone, S.R.; Goris, J.; Merlevede, M Biochemistry 30, 3589-3597, 1991
A;Title: Structure of the 55-kDa regulatory subunit of protein phosphatase 2A: evidence A;Secession: C38351
A;Accession: C38351
A;Status; preliminary
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D95972
D95972
Cycbable sugar uptake ABC transporter periplasmic solute-binding protein precursor SMb21
C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: D95972
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
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C;Species: Nicotiana tabacum (common tobacco)
C;Species: Nicotiana tabacum (common tobacco)
C;Accession: S57820
R;Bucher, M.; Brander, K.A.; Sbicego, S.; Mandel, T.; Kuhlemeier, C.
Plant Mol. Biol. 28, 739-750, 1995
A;Reference number: S57819; MUID:95375236; PMID:7647304
A;Status: S7819; MUID:95375236; PMID:7647304
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
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C;Keywords: carbon-carbon lyase; carboxy-lyase
F;1-405/Product: pyruvate decarboxylase #status experimental <MAT>
F;271-317/Domain: thiamin pyrophosphate-binding domain homology <TPB>
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                                                                                                                      Score 18; DB 2; Length 405;
Pred. No. 8.3e+02;
0; Mismatches 3; Indels
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A,Cross-references: EMBL:X81854
C,Superfamily: thiamin pyrophosphate-binding domain homology
C,Superfamily: thiamin pyrophosphate-binding comain homology
C,Steywords: carbon-carbon lyase; carboxy-lyase
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Pred. No. 8.5e+02;
0; Mismatches 3;
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C; Keywords: phosphoric monoester hydrolase
                                                                                                                   Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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ilarity 57.1%;
Conservative
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Matches 4; Conservative
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Best Local Similarity
4; Conserve
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A; Residues: 1-412 < MAY>
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By hosphatase 2-alpha regulatory chain - human

By Alternate names: phosphorotein phosphatase 2A-alpha 55K regulatory chain B

C;Species: Homo sapiens (man)

C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-Jul-2004

C;Accession: A38351

R;Mayer, R.E.; Hendrix, P.; Cron, P.; Matthies, R.; Stone, S.R.; Goris, J.; Merlevede, W

A;Title: Structure of the 55-kDa regulatory subunit of protein phosphatase 2A: evidence

A;Reference number: A38351

A;Attitle: A38351

A;Attitle: A38351

A;Attitle: MuD:91198016; PMID:1849734

A;Reterence number: A38351

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A;Gene: GDB:PPP2R2A
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Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
EMBL, ARO16942, AAO78999.1; ..
Complete proteome; Hypothetical protein.
SEQUENCE 116 AA, 11869 MW; DFAC729A3C3B9FAC CRC64;
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PubMed=1244438; DOI=10.1038/nature01184;
Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita S., Honda M., Ichikawa Y., Idonuma A., Ilijima M., Ikeda M.,
Ikeno M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;
Draft sequence of the Glardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Giardia lamblīa ATCC 50803.
Bukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
                                                                                          h Similarity 57.1%; Pred. No. 1e+03; Jength 116; 4; Conservative 0; Mismatches 3; Indels
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Similarity 57.1%; Pred. No. 1.1e+03;
4; Conservative 0; Mismatches 3; Indels
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SEQUENCE 126 AA; 13845 MW; 2BE6EEB9F73D7D7D CRC64;
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01-UTN-2003 (TFEMBLrel. 2:
01-OCT-2003 (TFEMBLrel. 2:
B1139B11.11 proctein.
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STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550808; PubMed=12663928; DOI=10.1126/science.1080029;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
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Q8evls 1
Q94em8
Q6abx6
Q926t3
Q926t3
Q71vt6
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Q91q8
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Q98my9
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Q6n130
Q9zp53
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Q8n1p4
Q92qw1
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07z7h3
083b80
07pj50
08fly3
09h6p6
09x0t1
097dg9
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O86mw2
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Bacteroidaceae; Bacteroides.
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Q9ZPS3

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Q87Z7H3
Q83BB0
Q7Z7H3
Q8FLX3
Q9FLX6
Q9YDG1
Q97DG1
Q97N37
ASSY HALN1
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Q7W717
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OrderedLocusNames=BT3794;
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 NCBI_TaxID=818;
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01-JUN-2003
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Matches 4; Conservative
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SEQUENCE FROM N.A.
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Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K. Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (COT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AV060702; AAL28260.1; -
FlyBase; FBGN0037525, CG17816.
SEQUENCE 159 AA; 17663 MW; C33175B9B3436C4D CRC64;
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Boptera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                        "The genome sequence and structure of rice chromosome 1."; Mature 420:312-316(2002).
BMBL; AP004369; BAB90783.1; -.
HSSP; O82040; 1K9U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.4%; Score 19; DB 2; Length 146; 57.1%; Pred. No. 1.3e+03; ive 0; Mismatches 3; Indels
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Calcium; Calcium-binding.
SEQUENCE 146 AA; 16257 MW; C6DDE4C8612A2E7C CRC64;
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GO, GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR002048; EF-hand.
InterPro; IPR010983; EF Hand like.
ProDom; PD000012; EF-hand, 2.
SWART; SM00054; EFh; 4.
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Q9NSN9;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2002 (TrEMBLrel. 22,
GH14459p.
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1095SM3
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Nucleic Acids Res. 31:6516-6523 (2003).
Nucleic Acids Res. 31:6516-6523 (2003).
-!- SIMILARITY: Contains 1 HTH tetR-type DNA-binding domain.
EMBL; BX248356; CAE4336.1; -.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009657; HTH_TetR.
                                                                Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Biotype gravis / NCTC 13129;
MEDLINE=2296544; PubMed=14602910; DOI=10.1093/nar/gkg874;
MEDLINE=2296544; PubMed=14602910; DOI=10.1093/nar/gkg874;
MEDLINE=2296544; PubMed=14602910; DOI=10.1093/nar/gkg874;
Pallen M.J. Bentley S.D., Besra G.S., Churcher C.M., James K.D., De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T., Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A., Rabbinowitsch E., Rutherford K.M., Thomson N.R., Unwin L., Whitchead S., Barrell B.G., Parkhill J.;
"The complete genome sequence and analysis of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                          PougeKa A., Wellenreuther R., Mewes H.W., Weil B., Wiemann S., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL161964, CAB82309.1; -.
Hypothetical protein.
SEQUENCE 173 AA, 19157 MW, B3CEF034C1E5D4BB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
NCBI_TaxID=1717;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 2; Length 173; Pred. No. 1.5e+03; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation.
SEQUENCE 222 AA; 24446 MW; 14DD3E055EBC79F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome; DNA-binding; Transcription;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence
05-JUL_2004 (TrEMBLrel. 27, Last annotat:
Putative tetR family regulatory protein.
Name-amtR; OrderedLocusNames=DIP0846;
Hypothetical protein DKFZp564B0982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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GO; GO:0007242; P:intracellular signaling cascade; IEA
                InterPro; IPR008973; C2 CalB.
InterPro; IPR02219; DAG_PE-bind.
Pfam; PF00130; C1 1; 1.
PRINTS; PR00109; C1 1; 1.
SMART; SM00109; C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 57.1%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01415; ANKYRIN.
                                                                                                                                              Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                   201 VATAAEF 207
                                                                                                                                                                                                       1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=URA3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                       Q691P2
Q691P2;
                                                                                                      Kinase
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EMBL, AK131548; BAD18682.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINEEI TOR NIGS61 / Serotype 01;
MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
MEDLINE=20406833; PubMed=10952301; Pettelin H., Richardson D.L.,
Gill S.R., Nelson K.E., Rash T.D., Tettelin H., Dragoi I.,
Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
Mexalanos J.J., Venter J.C., Fraser C.M.;
"DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.4%; Score 19; DB 2; Length 240; 57.1%; Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 AA; 26500 MW; F856E48C3BD6980E CRC64;
                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016491, F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000415; Nitroreductase.
                   240 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00881; Nitroreductase; 1.
                                                                                                                                                                                                                                                                                                                                                           Nature 406:477-483(2000).
EMBL, AE004158; AAF93880.1; -.
PIR, D82288, D82288.
HSSP, Q56691; 1BKJ.
TIGR; VC0715; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein FLJ16784. Homo sapiens (Human).
                                                                                      NADPH-flavin oxidoreductase.
                                                                                                    OrderedLocusNames=VC0715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
4; Conserve
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SEQUENCE 240 AA
                                                                                                                  Vibrio cholerae
                                                                                                                                                           NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                  cholerae.
                Q9KU15
Q9KU15;
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                                                                                                         Gaps
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Ankyrin repeat protein-like.
Name=OSJNBa0039D04.6;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Metschnikowiaceae; Clavispora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
"Oryza sativa nipponbare(GA3) genomic Clone:OSJNBA0039004.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AP006753; BAD32119.1; -.
PiterPro; IPR002110; ANK.
                                                Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.4%; Score 19; DB 2; Length 255; 57.1%; Pred. No. 2.1e+03; ive 0; Mismatches 3; Indels
SEQUENCE 243 AA; 27566 MW; 23D41825EB9F782D CRC64;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TremBrel. 26, Last annotation update)
                                                86.4%; Score 19; DB 2;
57.1%; Pred. No. 2e+03;
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                                                                                                    0; Mismatches
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PROSITE; PS50297; ANK REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                           PRT;
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Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                   39 VTTTÄEF
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                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Q8XBJ2;
                                                                                                                                                                         Q96L14;
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                                                                                                                               RESULT 12
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-!- CATALYTIC ACTIVITY: Orocidine 5'-phosphate = UMP + CO(2).
-!- SATHWAY: Parimidine biosynthesis.
-!- SATHWAY: Balongs to the OWP decarboxylase family.
EMBL, AB006207; BAA24611.1; --
HSSP: P03962; IDQW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016829; F:1yase activity; IEA.
GO; GO:0004590; F:1yase activity; IEA.
GO; GO:0006221; P:pyrimidine base biosynthesis; IEA.
GO; GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA.
InterPro; IPR001754; OMPdecase.
InterPro; IPR011060; RibP_bind_barrel.
Pfam; PF00215; OMPdecase:
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                             GO:0016829; Filyase activity; IEA.
GO:0004590; F:orotidine-5'-phosphate decarboxylase activity; IEA.
GO:0006207; P:'de novo' pyrimidine base biosynthesis; IEA.
GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA.
           Francois F., Chapeland-Leclerc F., Villard J., Noel T.; "Development of an integrative transformation system for the opportunistic pathogenic yeast Candida lusitaniae using URA3 as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                              STRAIN=CBS 6936;
Francois-Vadrot F., Chapeland-Leclerc F., Villard J., Noel T.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Orotidine 5'-phosphate = UMP + CO(2).
                                                                                                                                                                                                                                                                                                                                                                           Length 264;
                                                                                                                                                                - PATHWAY: Pyrimidine biosynthesis.
- I- SIMILARITY: Belongs to the OMP decarboxylase family.
- I- SIMILARITY: Belongs to the OMP decarboxylase family.
- I- SIMILARITY: Belongs to the OMP decarboxylase family.
- I- SIMILARITY: Belongs to the OMP decarboxylase family.
- I- SIMILARITY: Belongs to the OMP decarboxylase ac
- GO: GO: 0004529; F: Iyase activity; IEA.
- GO: GO: 0004590; F: Orocidine-5'-phosphate decarboxylase ac
- GO: GO: 000421; P: Yer imidine base biosynthesis;
- FFEM: PF00215; OMPdecase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
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SEQUENCE 267 AA; 29521 MW; 48D2C8CBFF85846B CRC64;
                                                                                                                                                                                                                                                                                                                                 Decarboxylase, Lyase, Pyrimidine biosynthesis.
SEQUENCE 264 AA, 28913 MW, 98949F050BBEB79B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Cotidine-5'-phosphate decarboxylase (EC 4.1.1.23).
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Pred. No. 2.2e+03;
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PROSITE; PS00156; OMPDECASE; 1.
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PROSITE; PS00156; OMPDECASE; 1.
                                                                                                                                                                                                                                                                                                                                                                           86.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida tropicalis (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 57.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                      feast 21:95-106(2004).
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                                                                                                  SEQUENCE FROM N.A.
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 STRAIN=CBS 6936;
                                                        selection marker
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042694;
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Richards R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,
A plokins R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,
A papleron M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
A Hakebley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Generation and initial analysis of more than 15,000 full-length human
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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     Length 267;
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Pred. No. 2.4e+03;
                                                     Indels
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Straubberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014590; AAH14590.2; -.
Hypothetical protein.
SEQUENCE 293 AA; 32648 MW; 74904E44B67399F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
Score 19; DB 2; Ler
Pred. No. 2.2e+03;
0; Mismatches 3;
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10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Name-yfeU; OrderedLocusNames=z3693, ECs3299;
Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                      293 AA.
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  86.4%;
57.1%;
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Best Local Similarity 57.1.
A; Conservative
                                                        4; Conservative
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                                       STRAIN=206.HI / CT0703 / ATCC 700928 / UPEC; MEDLINE=2388234; PubMed=12471157; DOI=10.1073/pnas.252529799; WEICH R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Masko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
-!- SIMILARITY: Belongs to the GCKR family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 1; Length 298; Pred. No. 2.5e+03; 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMĀIN 56 214 SIS.
SEQUENCE 298 AA; 31105 MW; 3F6DECAE3F784994 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YFEU ECOLI STANDARD; PRT; 298 AA. P76535; P76965; P76966; P76967; 01-NOV-1997 (Rel. 35, Created) LNOV-1997 (Rel. 35, Last sequence update) 25-JAN-2005 (Rel. 46, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=yfeU; OrderedLocusNames=b2428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGRO0274; GCKR like; 1.
PROSITE; PS01272; GCKR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; ME_00068; -; 1.
InterPro; IPR005486; GCKR.
InterPro; IPR005488; GCKR_like.
InterPro; IPR001347; SIS.
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Best Local Similarity 57.1%;
Matches 4; Conservative
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                          SEQUENCE FROM N.A.
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YFEU ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
STRAIN-0157-117 / Sakai / RIMD 0509952 / EHEC;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnshi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P. S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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57.1%; Pred. No. 2.5e+03;
tive 0; Mismatches 3;
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10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 8:11-22(2001).
-!- SIMILARITY: Belongs to the GCKR family.
-!- SIMILARITY: Contains 1 SIS domain.
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Escherichia coli 06.
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TIGRPAMB; TIGR00274; GCKR like; 1.
PROSITE; PS01272; GCKR; 1.
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                          Enterobacteriaceae; Escherichia
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InterPro; IPR005486; GCKR.
InterPro; IPR005488; GCKR_like.
InterPro; IPR001347; SIS.
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                                                                                                SEQUENCE FROM N.A.
                                            NCBI_TaxID=83334;
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ID YFEU ECOL6
AC Q8FFE0;
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Best Loc Matches

RESULT 14

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Bordetella pertussis.
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                                                                     Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takhahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamaqata S., Horiuchi T.; "Construction of a contiguous 874-kb sequence of the Escherichia colista sequence corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Snigelia ilexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                           Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B., "Enrichment of low abundance proteins of Escherichia coli by hydroxyapatite chromatography." |
Electrophoresis 20:2181-2195(1999).
-!- SIMILARITY: Belongs to the GCRR family.
-!- SIMILARITY: Contains 1 SIS domain.
-!- CAUTION: Ref. 2 sequence differs from that shown due to a frameshift in position 87.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.4%; Score 19; DB 1; Length 298; 57.1%; Pred. No. 2.5e+03; tive 0; Mismatches 3; Indels
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298 AA; 31220 MW; 34FE8F878E8B3077 CRC64;
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29-MAR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=yfeU; OrderedLocusNames=SF2481, S2629;
                                                                                                                                                                                                                                                                                 Enterobacteriaceae; Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 57.1
es 4; Conservative
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Q83QN4;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibo.ch).
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MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
                                                                                                                                                               "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
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Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella flexnari serotype Za strain 2457T.";
Infect. Immun. 71:277-2786(2003).
-!- SIMILARITY: Belongs to the GCKR family.
-!- SIMILARITY: Contains 1 SIS domain.
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Alcaligenaceae, Bordetella.
                                                                                                                                                                                                                                                                                                                                                                STRAIN=2457T / ATCC 700930 / Serotype 2a,
MEDLINE=22590274; PubMed=12704152;
DOI=10.1128/INI.71.5.2775-2786.2003,
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
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31183 MW; FB63F15725C1091F CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
101-ORT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
OrderedLocusNames=BP0330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 AA.
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InterPro; IPR005486; GCKR.
InterPro; IPR005488; GCKR_like.
InterPro; IPR001347; SIS.
Pfam; PP01380; SIS; 1.
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"Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:R77-R77(2004).

EMBL; AR0171331.1; -.

Hypothetical protein.

SEQUENCE 379 AA; 44618 MW; F3D59CE9A9F47F6E CRC64;
                                                                                                                                                                                        December 15077118; DOI=10.1038/nbt959; Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Signati R., Haveman S.A., Hemme C.L., Paulsen I.T., Baugherty S.C., Desoy R.T., Dodson R.J., Durkin A.S., Madipu R., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Lambda integrase-like, N-terminal, DNA breaking-
rejoining enzyme, catalytic core)
ORFNames-BL01373, BLi01428;
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                                                                     Bacteria, Proteobacteria, Deltaproteobacteria, Desulfovibrionales,
Desulfovibrionaceae, Desulfovibrio.
NCBI_TaxID=882;
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                                                 Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.4%; Score 19; DB 2; Length 377
57.1%; Pred. No. 3.18+03;
ive 0; Mismatches 3; Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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                            OrderedLocusNames=DVU0125;
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PubMed=15383718;
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EMBL, AY268839; AAQ1568.1; -.
GO; GO:0008171; F:O-methyltransferase activity; IEA.
GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR001601; Methyltransf.
InterPro; IPR009051; SAM bind.
InterPro; IRR009058; Wing ha.
Methyltransferase; Transferase.
SEQUENCE 355 AA; 39842 MW; DD408079B18D8F71 CRC64;
                                                                                                                                                                           Nat. Genet. 35:32-40(2003).
BMBL; BX640411; CAR40707.1; -.
GO; GO:000288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
InterPro; IPR005064; UPP0065.
Chillingworth T., Collins M., Cronin A., Davis P., Boggett J., Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norbersak H., O'Neil S., Ormond D., Price C., Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares R., Squares S., Stevens K., Unwin L., Whitchead S., Barrell B.G., Maskell D.J., "Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis, and Bordetella bronchiseptica.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ounaroon A., Decker G., Schmidt J., Lottspeich F., Kutchan T.M.; "(R.,8)-Reticuline 7-0-methyltransferase and (R.)8-norcoclaurine 6-0-methyltransferase of Papaver somniferum - cDNA cloning and characterization of methyl transfer enzymes of alkaloid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Papaver somniferum (Opium poppy).
Babaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, Ranunculales, Papaveraceae; Papaver.
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                                                                                                                                                                                                                                                                                  proteome; Hypothetical protein. 338 AA; 34618 MW; 65F3D103502CE118 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
Last annotation update)
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Pred. No. 2.8e+03;
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Best Local Similarity
4, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 VAASAEF 293
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Plant J. 36:808-81
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05-JUL-2004
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                                                                                                                                                                                                                                                                                    Complete
SEQUENCE
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Q6WUC2

RESULT 18

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Q72FT8

Matches

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RESULT 19 Q72FT8 ID Q72FT AC Q72FT DT 05-JU DT 05-JU

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01-NOV-1998 (TrEMBLrel. 08, Created
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NCBI_TaxID=160488;
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TIGRFAMS; TIGR00797; matE; 1.
                                                                                                                                  EMBL; AP003282; BAB64772.1;
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Q88CB9
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Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
Ikeno M., Itoh Y., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
Nagasaki H., Nakashima M., Nakama Y., Nakamura M.,
Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name-FIEK9.6;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzees; Oryza.
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                                 86.4%; Score 19; DB 2; Length 379; 57.1%; Pred. No. 3.1e+03; ive 0; Mismatches 3; Indels
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2002 (TrEMBLrel. 22,
P0583G08.7 protein.
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Query Match
Best Local Similarity 5/...
Best Local 4/ Conservative
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nes 4; Conservative
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                                                                                                                                                                                                                               VAAAAEF 51
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OC 0942T2
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Q9ZVTS
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MEDLINE=22423060; PubMed=12534463;
Nelson K.B., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moest,
Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Bun M.Y., Yano M., Jiang J., Gojobori T., "The genome sequence and structure of rice chromosome 1."; Nature 420:312-316(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas putida (strain KT2440).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.4%; Score 19; DB 2; Length 435; Best Local Similarity 57.1%; Pred. No. 3.5e+03; Matches 4; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                            Gramene; Q947T2; -.
Interpro; IRRO04314; DUP239.
PÉmi; PF03080; DUP239; 1.
SEQUENCE 435 AA; 47559 MW; 49CB0F59D6B46DF5 CRC64;
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01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MATE efflux family protein.
OrderedLocusNames=PP5262;
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GO; GO:0015297; F:antiporter activity; IEA.
GO; GO:0015238; F:drug transporter activity; IEA.
GO; GO:0006855; P:multidrug transport; IEA.
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Sockett R.E., Schuster S.C.; "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from
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STRAIN=HD100 / DSM 50701 / ATCC 15156 / NCIB 9529;
STRAIN=HD100 / DSM 50701 / ATCC 15156 / NCIB 9529;
PubMed=14752164; DOI=10.1126/science.1093027;
Rendullic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales,
Bdellovibrionaceae, Bdellovibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO: GO:0007010; P:cytoskeleton organization and biogenesis; IEA InterPro; IPR002097; Profilin.
                                                                                                                          Vibrio vulnificus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                        Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 h 86.4%; Score 19; DB 2; Length 516; Similarity 57.1%; Pred. No. 4.1e+03; 4; Conservative 0; Mismatches 3; Indels
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Pred. No. 4.16+03;
                                                                                                                                                                                                                                                                                                       "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AED16800; AAO09608.1; -.
Complete Proteome.
SEQUENCE 516 AA; 57283 MW; IDC881279BD2C1EF CRC64;
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                                            Last sequence update)
Last annotation update)
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Last annotation update)
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EMBL; BX842649; CAE79080.1; -
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0003709; F:actin binding; IEA.
GO; GO:0007010; P:cytoskeleton organizatio
                         Created)
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                     01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26, Predicted membrane protein. OrderedLocusNames=VV11134;
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Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity
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SEQUENCE 522 AA;
                                                                                                                                                                                   NCBI_TaxID=672;
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Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
"Comparative genome analysis of Vibrio vulnificus, a marine
                                                                                                                                                                                                                                                                Romine M.F., Stillwell L.C., Wong K.-K., Thurston S.J., Sisk E.C., Sensen C., Gaasterland T., Fredrickson J.K., Saffer J.D.; "Complete sequence of a 184-kilobase catabolic plasmid from Sphingomona aromaticivorans F199-"; J. Bacteriol. 181:158-vrans F199-"; J. Bacteriol. 181:158-vrans F199-"; PRO79317; AAD03948.1; -...
EMBL; AF079317; AAD03948.1; -...
FILLETPC: IPR010927; TraH.
Plasmid; Signal.
                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Novosphingobium.
NCBI_TaxID=48935;
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 2; Length 484; Pred. No. 3.9e+03; 0; Mismatches 3; Indels
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Pred. No. 4.1e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 AA; 52034 MW; 992DC004E93C4C40 CRC64;
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SEQUENCE 516 AA; 57208 MW; 5626021DC1B521A3 CRC64;
01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Pilus assembly and synthesis protein precursor.
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                                                                                                                                                                                                                                               MEDLINE=99175459; PubMed=10049392;
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EMBL; AP005330; BAC92857.1; -.
                                                                                   Sphingomonas aromaticivorans.
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nes 4; Conservative
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                                                                                                        Plasmid pNL1
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MEDINE-238825; PubMed=1247912; DOI=10.1073/pnas.242603899;

Altausher R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N. K.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N. K.,

Hopkine R.F., Jordan H., Moore T., Max S.I., Mang J., Heish F.,

Aspleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wakarn P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Raba S.S., Mochey K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Brakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Jones S.J., Maring M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Maring M.J., Smailus D.E., Schnerch A., Schein J.E.,

Radencation and initial analysis of more than 15,000 full-length human
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                                                                                                                                  Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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STRAIN=JCM 10545 / 7;
STRAIN=JCM 10545 / 7;
MEDLINE=214565165 PubbMed=11572479;
Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.
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EMBL; BC044201; AAH44201.1; -.
ZFIN; ZDB-GENE-030131-9382; zgc:55619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 575 AA; 66162 MW; A3EDACD583A73531 CRC64;
               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein zgc:55619.
ORFNames=zgc:55619;
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Last annotation update)
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STRAIN=AB; TISSUE=Whole body;
Strausberg R.;
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01-MAR-2004 (TrEMBLrel. 26, 1
Hypothetical protein ST2017.
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A diffontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Ajgle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Despons L., Fabre E., Fairhead C., Confanioleri F., de Daruvar A.,
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Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
A Wincker P., Souciet J.L.,
I "Genome evolution in yeasts.";
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Yarrowia lipolytica chromosome F of strain CLIB99 of Yarrowia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 2; Length 599;
Pred. No. 4.7e+03;
0; Mismatches 3; Indels
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Pred. No. 5.5e+03;
0; Mismatches 3; Indels
                                                                                                                   "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
EMBL; AP000988; BAB67116.1; -.
InterPro; IPR008928; GlyCo_trans_6hp.
InterPro; IPR010916; TONB Box N.
PROSITE; PS00430; TONB BDEPENDENT REC_1; UNKNOWN_1.
Complete proteome; Hypothetical protein.
SEQUENCE 599 AA; 69660 MW; F8B94CAE7731D119 CRC64;
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InterPro; IPR007244; MaxLO_Actrans.
Pfam; PF04112; MaxLO; 1.
SEQUENCE 712 AA; 79869 MW; 4E5D512544154E11 CRC64;
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57.1%;
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Best Local Similarity 57.1%;
Matches 4; Conservative
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ORFNames=YALIOF08591g;
Yarrowia lipolytica CLIB99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kchara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
"Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                       usually bicarbonate (By similarity).
-!- DOMAIN: Composed of two homologous domains (By similarity).
-!- SIMILARITY: Belongs to the transferrin family.
EMBL; US1824, AAC64660.1; -.
HSSP; P56410; IAOV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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SEQUENCE 995 AA; 110118 MW; DCF10D729E67A533 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradyřhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.4%; Score 19; DB 2; Length 977; 57.1%; Pred. No. 7.4e+03; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR01156; Peptidas 560.
Pfam; PF00405; Transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM0094; TR FER; 2.
PROSITE; PS00206; TRANSFERRIN 2; 1.
Iron transport; Metal-binding; Signal; Transport.
I 22 Potential; CHAIN 23 977 Pacifastin heavy chain.
SEQUENCE 977 AA; 106866 MW; SEF1706133350E99 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glutamate-ammonia-ligase adenylyltransferase.
Name=glnE; OrderedLocusNames=blril33;
                                                                                                                                                                                                                                                                                              GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008199; F:ferric iron binding; IEA.
GO; GO:0006819; P:iron ion homeostasis; IEA.
GO; GO:0006826; P:iron ion transport; IEA.
GO; GO:0006810; P:transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    488 VSAAAEF 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VXXXAEF 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-USDA110;
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-!- PATHWAY: Involved in glycolysis and in gluconeogenesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the GPI family.
C -!- SIMILARITY: Belongs to the GPI family.
R GO; GO:0004347; F:glucose-6-phosphate isomerase activity; IEA.
GO; GO:0004801; F:transaldolase activity; IEA.
GO; GO:0005953; F:isomerase activity; IEA.
GO; GO:000595; P:arabolydrate metabolism; IEA.
R GO; GO:0006994; P:glucose-cphosphate shunt; IEA.
R GO; GO:0006095; P:glycolysis; IEA.
R GO; GO:0006095; P:glycolysis; IEA.
R InterPro; IPR001472; Tal mycobact.
R InterPro; IPR00142; Tal mycobact.
R Pfam; PF00342; PGI; I. Tansaldolase.
R Pfam; PF00342; PGI; I. Tansaldolase.
R Pfam; PF00342; PGI; I. Tansaldolase.
                                                                                                                                                                                                                                                                                                                                                                                                                Gluconobacter oxydans (Gluconobacter suboxydans).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales,
Acetobacteraceae, Gluconobacter.
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MEDLINE=97338078; PubMed=9192625; DOI=10.1073/pnas.94.13.6682;
Liang Z., Sottrup-Jensen L., Aspan A., Hall M., Soderhall K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Sugiyama M., Suzuki S., Tonouchi N., Yokozeki K.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transaldolase and glucose-6-phosphate isomerase bifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Pacifastin heavy chain precursor.
Pacifastaus leniusculus (Signal crayfish).
Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Astacidea;
Astacoidea; Astacidae; Pacifastacus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.4%; Score 19; DB 2; Length 957; 57.1%; Pred. No. 7.2e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             977 AA.
                                                                                                                                                                                  957 AA.
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                                                                                                                                                                            PRELIMINARY;
                              300 VTSSAEF 306
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                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                           Q76EM6;
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P91775
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1 VXXXAEF 7
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                                                 Best Local Similarity
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  ANK repeat.
                                       Query Match
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Q92K44
                                                              Matches
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A Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
Mollet B., Mercenier of the probiotic intestinal bacterium
Lactobacillus johnsonii NCC 533.";
Lactobacillus johnsonii NCC 533.";
L. Proc. Natl. Acad Sci. U.S.A. 101:2512-2517(2004).
T. SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
R. REBL; ABCOTION: Attached to the cell wall peptidoglycan by
an amide bond (By similarity).
R. GO: GO: 0009986; C:cell surface; IEA.
InterPro: IPR001899; Gram_pos_anchor.
R. Pfam; PF00746; Gram_pos_anchor;
R. Pfam; PF00746; Gram_pos_anchor;
R. Pfam; PF00746; Gram_pos_anchor;
R. Pfam; PS081TE; PS50847; GRAM POS_ANCHORING;
M. Cell wall Complete proteome; Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (WAR-2003) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.4%; Score 19; DB 2; Length 1096; 57.1%; Pred. No. 8.2e+03;
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Giardia lamblia ATCC 50803.
Bukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
                                                                                                                                                Lactobacillus johnsonii.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1096 AA; 114350 MW; 4C8A938FB8FAC284 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                    Last sequence update)
Last annotation update)
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InterPro; IPR00110; ANK.
Pfam; PF00023; Ank; 9.
PRINTS; PR01415; ANK/REIN.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                        Created)
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                                                                                                05-JUL-2004 (TrEMBLrel, 27, 05-JUL-2004 (TrEMBLrel, 27,
                                                                                     05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                        OrderedLocusNames=LJ0391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 57.1
1es 4; Conservative
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                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptidoglycan-anchor.
SEQUENCE 1096 AA;
 816 VSASAEF 822
                                                                                                                          Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 VSTSÁÉF 295
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                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                        NCBI_TaxID=33959;
                                                                                                                                                                                                                             STRAIN=NCC 533;
PubMed=14966310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=WB C6;
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                                    RESULT 34
Q74L34
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Q7QTJ4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21396507; PubMed=11481430; DOI=10.1073/pnas.161294398; Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; Sinorhizobium mellioti strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 98:3877-9882(2001).

EMBL; ALS9189; CAC46716.1; -
Complete protecome; Hypothetical protein.

SEQUENCE 1234 AA; 130531 MW; 772A245CD29F56IC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NGBL_TaxID=382;
                                                         86.4%; Score 19; DB 2; Length 1191; 57.1%; Pred. No. 8.8e+03;
1191 AA; 132435 MW; 70A77664DD550A2D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SMc01454.
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Last annotation update)
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                                                                                                                        0; Mismatches
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Similarity 57.1%;
4; Conservative
                                                                                        Similarity 57.1%;
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                311 VSATAEF 317
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Best Local Similarity
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DOI=10.1128/JB.185.7.2330-2337.2003,
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparive genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
J. Bacteriol. 185:2330-2337(2003).
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TISSUB-Brain;
MEDLINE-98116662; PubMed-9455484;
Seki N., Ohira M., Nagage T., Ishikawa K., Miyajima N., Nakajima D.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                        Length 1266;
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                                                                                                                                                                                    86.4%; Score 19; DB 2; Length 126
57.1%; Pred. No. 9.4e+03;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 2; Length 146
Pred. No. 1.1e+04;
0; Mismatches 3; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00498; FHA; 1.
SMART; SM00240; FHA; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
SEQUENCE 1460 AA; 161436 MW; BAD23EBCA19B65F0 CRC64;
                                                                                                                               EMBL; AE016845; AA070819.1; -.
SEQUENCE 1266 AA; 138744 MW; 339C4A88D35922B2 CRC64;
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last annotation update)
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   MEDLINE=22531367; PubMed=12644504;
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InterPro; IPR000253; FHA.
InterPro; IPR008984; SMAD_FHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIAA0470 protein (Fragment)
Name=KIAA0470;
Homo sapiens (Human).
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Best Local Similarity 57.1.
4, Conservative
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                                                                                                                                                                                                          Best Local Similarity 57.1
Matches 4; Conservative
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TISSUE=Brain;
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                                                                                                                                                                                          Query Match
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Q7LGA9
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Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Mhitchead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
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Enterobacteriaceae; Salmonella.
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Enterobacteriaceae, Salmonella.
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                                                                        Nature 413:848-852(2001).
EMBL, AL6221278; CAD07884.1; -.
COMDLETE TOTCHOME.
SEQUENCE 1266 AA, 138661 MW, ECEA91FE03086C91 CRC64;
                                                                                                                                                                                                          3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              Q8ZLP4;
CHAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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Pred. No. 9.4e+03;
0; Mismatches 3;
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Salmonella typhimurium.
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                                                                                                                                                                      86.4%;
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Best Local Similarity 57.1%,
Best Local 4; Conservative
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OrderedLocusNames=t3284;
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STRAIN=Ty2 / ATCC 700931;
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Best Local Similarity
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EMBL; AB022657; BAA83378.1; -.
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'Characterization of cDNA clones in size-fractionated cDNA libraries
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR008984; SMAD_FHA.
InterPro; IPR00498; FHA; 1.
Pram; PR00498; FHA; 1.
PROSITE; PS50006; FHA; 1.
PROSITE; PS50006; FHA, DOMAIN; 1.
SEQUENCE 1486 AA; 164568 MW; 79312F1C5CB9D04F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 1472 AA; 162839 MW; 81C2CDC135B45093 CRC64;
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Hara Y., Adachi Y.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
KARP-1-binding protein 2 (KAB2)
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01-MAY_2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
KARP-1-binding protein 1 (KAB1).
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                            from human brain.";
DNA Res. 4:345-349(1997).
EMBL; AB007939; BA432315.2; -..
FIR; T00095; T00095.
InterPro; IPR009594; SMAD_FHA.
InterPro; IPR009894; SMAD_FHA.
SMART; SM00240; FHA; 1...
SWART; SM00240; FHA; 1...
NAW TEP.
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Best Local Similarity 57.1:
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Matches 4; Conservative
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090008
AC 09000
AC 09000
DT 01-MA
DT 0
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STRAIN=CLIP 11562 / Serovar 6a;

MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;

A Glaser P., Frangeul L., Buchtrisser C., Rusniok C., Amend A.,

A Glaser P., Berche P., Bloecker H., Brandt P., Chakraborty T.,

A Charbit A., Chetouani F., Couve B., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud B., Durant L., Dussurget O.,

Brian K.-D., Faihi H., Garcia-del Portillo F., Garrido P.,

A Gautier L., Goobel W., Keft J., Kuhn M., Kunst F., Kurapkat G.,

Jones L.-M., Kaerst U., Keft J., Kuhn M., Kunst F., Kurapkat G.,

Andueno E., Maltournam A., Mata Vicente J., NG E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Romenel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Nordsiek G., Novella S.,

Comparative genomics of Listeria species.";

Science 294:849-852(2001).

BMBL, AL596163; CAC95365.1; -.

RIR, AEL149; AE1449.

BMARI, SMO0060; FN3; 1.

ROMDEL PROLEOME.

SMARI, SMO0060; FN3; 1.

Complete proteome.

SQUENCE 1946 AA, 215361 MM; DAIB48630F9B62B3 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Yarrowia lipolytica chromosome F of strain CLIB99 of Yarrowia
                                                                                                                                                                                                                                             Query Match 86.4%; Score 19; DB 2; Length 1584; Best Local Similarity 57.1%; Pred. No. 1.2e+04; Matches 4; Conservative 0; Mismatches 3; Indels
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Pred. No. 1.4e+04;
0; Mismatches 3; Indels
Interpro; IPR000253; FHA.
Interpro; IPR008984; SMAD_FHA.
Pfam; PF00498; PHA; 1.
SMART; SM00240; FHA, 1.
PROSITE; PS50006; FHA DOMAIN; 1.
SEQUENCE 1584 AA; 175321 MW; A99D76ED374531F0 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Best Local Similarity 57.1%;
Matches 4; Conservative
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ORFNames=YALI0F20724g;
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                                                                                                                                                                                                                                                                                                                                                                                                1 VXXXAEF
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                           STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
Wormbase Consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 6 EGF-like domains.
EMBL; U40420; AAA81430.1; -.
FIR; T16305; T16305.
WormBase; WGGene00018237; F40F4.6.
WormPep; F40F4.6; CE04536.
GO; GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                   "The sequence of C. elegans cosmid F40F4."; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
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PROSITE; PS50234; VWFA; 1.
EGF-like domain; Hypothetical protein.
SEQUENCE 2214 AA; 243435 MW; B0B38'
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InterPro; IRR0004219; EGF 2.
InterPro; IRR0004210; IEGF 1.
InterPro; IRR0004104; IEGF.
InterPro; IRR001304; IEGF.
InterPro; IRR001304; IEGF.
InterPro; IRR001305; WWF A.
Pfam; PP00008; EGF; I.
Pfam; PP000059; Lectin C; I.
Pfam; PP000059; Lectin C; I.
SWART; SW00034; CLECT; I.
SWART; SW00181; EGF; 3.
SWART; SW00181; EGF; 3.
SWART; SW00181; EGF; 3.
PROSITE; PS00041; EGF 1; PROSITE; PS00042; EGF 1; ECTIN PROSITE; PS00022; EGF 1; EFCTIN PROSITE; PS01186; EGF 2; 3.
Hypothetical protein F40F4.6.
Name=F40F4.6; ORFNames=F40F4.6;
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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Matches 4; Conservative
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                                            Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
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Q6E7J8
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                                                                                                                                                                Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J., M., Beyne E., Blarkasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Borspons L., Rabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joset P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Micaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia P., Mesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weisenbach J.,
Wincker P., Souciet J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; CR382132; CAG78485.1; -...
GO; GO:0005634; F.ATP binding; IEA.
GO; GO:0008026; F.ATP binding; IEA.
GO; GO:0008026; F.ATP-dependent helicase activity; IEA.
GO; GO:0003677; F.DNA binding; IEA.
GO; GO:0003679; F.DNA-directed RNA polymerase activity; IEA.
GO; GO:0001666; F:DNA-directed Binding; IEA.
GO; GO:00015668; F:Type III site-specific deoxyribonuclease ac. . .; IEA.
GO; GO:000370; P:DNA restriction; IEA.
GO; GO:000350; P:Type III site-specific deoxyribonuclease ac. . .; IEA.
GO; GO:000350; P:Type III site-specific deoxyribonuclease ac. . .; IEA.
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                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.
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SMART; SM00611; SEC63; 2.
ATP-binding; Helicase; Hydrolase.
SEQUENCE 2106 AA; 234728 MW; 772389CAFP107619 CRC64;
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Interpro; IPR001410; DEAD.
Interpro; IPR011545; DEAD/DEAH N.
Interpro; IPR001650; Helicase C.
Interpro; IPR006993; ResIII.
Interpro; IPR011260; RNAP alpha C.
Interpro; IPR004179; Sec63.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
Yarrowia lipolytica CLIB99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF04851; ResIII; I. Pfam; PF02889; Sec63; 2. SMART; SM00382; AAA; 2. SMART; SMO0487; DEXDC; 2.
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Matches 4; Conservative
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                                                              NCBI_TaxID=284591;
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                                                                                                          SEQUENCE FROM N.A.
                                                                                                                               STRAIN-CLIB99;
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                                                                                                                                                      Genolevures;
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020219 RESULT 46 Q20219 ID Q2021 AC Q2021 DT 01-NO DT 01-NO DT 01-NO

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9 VGTTÄEF 15
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Best Local Similarity
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                                                                                                                                          Complete proteome. SEQUENCE 39 AA;
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TX3A AGEAP
ID TX3A AGEAP
AC P33034;
DT 01-0CT-1993 (
DT 05-JUL-2004 (
                                                                                                                                                                                                                                                                                                                                    Name=pilB;
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Matches
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                                                                                         "Structure and Biosynthesis of the Jamaicamides, New Mixed Polyketide-
Peptide Neurotoxins from the Marine Cyanobacterium Lyngbya
majuscula.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
                                                              PubMed=15217615; DOI=10.1016/j.chembiol.2004.03.030;
Edwards D.J., Marquez B.L., Nogle L.M., McPhail K., Goeger D.E.,
Roberts M.A., Gerwick W.H.;
                                                                                                                     Chem. Biol. 11:817-833(2004).
-1- COFACTOR: Pyridoxal phosphate (By similarity).
-1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                           SIMILARITY: Belongs to the group II decarboxylase family
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Pfam; Proofes and Production; 1.

Pfam; Proofes and Productyleynt; 1.

Pfam; Proofes and Probles and Production; 1.

Pfam; Proofes and Production; 2.

Pfam; Proofes and Production; 2.

Proofes and Proofes and Production; 2.

PROSITE; PROOFES and Proceed and Production; 2.

PROSITE; Proofes and Procedure; 3.

Proofes and Proofes and Production and Production and Production and Production and Production and Proofes and Proofes and Adolts MW; DBF0D4AC0681FP24 CRC64;
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Last annotation update)
          Bacteria; Cyanobacteria; Oscillatoriales; Lyngbya.
NCBI_TaxID=158786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 57.1
les 4; Conservative
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                                             SEQUENCE FROM N.A.
        majuscula
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Q8F054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 48
Q8F054
DD Q8F05
AC Q8F05
DT 01-MA
DT 01-MA
DT HYPOKI
OR Order
OS Lepto
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SEQUENCE FROM N.A.

STRAIN=SeGOL / Serogroup Icterohaemorrhagiae / Serovar lai;
STRAIN=SeGOL / Serogroup Icterohaemorrhagiae / Serovar lai;
MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
A Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miaco Y.-G., Xu H.,
Zhang Y.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
A Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yaco Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guc X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.;
"Unique physiological and pathogenic features of Leptospira
Interrogans revealed by whole-genome sequencing.";
REMBL; AEO11520; AAN50841.1; -.
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PubMed=15057449;
Yang Y.C., Chou C.P., Kuo T.T., Lin S.H., Yang M.K.;
Yang Y.C., Chou Ensitivity of Xanthomonas axonopodis pv. citri to the infection of filamentous bacteriophage Cf.";
Curr. Microbiol. 48:251-261(2004).
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Pred. No. 8.3e+02;
0; Mismatches 3; Indels
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Kou T.T., Yang Y.C., Chou C.P., Yang M.K.;

Indiana M. Yang M. Y
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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(Rel. 27, Last sequence update)
(Rel. 44, Last annotation update)
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Similarity 57.1%;
4; Conservative (
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Indels

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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
P0459B04.5 protein (P0659H10.23 protein).
Name=P0459B04.5; Synonyms=P0659H10.23;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
NCBI_TAXID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 84;
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Last annotation update)
Pred. No. 1.46+03;
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Pred. No. 1.5e+03;
1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                        84 AA
                                                    0; Mismatches
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42.9%;
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                       57.1%;
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Les 3, Conservative
                                                    4; Conservative
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 420:312-316(2002)
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                                                                                                                                                              42 VGTSAEF 48
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                          Best Local Similarity
                                                                                                      1 VXXXAEF 7
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Matches
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Plochemistry 33:5088-5108(1994).

Plochemistry 33:5088-5108(1994).

Plochemistry of this toxin is a potent blocker of N-type calcium channels. This toxin is a potent blocker of N-type calcium channels. It also blocks L-type calcium channels, but with less potency than omega-Aga-IIIA. It does not block T-type channels. It blocks calcium currents in locust thoracic neurones, but does not block housefly neuromuscular transmission presynaptically.
                                                                                                                                                                                                                                                                                                                                                 Parol. Biol. 100. Mem. 267:2610-2615(1992).

-!- FUNCTION: Omega-agatoxin are antagonist of voltage-sensitive calcium channels. They block insect neuromuscular transmission presynaptically. Potent blocker of N- and L-type calcium channels.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- FTW: Contains six disulfide bonds (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, A42335; A42335.
Calcium channel inhibitor; Direct protein sequencing;
Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
SEQUENCE 76 AA; 8518 MW; 6A715CAC9591888B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
                                                                                                                                                                                                                   TISSUE-Venom;
PEDLINE-2921293151; PubMed=1310319;
Venema V.J., Swiderek K.M., Lee T.D., Hathaway G.M., Adams M.E.;
"Antagonism of synaptosomal calcium channels by subtypes of omega-
                                                 Agelenopsis aperta (Funnel-web spider).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Arancomorphae; Entelegynae; Agelenidae; Agelenopsis.
NCBI_TaxID=6908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Araneae,
Araneomorphae, Entelegynae, Agelenidae, Agelenopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ertel E.A., Warren V.A., Adams M.E., Griffin P.R., Cohen C.J., Smith M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, VARIANTS SER-29 AND ARG-35, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.8%; Score 18; DB 1; Length 76; 57.1%; Pred. No. 1.46+03; ive 0; Mismatches 3; Indels
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-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- PTM: Contains six disulfide bonds (Probable).
-!- SIMILARITY: Belongs to the omega-agatoxin family.
PIR; C54252; C54252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium channel inhibitor; Direct protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D5C63C3AE8C95BB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
06-Grappa - Agarant IIIB (Omega-Aga-IIIB).
Agelenopsis aperta (Funnel-web spider).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 AA.
                    Omega-agatoxin IIIA (Omega-Aga-IIIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N -> S.
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MEDLINE=94227039; PubMed=8172884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8620 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6908;
                                                                                                                                                                                                                                                                                                                                   agatoxins.";
J. Biol. Chem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TX3B AGEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                         SEQUENCE
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30 VGSSAEF 36
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 96 AA;
                                                                                                                                                                                                                          27
41
76
82
92
92 AA;
  NCBI_TaxID=10141;
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MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2; Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C., Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R., Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S., Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                             Name=B1120F06.135; Synonyms=B1272H04.1;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caviã porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria, Rodentia, Hystricognathi; Caviidae, Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki T., Matsumoto T., Katayose Y.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P20658,
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Protein 10 (29 KDa calcium-binding protein, brain-specific)
(Fragments)
                                                                                                                          Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki T., Matsumoto T., Katayose Y.;
"Oryas astiva nipponbare(GA3) genomic DNA, chromosome 7,
clone:B1272H04";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%; Score 18; DB 2; Length 88; 57.1%; Pred. No. 1.6e+03;
                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-GCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein B1120F06.135 (Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AP005830; BAC84533.1; -. EMBL, AP006479; BAD32057.1; -.
                                                                 "Origins of highly mosaic mycobacteriophage genomes.";
Cell 113:171-182(2003).
EMBL; AY129318, AAN12718.1; -
EEQUENCE 88 AA, 10324 MW; SD13C1010CA698SE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 88 AA; 10001 MW; 693B4D3224B4D010 CRC64;
                                                                                                                         81.8%; Score 18; DB 2; I
57.1%; Pred. No. 1.6e+03;
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les 4; Conservative
                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                            50 VSVAAEF 56
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                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                      1 VXXXAEF 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                             clone:B1120F06."
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Q6YVE3;
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CAVPO
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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DAR Res, 9:189-197(2002).
EMBL; AP005936; BAC45816.1; -.
GO; GO:0016020; C:membrane; IEA.
TISSUB=Brain;
MEDLINE=9009311; PubMed=2602362;
MEDLINE=9009311; PubMed=2602362;
Winsky L., Nakata H., Martin B.M., Jacobowitz D.M.;
"Isolation, partial amino acid sequence, and immunohistochemical localization of a brain-specific calcium-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 86:10139-10143(1989).
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0
                                                                                                                                                                                                --- MISCELLANEOUS: Binds calcium.
--- SIMILARITY: Belongs to the calbindin family.
--- SIMILARITY: Contains 6 EF-hand calcium-binding domains.
PIR, A34520; A34520.
InterPro; IPR002048; EF-hand.
InterPro; IPR01983; EF-Hand like.
PROSTIE; PS00018; EF-HAND; PĀRITAL.
CAlcium-binding; Direct protein sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 1; Length 92;
Pred. No. 1.7e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11067 MW; D1CCD66C148A7F6A CRC64;
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Last annotation update)
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Pfam; PF02325; YGGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%;
57.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bs10551 protein.
OrderedLocusNames=bs10551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bradyrhizobium japonicum.
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13 VQSTAEF 19
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Matches
                                                                    RESULT 58
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                                                                                           27KQL8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 430:35-44(2004).

-! PUNCTION: Important for transcription initiation. The SPT4/5/6

-! PUNCTION: Important for transcription initiation. It may normally complex is required for transcription initiation. It may normally act to repress transcription at a variety of loci, and also plays a role in chromatin structure or assembly. Metal binding is important for its function (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99087905; PubMed-9871119;
Hikkel I., Gbelska Y., Subik J.;
Identification and functional analysis of a Kluyveromyces lactis
homologue of the SPT4 gene of Saccharomyces cerevisiae.";
Curr. Genet. 34:375-378(1998)
                                                                                                                                                                                                                                                                            Kluyveromyces lactis (Yeast).
Bukaryota: Fungi; Ascomycota: Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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81.8%; Score 18; DB 1; Length 102;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y similarity.
869070285CF7917C CRC64;
                                                                                                                                                                              15-JUL-1998 (Rel. 36, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-DCT-2014 (Rel. 45, Last annotation update)
Name=SPT4; OrderedLocusNames=KLLAOB07997g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF06093; Spt4; 1.
Nuclear protein; Transcription; Zinc-finger.
                                                                                                              102 AA.
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                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
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                                                                                                                                                                                                                                                                       Kluyveromyces lactis (Yeast)
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                                                                                                              STANDARD;
41 VSAVAEF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-JBD100
                                                                                                         SPT4 KLULA
P81205;
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                                                                                                                                                                                                                                                      MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097; MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.W., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlamb A.H., Fraunholz M.J., Rose D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                          Plasmodium falcíparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h Similarity 57.1%; Pred. No. 1.9e+03; 4; Conservative 0; Mismatches 3; Indels
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Krnajski Z., Gilberger T.W., Walter R.D., Mueller S.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ277839; CAB90828.1; --
HSSP; P80028; 1EP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 AA; 11716 MW; 0129998AEB88770C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005489; F:electron transporter activity; IEA. GO; GO:0006118; P:electron transport; IEA.
                                                                      Last sequence update)
Last annotation update)
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Last annotation update)
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                                                  Created)
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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InterPro; IPR005746; Thioredoxin.
InterPro; IPR006663; Thioredox_dom2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE014825; AAN37158.1; -. HSSP; P10599; LAUC.
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                                          05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 419:498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Redox-active center.
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GO; GO:0005489; F:electron transporter activity; IEA

1 VXXXAEF 7

Gaps

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"Arthrobacter aurescens TC1 Atrazine Catabolism Genes trzN, atzB, and atzC Are Linked on a 160-Kilobase Region and Are Functional in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEGUENCE FROM N.A.
SETRAILE-S188C / AB972;
MEDLINE-S181326; PubMed=9169870;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.,
"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.",
Nature 387:44-87(1997).
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"Creation of the YFLEX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system."; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical 13.0 kDa protein in SNPI-GPP1 intergenic region.
                                                                                                                                                                                                                                                                                                                                             Similarity 57.1%; Pred. No. 2e+03; 4; Conservative 0; Mismatches 3; Indels
                                                           Becherichia coli.";
Appl. Environ. Microbiol. 70:4402-4407 (2004).
EMBL, AX456694. AAS20147.1; -.
InterPro; IPR008651; Hic8.
InterPro; IPR010985; Met_repress_like.
Pfam; PP05534; Hic8; 1...
Hypochetical protein; Plasmid.
SEQUENCE 113 AA; 12762 MW; 85AF588567AA5328 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 23 Potential.
121 AA; 13030 MW; 18B23D652939CDD2 CRC64;
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GermOnline; 139596; -.
SGD; S000001321; YIL059C.
Hypochetical protein; Transmembrane.
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EMBL; AY693258; AAT93277.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=YIL059C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 VATVÁÉF 32
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P40520;
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YIF9_YEAST
      RAT RAT DE RAT D
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FAMEL, AFS13895; AANTG283.1; -

Hypothetical protein; Plasmid.

SEQUENCE 106 AA; 11488 MW; E28127026C785A91 CRC64;
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PubMed-15240330; DOI=10.1128/AEM.70.7.4402-4407.2004;
Sajjaphan K., Shapir N., Wackett L.P., Palmer M., Blackmon B.,
Tomking J., Sadowsky M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pAA1.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Micrococcineae, Micrococcaceae, Arthrobacter.
NCBI_TaxID=43663,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                81.8%; Score 18; DB 2; Length 104; 57.1%; Pred. No. 1.9e+03; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%; Score 18; DB 2; Length 106; 57.1%; Pred. No. 1.9e+03;
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                                                                                                                                                                                                                                                                                 104 AA; 11716 MW; 0129998AEB88770C CRC64;
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Last annotation update)
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Last annotation update)
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GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                     TIGRFAMB; TIGR01068; thioredoxin; 1. PROSITE; PS00194; THIOREDOXIN; 1.
                          InterPro; IPR006662; Thiored.
InterPro; IPR005746; Thioredoxin.
InterPro; IPR00663; Thioredox dom2.
Pfam; PF00085; Thioredoxin; 1.
PRINTS; PR00421; THIOREDOXIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein. Arthrobacter aurescens.
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les 4; Conservative
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Plasmid pEN2701.
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60 SKZ5
AC 065KZ
AC 065KZ
DT 05-JU
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DT 05-JU
DT 05-JU
DE HYPOL
OG Plasm
OG Plasm
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Gaps

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moser, 60:0003677; F:DNA binding; IEA.
GO; GO:0000156; F:two-component response regulator activity; IEA.
GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
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    predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Uncharacterized hematopoietic stem/progenitor cells protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 2; Length 134;
Pred. No. 2.4e+03;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%; Score 18; DB 2; Length 137; 57.1%; Pred. No. 2.4e+03; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50110; RESPONSE RECULATORY; 1.
Complete proteome; Phosphorylation; Sensory transduction.
SEQUENCE 134 AA; 15035 MW; A76AF72470EA58EF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14995 MW; 88B77FDD35F50F93 CRC64;
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InterPro; IPR001109; Response_reg.
Pfam; PP00072; Response_reg; IProDom; PD000039; Response_reg; I.
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57.1%;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Hypothetical protein.
OrderedLocusNames=RPA2246;
                                                                      Science 303:689-692(2004).
EMBL; BX842652; CAE80226.1;
HSSP; P06143; IAB6.
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                                             genomic perspective.
Science 303:689-692(
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Best Local Similarity
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Best Local Similarity
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    RETT AND DESCRIPTION OF SECTION O
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STRAIN=C2A / ATCC 35395 / DSM 2834;

STRAIN=C2A / ATCC 35395 / DSM 2834;

MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;

MACADAN JE., Nubbaum C., ROY A., Endrizzi M.G., Macdonald P., Allan N., Dalagan J.E., Sumer D., Brown A., Allan N., Dalagan J.E., Sumer D., Brown R., Allan N., Dalage-Thomann N., DeArellano K., Johnson R., Linton L., McKernan R., Talamas J., Tirrell A., Vew. A., McKernan P., McKernan K., Talamas D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kurstrow D.E., Grahame D.A., Guss A.M., Leigh J.A., Li W., Liu J., Mukhopadhay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Rrych J.G., Jarrell K.P., Jing H., Macario A.J.L., Paulsen I.T., A., McCall K., M., Swanson R.V., Zinder S.H., Lander E., McCall W.W., Birren B., Rever J.G., Lander S.H., Lander S.H., Cand physiological diversity.";

The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";

EMBL, ABO11092; AAM07154.1; -.
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PubMed=14752164; DOI=10.1126/science.1093027;
Redulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
Sockett R.E., Schuster S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales, Bdellovibrionaceae, Bdellovibrio.
NCBI_TaxID=959;
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Score 18; DB 1; Length 121;
Pred. No. 2.2e+03;
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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57.1%; Pred. No. 2.2e+03;
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Name=chey, OrderedLocusNames=Bd2409;
Bdellovibrio bacteriovorus.
                                57.1%;
    81.8%;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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                                                                              4; Conservative
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                                         Best Local Similarity
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SEQUENCE 123 AA
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    Query Match
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AC 08TJII
DT 01-JU
DE Predi
CO Mcha
CO Mch
CO Mc
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MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;

MG W V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

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Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Preitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

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Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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MEDLINB=21235186; PubMed=11337471; DOI=10.1101/gr.GR-1697R;

MEDLINB=21235186; PubMed=11337471; DOI=10.1101/gr.GR-1697R;

Meissenbach A., Mauger S., Jaillon O., Malarme K.,

"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";

Genome Res. 11.731-753 (2001).

-! SIMILARITY: Belongs to the dps family.

EMBL; AE006432; AAK06123.1; -.
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Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                         Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
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Last annotation update)
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InterPro; IPR009078; Perritin/RR_like.
InterPro; IPR008331; Perritin_Dps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-heme iron-binding ferritin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01346; HELNAPAPROT. ProDom; PD149803; DPS; 1. PROSITE; PS00818; DPS 1; 1. Complete proteome.
   OrderedLocusNames=VNG1907H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00210; Ferritin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; H84341; H84341.
Complete proteome.
SEQUENCE 147 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A86878; A86878.
HSSP; P80725; 1QGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 VSSRÁEF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conserva
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Best Local Similarity
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1360;
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Q9CE23
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MEDLINE=97404455; PubMed=9256512; DOI=10.1073/pnas.94.17.9504;

MEDLINE=97404455; PubMed=9256512; DOI=10.1073/pnas.94.17.9504;

MEDLINE=97404455; PubMed=9256512; DOI=10.1073/pnas.94.17.9504;

Tisolation and characteridation of an amino acid-selective channel
Tisolation and characteridation acid-selective channel
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Tisolation acid-
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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42.9%; Pred. No. 2.6e+03;
ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%; Score 18; DB 2; Length 141; 57.1%; Pred. No. 2.5e+03; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2003 (TrEMBLrel. 24, Vng1907h.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pisum sativum (Garden pea).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 42.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 VSDSAEF 117
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                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                    NCBI_TaxID=1076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Core protein.
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Q9HNXO;
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RESULT 68

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Bradyrhizobiaceae; Bradyrhizobium.
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                                                              STRAIN-USDA110;
               NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUCR
                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09A714;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                    STRAIN=DSM 9790 / ATCC 700027;
PubMed=15184674; DOI=10.1073/pnas.0401356101;
Fuetcerer O., Angelov A., Liesegang H., Gotteschalk G., Schleper C.,
Schepers B., Dock C., Antranikian G., Liebl W.;
"Genome sequence of Picrophilus torridus and its implications for life around pH 0.";
                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 101:9081-9096 (2004).

-1- FUNCTION: This protein binds specifically to 23S rRNA. It makes multiple contacts with different domains of the 23S rRNA in the assembled 50S subunit and ribosome (By similarity).

-1- FUNCTION: The globular domain of the protein is located near the polypeptide exit tunnel on the outside of the subunit, while an extended beta-hairpin is found that lines the wall of the exit tunnel in the center of the 70S ribosome (By similarity).

-1- SUBUNIT: Part of the 50S ribosomal subunit.

-1- SIMILARITY: Belongs to the ribosomal protein L22P family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_01331; -; 1.
ProDom; PD01032; Ribosomal_L22; 1.
PROSITE; PSO0464; RIBOSOMAL_L22; FALSE NEG.
COMplete proteome; Ribosomal_protein; RNA-binding; rRNA-binding SEQUENCE 149 AA; 16731 MW; A80FA918151BA217 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blr6079 protein.
OrderedLocusNames=blr6079;
Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                     Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Picrophilaceae; Picrophilus.
NCBI_TaxID=82076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%; Score 18; DB 1; Length 149; 57.1%; Pred. No. 2.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                      25-OCT-2004 (Rel. 45, Last Sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) 50S ribosomal protein L22P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 AA.
                                                                                                                            149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%; Pred. .v. +ive 0; Mismatches
                                                                                                                                                                                                                        Name=rpl22p, OrderedLocusNames=PT00645;
Picrophilus torridus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                        25-OCT-2004 (Rel. 45, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE017261; AAT43230.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                          STANDARD;
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                                           69 VSTLAÈF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSANAEF 98
             7
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             VXXXAEF
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01-JUN-2003 (
01-JUN-2003 (
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                                                                                                                                      Q6L1C2;
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                                                                                                           RL22_PICTO
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0894B8
AC 0894BB
AC 0894B
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-OC
DE Blr60
GN Order
CO Bacte
CO Bacte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 19089 / CB15;
MEDLINE=21173699 PubMed=11259647; DOI=10.1073/pnas.061029298;
MEDLINE=21173699 PubMed=11259647; DOI=10.1073/pnas.061029298;
MINITAMENT W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nalson K.E.,
Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                     "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
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0
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Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-!- FUNCTION: Involved in saturated fatty acids biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (9 similarity).
                                                                                                                                                                                                                                                                                                                                                                81.8%; Score 18; DB 2; Length 151;
57.1%; Pred. No. 2.6e+03;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                         151 AA; 16840 MW; 7AAAD1AC94717AC4 CRC64;
                                                                                                                            Bradyrhizobium japonicum USDA110.";
NDA Res. 9:189-197 (2002).
EMBL, APOD5957; BAC5144.1; -.
GO: GO:0045735; F:nutrient reservoir activity; IEA.
                                                                                                                                                                                                               InterPro; IPR006045; Cupin.
InterPro; IPR007113; Cupin region.
InterPro; IPR011051; RmIC_like_cupin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
MEDLINE=22484998; PubMed=12597275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE005865; AAK23887.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                 Pfam; PF00190; Cupin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 VAMAAEF 140
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Kenopus laevis (African clawed frog)
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                                                                            SEQUENCE FROM N.A.
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                           TISSUE=Intestine;
                                                                                        TISSUE=Intestine;
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                                                    NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
TIGR, CC1912; -.
HAMARP; MF 00406; -; 1.
InterPro: IPRO106684; FabZ.
InterPro; IPRO06684; FabZ.
InterPro; IPRO10684; Tidoestr_supf.
Pfam; PF03061; 4HBT; 1.
TIGRAMAR TIGRO1750; fabZ; 1.
Complete proteome; Lipid A biosynthesis; Lipid synthesis; Lyase.
ACT_SITE S9 By similarity.
SEQUENCE 159 AA; 17443 MW; 2C7EAA8668EA0141 CRC64;
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MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
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                                                                                                                         81.8%; Score 18; DB 1; Length 159
57.1%; Pred. No. 2.8e+03;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 AA; 18035 MW; 6CB7E15CDAC6FC75 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
010-MAR-2004 (TERBMLrel. 26, Last annotation update)
Protein phosphatase 2 regulatory subunit B (Fragment).
                                                                                                                                                                                                                                                                                               (TrEMBLrel. 24, Last sequence update) (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 AA.
                                                                                                                                                                                                                                                                                       Created)
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MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP005021; BAC67769.1; -.
                                                                                                                                                                                                                                                                                                                                                 Streptomyces avermitilis.
                                                                                                                                     Local Similarity 57.1 les 4; Conservative
                                                                                                                                                                                                                                                                                                                                  OrderedLocusNames=SAV60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                                                                                                                                                                                142 VAAEAEF 148
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                                                                                                                                                                           1 VXXXAEF 7
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01-JUN-2003 (
01-JUN-2003 (
                                                                                                                           Query Match
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Q9DDR2;
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Q9DDR2
ID Q9DDR
AC Q9DDR
DT 01-MA
DT 01-MA
DE Prote
                                                                                                                                                   Matches
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STRAIN=C2A (ANT.).

SURCENCE FROM N.T.

SURCENCE FROM N.T.

MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;

A Galagan J.E., Nusbaum C., Roy A., Endrizzia M.G., Macdonald P.,

A FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

A Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

A Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C.,

Perry J.G., Jarrell K.R., Swanson R.V., Zinder S.H., Lander E.,

A Metcalf W.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic

Genome Res. 12:532-542(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watson M.D.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: Contains 3 WD repeats.

EMBL; AF305084; A645003.1; -.

GO; GO:0000159; C:protein phosphatase type 2A complex; IEA.

GO; GO:0000861; F:protein phosphatase type 2A regulator activity; IEA.

GO; GO:0007165; P:prignal transduction; IEA.

InterPro; IFR010049; PD2A_FR55.

InterPro; IFR000009; PD2A_FR55.

InterPro; IFR000008; PD2A_FR55.
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                                                                                                                                                                                                                                           Minter R., Horton J.D., Watson M.D.;
"Development of Antibody Technology to Identify Natural Killer Cell
"Surface Antigens in Xenopus laevis.";
Thesis (1999), University of Durham, South Rd., Durham, UK.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 AA; 20210 MW; BD84B23CA0F80880 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Name-pfpI; OrderedLocusNames=MA1654;
Methanosarcina acetivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
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PRINTS; PR00600; PP2APR55.
SMART; SM00320; WD40; 3.
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                                                                     Xenopodinae; Xenopus
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1 VXXXAEF 7
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  [1]
SEQUENCE FROM N.A.
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Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
de Oliveira J.C.P., Wood D., de Oliveira M.C., Miyaki C.Y.,
Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorry H.A.,
Ferro M.I.T., Gagliardi P.R., Giglioti E., Goldman M.H.S.,
Goldman G.H., Kimura E.T., Perro E.S., Kuramae E.E., Lemos E.G.M.,
Lemos M.V.P., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.,
"The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
xyli subsp. xyli.",
Mol. Plant Microbe Interact. 17:827-836(2004).
                                                                                                                                                                                                                                                                                       Gaps
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Viruses, deDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
NCBI_TaxID=227470;
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
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                                                                                                                                                                                                                            Length 179;
                                                                                                                                                                                                                                                                                    3; Indels
                          HSSP; 059413; 1G21.
GO; GO: 0008233; F:peptidase activity; IEA.
InterPro; IPR002818; Thid/Pfp1.
Pfan; PF01965; D.1 Pfp1; 1.
Complete protecome; Protease.
SEQUENCE 179 AA; 19359 MW; E0FDC30D4BF4F456 CRC64;
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Last annotation update)
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Last annotation update)
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Pred. No. 3.1e+03;
0; Mismatches 3;
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  EMBL; AE010838; AAM05062.1; -
                                                                                                                                                                                                                         81.8%;
57.1%;
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                                                                                                                                                                                           Query Match
Best Local Similarity 57.11,
Best Local 6, Conservative
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IAATAEF 95
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nes 3; Conserv
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SEQUENCE 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=15305603;
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Q6AC19;
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106AC19
10 C06AC1
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Rhabditidae, Peloderinae, Caenorhabditis.
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Petrov V., Nolan J., Bertrand C., Letarov A.V., Krisch H.M., Karam J.D.,
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     Length 186;
                                                                                                                                                                                                                                                                                                               Score 18; DB 2; Length 186 Pred. No. 3.2e+03; 0; Mismatches 3; Indels
                                                                                                                                    Petrov V., Nolan J., Karam J.D.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX266303; AAQ17763.1; -.
Hypothetical protein and protein sequence 186 AA; 21839 MW; 45060CC5F8B03B11 CRC64;
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Bradshaw-Cordum H., Scott K., Graves T.;
"The sequence of C. elegans cosmid Y11F9AL";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston R.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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EMBL; AC024200; AAF35997.2; -.
HSSP; Q9LRB7; 11YM.
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(TrEMBLrel. 26, Last ann
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MEDLINE=99069613; PubMed=9851916;
WormBase Consortium;
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57.1%;
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Best Local Similarity 57...
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193 AA.

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A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Ahgle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Ferry-Dumazet H., Groppi A.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Oziar-Kalogeropoulos O.,
Pellenz S., Pottier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., With B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
T., "Genome evolution in yeasts.";
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Saccharomycetales, Dipodascaceae, Yarrowia.
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                                                                                                                                              Length 189;
     GO, GO:0000151; C:ubiquitin ligase complex; IEA.
GO, GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:000870; F:zinc ion binding; IEA.
GO; GO:0016567; P:protein ubiquitination; IEA.
InterPro; IPR001841; Znf ring.
PFam; PF00097; Zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                            81.8%; Score 18; DB 2; Length 189
57.1%; Pred. No. 3.2e+03;
cive 0; Mismatches 3; Indels
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                               SMART; SM00184; RING; 1.
PROSITE; PS50089; ZF RING 2; 1.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 189 AA; 21048 MW; 7BDA2D05F0362CD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; CR382128; CAG83427.1; -.
SEQUENCE 193 AA; 22016 MW; 939292835977B6BF CRC64;
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Last annotation update)
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WormPep; Y71F9AL.10; CE31386.
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Yarrowia lipolytica CL1B99
                                                                                                                                Query Match
Best Local Similarity 57.1
Best Local 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 430:35-44(2004)
                                                                                                                                                                                                                     37 VMTAÄĖF 43
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                                                                                                                                                                                                                                                                                                                               STRAIN=2603 V/R / Serotype V,
MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
Radune D., Redorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchardon P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin E., Tice H.;
Richardson P., Rubin E., Tice H.;
"Complete genome sequence of Bacillus cereus ZK.";
"Complete Genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CP000001; AAU19332.1; -.
SEQUENCE 194 AA; 22360 MW; CCCECE4FIC508863 CRC64;
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57.1%; Pred. No. 3.3e+03;
cive 0; Mismatches 3; Indels
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                                                                                                                                                 Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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NCBI_TaxID=288681;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Group-specific protein.
                      01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Created)
                                                                                   Membrane protein, putative.
OrderedLocusNames=SAG0250;
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Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                           NCBI_TaxID=216466;
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SEQUENCE 193 AA
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MEDLINE=22608306; PubMed=12692562;
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Best Local Similarity 57.1.,
A; Conservative
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STRAIN=A3(2) / M145;
STRAIN=E1996410; PubMed=12000953; DOI=10.1038/417141a;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornaby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
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Mature 417.141-147(2002)

EMBL; A1939125; CAA16476.1;
PIR; T34819; T34819.
PO Go.003824; F.catalytic activity; IEA.

InterPro; IPR006683; Thioestr_supf.

Pfam; PP03061; 4HBT; 1.
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MEDLINE-21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
MEDLINE-21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
MEDLINE-21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
Shinose M., Takahashi C., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                       Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome; Hypothetical protein.
SEQUENCE 194 AA; 20474 MW; 9FE391B9E3CED80E CRC64;
                                                                                                                                                     (TrEMBLrel. 06, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                               194 AA.
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                                                                                                                        Created)
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                                                               PRT;
                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, L
01-OCT-2003 (TrEMBLrel. 25, L
Hypothetical protein SCO5867.
ORFNames=SC2E9.08;
                                                                                                                  01-JUN-1998 (TrEMBLrel. 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 57.1 les 4; Conservative
                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MA-4680;
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                                                            054133
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0082KK3
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AC 0082KK
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RESULT 82
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RECORDENCE FROM N.A.

SUBDENCE FROM N.A.

RECORDENCE FROM N.A.

RECORDENCE A.TR. de Almeida D.F., Hungaria M., Guinaraes C.T.,

RA Antenio R.V., Almeida F.C., Hungaria M., Guinaraes C.T.,

RA Antenio R.V., Almeida F.C., Hungaria M., Guinaraes C.T.,

RA Antenio R.V., Andrade E.M., Araripe J., de Araujo M.F.F.,

RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,

RA Batista J.S., Azevedo V., Baptista A.J., Batcaus L.A.M.,

RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

RA Carvalho C.M.B., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,

Carvalho C.M.B., Cascardo J.C.M., Faguades N., Burity H.A.,

RA Carvalho C.M.B., Candardo B.S., Ferrari L.P., Ferro J.A.,

RA Ferro M.IT., Franco G.R., Freitas N.S.A., Furlan L.R.,

RA Ferro M.IT., Franco G.R., Freitas N.S.A., Furlan L.R.,

RA Gazzinelli R.T., Gomes B.A., Goncalves P.R., Garangeiro T.B.,

Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,

RA Madeira H.M.F., Manfio G.P., Maranhao A.G., Martins W.S.,

di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,

RA Perixo P.F.C., Parente J.A., Pedrosa P.O., Pena S.D.J., Perrira J.O.,

RA Paixao R.F.C., Parente J.A., Schoreider M.P.C., Seuanez H.N.

RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.N.

RA Santos B.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.

Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,

Santos R.B., Santos F.R., Scheneider M.P. C., Seuanez H.N.

Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes R. S., Streindel M., Teixeira S.R., Urmenyi T.,

RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,

RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,

RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.,
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:556-531(2003).
BMBL, AP005030; BAC70111.1;
GO, GO.0003824; F:catalytic activity; IEA.
InterPro; IPR006683; Thioestr_supf.
InterPro; IPR06683; Thioestr_supf.
Complete proteome; Hypothetical protein.
SEQUENCE 194 AA; 20316 MW; 3BE41F14E45228D5 CRC64;
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Pred. No. 3.3e+03;
0; Mismatches 3; Indels
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Molybdopperin-guanine dinuclectide biosynthesis protein.
Name=mobA; OrderedLocusNames=CV1625;
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01-MAR-2004 (TrEMBLrel. 26, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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57.1%;
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201 AA;
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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Linases in eukaryote ribosomes.

SMILARITY: Belongs to the ribosomal protein S6e family.

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                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=cv. SRI, TISSUE=Leaf,
MEDLINE=93027271; PubMed=1408841;
Hansen G., Estruch J.J., Spena A.;
Hansen G., Estruch J.J., Spena A.;
"Tobacco CDNA encoding the ribosomal protein S6.";
"Tobacco CDNA encoding the ribosomal protein S6.";
Nucleic Acids Res. 20.5230-5230(1992).
I. FUNCTION: May play an important role in controlling cell growth and proliferation through the selective translation of particular
                                                Gaps
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0MR-2004 (TrEMBLrel. 26, Last annotation update)
Stratchin-MLCK (Fragment).
Name-Strn-MLCk,
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%; Score 18; DB 1; Length 199; 57.1%; Pred. No. 3.4e+03; tive 0; Mismatches 3; Indels
Pred. No. 3.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 AA; 22620 MW; 03EEBA0BD87B77F5 CRC64;
                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
40S ribosomal protein S6 (Fragment).
                                                                                                                                                                                                                                                  199 AA.
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                                              0; Mismatches
                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana tabacum (Common tobacco)
                    57.1%;
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nes 4; Conservative
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                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                   71 VTDAAĖF 77
                         Best Local Similarity
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                                                                                         1 VXXXAEF 7
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                                                                                                                                                                                                                                               RS6_TOBAC
P29345;
                                                                                                                                                                                                                                                                                                                                                                                   Name=RPS6;
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TS64 TOBAC
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Flyase, Fegnol 1988, Strn-Mlck.
Flyase, Fegnol 1988, Strn-Mlck.
GO; GO:0004685; F:calcium- and calmodulin-dependent protein k. . .; IDA.
GO; GO:0004687; F:myosin-light-chain kinase activity; IDA.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
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MEDLINE=9512920; PubMed=7828933; DOI=10.1016/0378-1119(94)00692-L;
Blisha B.G., Courvalin P.;
"Analysis of genes encoding D-alanine:D-alanine ligase-related enzymes in Leuconostoc mesenteroides and Lactobacillus spp.";
                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=20351481; PubMed=10891286; DOI=10.1006/jmbi.2000.3802;
Champagne M.B., Edwards K.A., Erickson H.P., Kiehart D.P.;
"Drosophila stretchin-MLCK is a novel member of the Titin/Myosin light
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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22150 MW; CFC118FDC3C423DD CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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InterPro; IPRO11127; Dala_Dala_lig_N.
Pfam; PF07478; Dala_Dala_lig_C; 1.
Pfam; PF01820; Dala_Dala_lig_N; 1.
                                                                                                                                                                                                                                            chain kinase family.";
7 Mol. Biol. 300:759-777(2000).
EMBL, AR257311; AAF90129-1;
HSSP; Q9UQH9; 1DJS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00409; IG; 2.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 152:79-83(1995).
EMBL; U08910; AAA87680.1; -.
HSSP; P71454; IEHI.
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211 AA.
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                   PRELIMINARY;
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                                                                                                                                                                                                                                                                     baculovirus infection.";
Virology 268:56-67(2000)
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                                                                                                                                                  Nucleopolyhedrovirus.
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                     NCBI_TaxID=74660;
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25-OCT-2004
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Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N., Kuwahara S., Hattori M., Hayashi T., Ohnishi Y.;
Genomic analysis of Bacteroides fragilis reveals extensive DNA inversions regulating cell surface adaptation.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
EMBL; AP00684; BA47782.1;
                                                                                                                                                                                                                                 PubMed=15240330; DOI=10.1128/AEM.70.7.4402-4407.2004; Sajjaphan K., Shapir N., Wackett L.P., Palmer M., Blackmon B., Tomkins J., Sadowsky M.J.; "Arthrobacter aurescens TCI Atrazine Catabolism Genes trzN, atzB, and atzC Are Linked on a 160-Kilobase Region and Are Functional in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococineae; Micrococcaceae; Arthrobacter.
NCBI_TaxID=43663;
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Bacteroidaceae; Bacteroides.
NCBI_TaxID=817;
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SEQUENCE 207 AA; 21741 MW; F10397D13AD2F10A CRC64;
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SEGUENCE 211 AA; 24442 MW; C86EC7A0D93BA917 CRC64;
                                 Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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EMBL, AX456696; AAS20024.1; ---
InterPro; IPR001763; Rhodanese-like.
FMART; SM00450; RhOdanese; 1.
SMART; SM00450; RHODANESE 3; 1.
 207 AA
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 PRT;
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PRELIMINARY;
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                                                              05-JUL-2004 (TrEMBLrel.
Hypothetical protein.
Arthrobacter aurescens.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VXXXAEF 7
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      Escherichia coli.
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                               05-JUL-2004
05-JUL-2004
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 Q6SKE7
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Q64XJ4
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RESULT 90

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A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Aajele M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Despons L., Fabre E., Fairhead C., Terry-Dunazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lewur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Oztar-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
I "Genome evolution in yeasts.";
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Yarrowia lipolytica CL1B99.
Eukaryota, Fungi; Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                   MEDICINE-20149221; PubWed=10683327; DOI=10.1006/viro.1999.0138; Li X., Barrett J., Pang A., Klose R.J., Krell P.J., Arif B.M.; "Characterization of an overexpressed spindle protein during a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 81.8%; Score 18; DB 2; Length 211; Best Local Similarity 57.1%; Pred. No. 3.6e+03; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Lauzon H.A.M., Jamieson P.B., Krell P.J., Arif B.M.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, A3127402; AAQ91712.1; -.
InterPro; IRR009661; DUF1251.
Pfam; PF06856; DUF1251, 1.
                                                                                           Choristoneura fumiferana defective nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 AA; 23673 MW; A24E6286DF93CA3A CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
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MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
Parkhill J. Wren B W., Mungall K.L., Ketley J.M., Churcher C.M., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
Witheread S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";
Nature 403:665-668 (2000).
PEMBL, AL139076; CAB73007.1; -.
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MEDLINE_21159325, PubMed=11466286;
DOI=10.1128/JB.183.16.4823-4838.2001;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P., Tatusov R.L., Bennett G.N., Koonin E.V., Snith D.R., Soucaille P., "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridum acetobutylicum.";

J. Bacteriol. 183:4823-48838 (2001).

EMBL, AE007723, AAK80184.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                       GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0016791; F:phosphoric monoester hydrolase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR005834; Debal like_hydro.
InterPro; IPR006383; HAD_SF_IB.
InterPro; IPR006385; HAD_SF_IB_hyp2.
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GO; GO:0016791; F:phosphoric monoester hydrolase activity; IEA. GO; GO:0016791; F:phosphoric monoester hydrolase activity; IEA. GO; GO:0008152; P:metabolism; IEA. InterPro; IPR065383; HAD SF_IB. InterPro; IPR065385; HAD SF_IB hyp2.

TIGRRAMS; TIGR01489; HAD-SF-IB; 1.
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Pred. No. 3.6e+03;
1; Mismatches 3; Indels
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TIGRFAMs; TIGRO1490; HAD-SF-IB-hypl; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 212 AA; 25015 WW; RA892FEBBDF54ED4 CRC64;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%;
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Best Local Similarity 42.5،
درم 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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SEQUENCE 213 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-20351481; PubMed=10891286; DOI=10.1006/jmbi.2000.3802;
Champagne M.B., Edwards K.A., Erickson H.P., Kiehart D.P.;
"Drosophila stretchin-MLCK is a novel member of the Titin/Myosin light
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
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Eukaryota, Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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                                                                                                                                                                                           3; Indels
                                  to the EMBL/GenBank/DDBJ databases.
          Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
EMBL; CR382128; CAG83321.1; -.
SEQUENCE 212 AA; 24023 MW; 95219C003E2B41E2 CRC64;
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Pred. No. 3.6e+03;
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J. Mol. Biol. 300:759-777(2000).
Bmbl; AR257310; AAF90128.1; -.
HSSP; O9UQH9; 1DJS.
FlyBase; FBgn0013988; Strn-Mlck.
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                                                                                                                                         81.8%;
57.1%;
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01-0CT-2000 (TrEMBLrel. 15, I
01-MAR-2004 (TrEMBLrel. 26, I
Hypothetical protein Cj0733.
OrderedLocusNames=Cj0733;
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 57...
4; Conservative
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SEQUENCE FROM N.A.
STRAIN=NCTC 11168;
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RESULT 93

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Bukāryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopiera; Endopterrygota; Diptera; Nematocera; Culicoldea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL, AAAB01008960; EAA11056.1; -.
SEQUENCE 217 AA; 24420 MW; FSAICC770B728ECB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h Similarity 57.1%; Pred. No. 3.7e+03; 4; Conservative 0; Mismatches 3; Indels
                                                                                                                  3; Indels
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                        22587 MW; 423CD8B32A67B7A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
AGCF6282 (ENSANGP00000018110).
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01-MDR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                               Score 18; DB 2; I
Pred. No. 3.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=agCG52667; Synonyms=ENSANGG0000015621;
ORFNames=ENSANGG0000015279;
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MEDLINE=22829867; PubMed=12949112;
                                                                 Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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OrderedLocusNames=PG1823;
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                        216 AA;
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Best Local Similarity
Matches 4; Conserv
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Complete proteome. SEQUENCE 216 AA;
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Q7MTV9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20151481; PubMed=10891286; DOI=10.1006/jmbi.2000.3802; Champagne M.B., Edwards K.A., Erickson H.P., Kiehart D.P.; "Drosophila stretchin-MLCK is a novel member of the Titin/Myosin light chain kinase family.";
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STRAIN=CGA009 / ATCC BAA-98;

STRAIN=CGA009 / ATCC BAA-98;

Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L., Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., Harrison F.H., Gibson J. Harwood C.S., "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";

Nat. Biotechnol. 22:55-61(2004).

EMBL, BX572597; CAR26936.i, ...

InterPro; IPR009013; Viral_att_shaft.
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BEMBL, AR257312; AAF90130.1; --

EMBL, AR254365; AAF90130.1; --

EMBL, AR264061; AAF90130.1; --

EMBL, AR264061; AAF90130.1; --

GO; GO:0004685; R:calcium- and calmodulin-dependent protein k.

GO; GO:0004685; R:wyosin-light-chain kinase activity; IDA.

InterPro; IPR007110; IG-like.
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                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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PROSITE; PS50835; IG_LIKE; 2.
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OrderedLocusNames=RPA1494;
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Matches 4; Conservative
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110 ISASAEF 116
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DOI=10.1128/JB.185.18.5591-5601.2003;
Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J., Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.

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Search completed: June 13, 2005, 13:59:45
Job time : 122 secs
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STRAIN=VPI-5482 / ATCC 29148;
STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550888; Pubmed=12663928; DOI=10.1126/science.1080029;
Xu J., Biursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2704-2076(2003).
EMBL; AEO16644; AAO79438-1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 219 AA; 25376 MW; SBDCE2094E688E55 CRC64;
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MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
Gojobori T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
OrderedLocusNames=BT4333;
Bacteroides thetalotaomicron.
Bacterria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
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Corynabacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Dewhirst F.E., Fraser C.M.;
"Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5601(2003).
EMBL; AE017178; AAQ66820.1; -..
TIGR; PG1823; -..
Complete proteome; Hypothetical protein.
SEQUENCE 217 AA; 23686 MW; DA473C25FF8851DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                    h 81.8%; Score 18; DB 2; Length 217; Similarity 57.1%; Pred. No. 3.7e+03; 4; Conservative 0; Mismatches 3; Indels
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Last sequence update)
Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Beet Local Similarity 57.1...
A; Conservative
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q89ZP3;
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08FUGS
AC 08FUGS,
DT 01-MAR,
DT 01-MAR,
DT 01-MAR,
DT 01-CAR,
DC 0
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1089283
10 089228
AC 089228
DT 01-JU
DT 01-JU
DT 01-JU
DE HYPOT
GN Bacte
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OC Bacte
OC Bacte
CO RATE
RR SEQUE
RR SEGUE
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Gaps
replacements responsible for the thermostability of Corynebacterium
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0
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                                                                                                                                                                               PROSITE; PS50206; RHODANESE 3; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 219 AA; 23127 MW; BE96467A6760F332 CRC64;
                          efficiens.";
Genome Res. 13:1572-1579(2003).
EMBL; AP005214; BAC16865.1; -.
InterPro; IPR001763; Rhodanese-like.
Pfam; PF00581; Rhodanese; 1.
SMART; SM00450; RHOD; 1.
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                                                                                                                                                                                                                                                                                                            Local Similarity
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